

# SEARCH REQUEST FORM

Requestor's Name: \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Date: \_\_\_\_\_ Phone: \_\_\_\_\_ Art Unit: \_\_\_\_\_

## Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

## STAFF USE ONLY

Date completed: <u>8/15</u>	Search Site	Vendors
Searcher: <u>D. Schaefer 308-4292</u>	<input type="checkbox"/> STIC	<input type="checkbox"/> IG
Terminal time: <u>75</u>	<input checked="" type="checkbox"/> CM-1 <u>GA-03</u>	<input type="checkbox"/> STN
Elapsed time: <u>14</u>	<input type="checkbox"/> Pre-S	<input type="checkbox"/> Dialog
CPU time: _____	Type of Search	<input type="checkbox"/> APS
Total time: _____	<input type="checkbox"/> N.A. Sequence	<input type="checkbox"/> Geninfo
Number of Searches: _____	<u>12</u> <input type="checkbox"/> A.A. Sequence	<input type="checkbox"/> SDC
Number of Databases: <u>5</u>	<input type="checkbox"/> Structure	<input type="checkbox"/> DARC/Questel
	<input type="checkbox"/> Bibliographic	<input checked="" type="checkbox"/> Other <u>Compugen + GCG</u>

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Schreiber, David

73393

From: Yu, Misook  
Sent: Wednesday, August 14, 2002 12:56 PM  
To: Schreiber, David  
Subject: 09/499,662

*Search notes*

David,

Is it possible search

1. (X, 18-30 aa)-SEQ ID NO:2-(X, 14 aa)-SEQ ID NO:3-(X, 32 aa)-SEQ ID NO:4-(X, 11 aa) string and
2. (X, 23aa)-SEQ ID NO:5-(X, 15 aa)-SEQ ID NO:6-(X, 32 aa)-SEQ ID NO:7-(X, 10 aa)?

All the SEQ ID NO are small peptides.

Please compare SEQ ID NO:50, 52, 54, 109, 107, 129, 131, 127 against each other. I would like to know what is the differences in the seqs. They are all 218 aa antibody light chain.

Please compare SEQ ID NO:89, 117, 143, 145, 147, 155 against each other.

Please search SEQ ID 129, 131, ~~127~~, 143, 145, 147, 157. They are all amino acid sequences either 218 or 451 aa.

Please search SEQ ID NO:1 (10aa)

Do I have to get approval from someone for these many seq searches?

Examiner Misook Yu, Ph.D.  
703-308-2454 (Phone)  
Art Unit 1642  
CM1-8E18 (Room)  
CM1-8E12 (Mail Box)

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 15:23:12 ; Search time 53.64 Seconds  
(without alignments)  
7.218 Million cell updates/sec

Title: US-09-499-662-1  
Perfect score: 59  
Sequence: 1 RTQNTKCRCK 10

Scoring table:  
BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	324	1	TNR6_RAT
2	59	100.0	332	1	TNR6_PIG
3	59	100.0	335	1	TNR6_HUMAN
4	55	93.2	323	1	TNR6_BOVIN
5	51	86.4	327	1	TNR6_MOUSE
6	40	67.8	468	1	T10A_HUMAN
7	39	66.1	272	1	TNR4_MOUSE
8	39	66.1	277	1	TNR4_HUMAN
9	37	62.7	360	1	WNT2_MOUSE
10	37	62.7	454	1	TR1A_MOUSE
11	36	61.0	58	1	SKC2_MESMA
12	36	61.0	59	1	SKC3_MESMA
13	36	61.0	219	1	NOLA_BRAEL
14	36	61.0	310	1	YAHB_ECOLI
15	36	61.0	326	1	VEGD_RAT
16	36	61.0	351	1	WN2B_XENLA
17	36	61.0	358	1	VEGD_MOUSE
18	35	59.3	36	1	SKC3_LEIOH
19	35	59.3	350	1	TNR2_BRARE
20	35	59.3	360	1	WNT2_HUMAN
21	35	59.3	413	1	YPRB_BACSU
22	35	59.3	440	1	T10B_HUMAN
23	35	59.3	842	1	ORP7_HUMAN
24	35	59.3	843	1	CO7_HUMAN
25	34	57.6	37	1	SKC2_LEIOH
26	34	57.6	37	1	SKCB_LEIOH
27	34	57.6	86	1	TAT_HVIND
28	34	57.6	99	1	TAT_HVIEL
29	34	57.6	148	1	VEGH_ORFN7
30	34	57.6	259	1	T10C_HUMAN
31	34	57.6	453	1	NRAM_IAWIL
32	34	57.6	454	1	NRAM_IAPUR
33	34	57.6	469	1	NRAM_IAPUR

#### RESULT 1

TNR6_RAT	ID	TNR6_RAT	STANDARD;	PRT;	324 AA.
AC	Q63199;				
DT	15-JUL-1999 (Rel. 38, Created)				
DT	15-JUL-1999 (Rel. 38, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen) (CD95).				
DE	DE				
GN	TNFRSF6 OR PT1 OR FAS.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-SPRAGUE-DAWLEY; TISSUE=Liver;				
RA	MEDLINE-94128114; Pubmed-7507668;				
RA	Kimura K., Yamamoto M., Wakatsuki T.;				
RT	"A variant mRNA species encoding a truncated form of Fas antigen in the rat liver."				
RL	Biochem. Biophys. Res. Commun. 198;666-674(1994).				
CC	-1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL T-CELLS, OR BOTH (BY SIMILARITY).				
CC	SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).				
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.				
CC	-1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.				
CC	-1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.				
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DR	EMBL; D26112; BAA05108.1; -				
DR	HSSP; P25445; IDDF.				
DR	InterPro; IPR000488; Death.				
DR	InterPro; IPR001368; TNFR_c6.				
DR	Pfam; PF00531; death; 1.				
DR	Pfam; PF00020; TNFR_c6; 3.				
DR	SMART; SM00005; DEATH; 1.				
DR	SMART; SM00208; TNFR; 3.				
DR	PROSITE; PS00652; TNFR_NGFR_1; 2.				
DR	PROSITE; PS00050; TNFR_NGFR_2; 2.				

P52172 drosophila  
P25509 placobdella  
P25510 placobdella  
P01499 apis mellif  
Q9ni16 mesobuthus  
P55950 callinectes  
O55038 mus musculu  
P12453 human immun  
P23252 hordium vul  
O62802 canis fami  
P22955 red clover  
P38565 xenopus lae

```
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 21
FT CHAIN 22 324
FT TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 6.
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 22 171
FT TRANSMEM 172 188
FT DOMAIN 189 324
FT REPEAT 43 79
FT REPEAT 80 123
FT REPEAT 124 163
FT REPEAT 219 303
FT DEATH.
FT CARBOHYD 43 43
FT CARBOHYD 114 114
FT CARBOHYD 132 132
FT CARBOHYD 324 324; 36835 MW; D25D583C909D9D09 CRC64;
SQ SEQUENCE 324 AA; 36835 MW; D25D583C909D9D09 CRC64;

Query Match 100.0%; Score 59; DB 1; Length 324;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
DB 117 RTQNTKCRCK 126

RESULT 2
TNR6_PIG STANDARD; PRT; 332 AA.
AC 077736;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen
DE (CD95)).
GN TNFRSF6 OR APT1 OR FAS.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
RT "Expression of apoptosis-associated genes in hibernating and stunned
RT myocardium of pig.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CC CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC -----
DR EMBL; AJ001202; CAA04596.1; -.
DR HSPF; P25445; 1DDF.
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DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00652; TNFR_NGFR_2; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 16
FT CHAIN 17 332
FT TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 6.
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 17 175
FT TRANSMEM 176 192
FT DOMAIN 193 332
FT CYTOPLASMIC (POTENTIAL).
FT REPEAT 45 81
FT REPEAT 82 125
FT REPEAT 126 164
FT REPEAT 227 311
FT DEATH.
FT CARBOHYD 38 38
FT CARBOHYD 116 116
FT CARBOHYD 332 332; 37592 MW; 5B8B03682756BF1B CRC64;
SQ SEQUENCE 332 AA; 37592 MW; 5B8B03682756BF1B CRC64;

Query Match 100.0%; Score 59; DB 1; Length 332;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
DB 119 RTQNTKCRCK 128

RESULT 3
TNR6_HUMAN STANDARD; PRT; 335 AA.
AC P25445;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen
DE (CD95)).
GN TNFRSF6 OR APT1 OR FAS OR FASL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Itoh N., Yonehara S., Ishii A., Yonehara M., Mizushima S.I.,
RA Sameshima M., Hase A., Seto Y., Nagata S.;
RT "The polypeptide encoded by the cDNA for human cell surface antigen
RT Fas can mediate apoptosis.";
RN Cell 66:233-243(1991).
RL [2]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 226-240; 269-291 AND 321-335.
RX MEDLINE=92268122; PubMed=1375228;
RA Oehm A., Behrmann I., Falk W., Pawlita M., Maier G., Klas C.,
RA Li-Weber M., Richards S., Dhein J., Trauth B.C., Ponstingl H.,
RA Krammer P.H.;
RT "Purification and molecular cloning of the APO-1 cell surface
RT antigen, a member of the tumor necrosis factor/nerve growth factor
RT receptor superfamily. Sequence identity with the Fas antigen.";
RN J. Biol. Chem. 267:10709-10715(1992).
RL [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Urinary bladder;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
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RP STRUCTURE BY NMR OF 218-335.
RX MEDLINE-97122332; PubMed-8967952;
RA Huang B., Eberstadt M., Olejniczak E.T., Meadows R.P., Fesik S.W.;
RT "NMR structure and mutagenesis of the Fas (APO-1/CD95) death domain.";
RL Nature 384:638-641(1996).
CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CC CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC SUICIDE OF MATURE T-CELLS, OR BOTH.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD95 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd95.htm".
CC -----
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CC -----
DR EMBL; M67454; AAA63174.1; -.
DR EMBL; X63717; CAA45250.1; -.
DR EMBL; BC012479; AAH12479.1; -.
DR PIR; A40036; A40036.
DR PIR; S24543; S24543.
DR PDB; 1DDF; 12-NOV-97.
DR MIM; 134637; -.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal;
KW 3D-structure.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 335 TUMOR NECROSIS FACTOR RECEPTOR
FT DOMAIN 17 173 SUPERFAMILY MEMBER 6.
FT TRANSMEM 174 190 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 191 335 POTENTIAL.
FT REPEAT 47 83 CYTOPLASMIC (POTENTIAL).
FT REPEAT 84 127 TNFR-CYS 1.
FT REPEAT 128 166 TNFR-CYS 2.
FT REPEAT 230 314 TNFR-CYS 3.
FT DOMAIN 238 314 DEATH.
FT CARBOHYD 118 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 335 AA; 37732 MW; 0139942535111410 CRC64;
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Query Match 100.0%; Score 59; DB 1; Length 335;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 RTQNTKCRCK 10
|
Db 121 RTQNTKCRCK 130
```

RESULT 4

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TNR6_BOVIN
ID TNR6_BOVIN STANDARD; PRT; 323 AA.
AC P51867;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE receptor) (Apoptosis-mediating surface antigen Fas) (Apo-1 antigen)
DE (CD95).
GN TNFRSF6 OR APT1 OR FAS.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-96226401; PubMed-8634151;
RA Yoo J., Stone R.F., Beattie C.W.;
RT "Cloning and characterization of the bovine Fas.";
RL DNA Cell Biol. 15:227-234(1996).
CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CC CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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CC -----
DR EMBL; U34794; AAC48546.1; -.
DR HSSP; P25445; 1DDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 323 TUMOR NECROSIS FACTOR RECEPTOR
FT DOMAIN 17 170 SUPERFAMILY MEMBER 6.
FT TRANSMEM 171 188 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 189 323 POTENTIAL.
FT REPEAT 45 80 CYTOPLASMIC (POTENTIAL).
FT REPEAT 81 124 TNFR-CYS 1.
FT REPEAT 125 163 TNFR-CYS 2.
FT REPEAT 238 306 TNFR-CYS 3.
FT DOMAIN 238 306 DEATH.
SQ SEQUENCE 323 AA; 36445 MW; 4D88A90E9E1F4892 CRC64;
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Query Match 93.2%; Score 55; DB 1; Length 323;
Best Local Similarity 90.0%; Pred. No. 0.0065;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RTQNTKCRCK 10  
 DB 118 RTQNTKCRCK 127

RESULT 5  
 TNR6\_MOUSE STANDARD; PRT; 327 AA.  
 AC P25446;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen) (CD95).  
 DE TNRFSF6 OR APT1 OR FAS.  
 GN Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92148151; PubMed=1371136;  
 RA Watanabe-Fukunaga R., Brannan C.I., Itoh N., Yonehara S., Copeland N.G., Jenkins N.A., Nagata S.;  
 RT "The cDNA structure, expression, and chromosomal assignment of the mouse Fas antigen.";  
 RL J. Immunol. 148:1274-1279(1992).  
 RN [2]  
 RP SEQUENCE OF 1-96 FROM N.A.  
 RX MEDLINE=93189576; PubMed=7680478;  
 RA Adachi M., Watanabe-Fukunaga R., Nagata S.;  
 RT "Aberrant transcription caused by the insertion of an early transposable element in an intron of the Fas antigen gene of lpr mice.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:1756-1760(1993).  
 RN [3]  
 RP VARIANT LPR.  
 RX MEDLINE=92195401; PubMed=1372994;  
 RA Watanabe-Fukunaga R., Brannan C.I., Copeland N.G., Jenkins N.A., Nagata S.;  
 RT "Lymphoproliferation disorder in mice explained by defects in Fas antigen that mediates apoptosis.";  
 RL Nature 356:314-317(1992).  
 CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- TISSUE SPECIFICITY: DETECTED IN VARIOUS TISSUES INCLUDING THYMUS, LIVER, LUNG, HEART, AND ADULT OVARY.  
 CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.  
 CC -!- DISEASE: DEFECTS IN TNRFSF6 ARE THE CAUSE OF A LYMPHOPROLIFERATION DISORDER (LPR) RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION.  
 CC -!- SIMILARITY: CONTAINS 3 TNRFSF6 REPEATS.  
 CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
 CC -----  
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 CC -----  
 DB EMBL; M83649; AAA37593.1; -

DR EMBL; S56490; AAB25700.1; -  
 DR EMBL; S56485; AAB25700.1; JOINED.  
 DR EMBL; S56486; AAB25700.1; JOINED.  
 DR PIR; A46484; A46484.  
 DR HSP; P25445; IDDF.  
 DR MGD; MGI:95484; Tnfrsf6.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR001368; TNRFSF6.  
 DR Pfam; PF00531; death; 1.  
 DR Pfam; PF00020; TNRFSF6; 3.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00208; TNRFSF6; 3.  
 DR PROSITE; PS00652; TNRFSF6\_1; 2.  
 DR PROSITE; PS00050; TNRFSF6\_2; 2.  
 DR PROSITE; PS0017; DEATH\_DOMAIN; 1.  
 KW Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal;  
 KW Disease mutation.  
 FT SIGNAL 1 21 TUMOR NECROSIS FACTOR RECEPTOR  
 FT CHAIN 22 327 SUPERFAMILY MEMBER 6.  
 FT DOMAIN 22 169 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 170 186 POTENTIAL.  
 FT DOMAIN 187 327 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 43 79 TNRFSF6 1.  
 FT REPEAT 80 123 TNRFSF6 2.  
 FT REPEAT 124 162 TNRFSF6 3.  
 FT DOMAIN 222 306 DEATH.  
 FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARIANT 246 246 I -> N (IN LPR).  
 FT SEQUENCE 327 AA; 37418 MW; F6BFFC5ACE356EEE CRC64;  
 SQ

Query Match 86.4%; Score 51; DB 1; Length 327;  
 Best Local Similarity 88.9%; Pred. No. 0.033;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TQNTKCRCK 10  
 DB 118 TQNTKCRCK 126

RESULT 6  
 T10A\_HUMAN STANDARD; PRT; 468 AA.  
 ID T10A\_HUMAN  
 AC 000220;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 10A precursor (Death receptor 4) (TNF-related apoptosis-inducing ligand receptor 1) (TRAIL receptor-1) (TRAIL-RL).  
 DE TNRFSF10A OR DR4 OR TRAILR1 OR APO2.  
 GN Homo sapiens (Human)  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97238921; PubMed=9082980;  
 RA Pan G., O'Rourke K., Chinnaiyan A.M., Gentz R., Ebner R., Ni J., Dixit V.M.;  
 RT "The receptor for the cytotoxic ligand TRAIL.";  
 RL Science 276:111-113(1997).  
 RN [2]  
 RP FUNCTION.  
 RX MEDLINE=98090092; PubMed=9430227;  
 RA Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;  
 RT "Death receptor 5, a new member of the TNFR family, and DR4 induce FADD-dependent apoptosis and activate the NF-kappaB pathway.";  
 RL Immunity 7:821-830(1997).  
 CC -!- FUNCTION: Receptor for the cytotoxic ligand TRAIL; mediates apoptosis in a caspase-dependent manner. Can trigger the nuclear

CC factor kappaB-pathway and can bind the cytoplasmic adapter  
CC molecule FADD/MOR1 which engages initiator caspases such as  
CC caspase 8 leading to subsequent activation of effector caspases  
CC that execute apoptotic death of the cell.  
CC -1- SUBUNIT: Can interact with TRADD and RIP.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- TISSUE SPECIFICITY: Widely expressed. High levels are found in  
CC spleen, peripheral blood leukocytes, small intestine and thymus,  
CC but also in K562 erythroleukemia cells, MCF7 breast carcinoma  
CC cells and activated T-cells.  
CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.  
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
CC  
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CC  
CC EMBL; U90875; AAC51226.1; -.  
CC MIM; 603611; -.  
CC HSP; P19438; LEXI.  
CC InterPro; IPR000488; Death.  
CC InterPro; IPR001368; TNFR\_c6.  
CC Pfam; PF00531; death; 1.  
CC Pfam; PF00020; TNFR\_c6; 2.  
CC SMART; SM00005; DEATH; 1.  
CC SMART; SM00208; TNFR; 2. DOMAIN; 1.  
CC PROSITE; PS00017; DEATH\_DOMAIN; 1.  
CC PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
CC PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
CC Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.  
KW SIGNAL 1 23 POTENTIAL.  
FT CHAIN 24 468  
FT TUMOR NECROSIS FACTOR RECEPTOR  
FT SUPERFAMILY MEMBER 10A.  
FT  
FT DOMAIN 24 239  
FT TRANSMEM 240 262  
FT DOMAIN 263 468  
FT REPEAT 147 188  
FT REPEAT 189 229  
FT REPEAT 229 468  
FT DEATH.  
FT DOMAIN 365 448  
FT POLY-ALA.  
FT DISULFID 132 145  
FT DISULFID 148 164  
FT DISULFID 167 180  
FT DISULFID 170 188  
FT DISULFID 190 204  
FT DISULFID 207 221  
FT DISULFID 211 229  
FT CARBOHYD 156 156  
FT N-LINKED (GLCNAC... ) (POTENTIAL).  
SQ SEQUENCE 468 AA; 50025 MW; 1E85DCDC2C8760F7 CRC64;

Query Match 67.8%; Score 40; DB 1; Length 468;

Best Local Similarity 66.7%; Pred. No. 3.9;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 TONTKCRCK 10  
1:|:|:|:|:|  
Db 183 TRNTACOCK 191

RESULT 7  
ID TNR4\_MOUSE STANDARD; PRT; 272 AA.  
AC P47741;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 4 precursor (OX40L  
DE receptor) (OX40 antigen).

GN TNFRSF4 OR TXGP1 OR OX40.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RC SEQUENCE FROM N.A.  
RP STRAIN=BALB/C;  
RX MEDLINE=94044750; PubMed=8228223;  
RA Calderhead D.M., Buhlmann J.E., van den Eertwegh A.J.,  
RA Claassen E., Noelle R.J., Fell H.;  
RT "Cloning of mouse OX40: a T cell activation marker that may mediate  
RT T-B cell interactions.";  
RL J. Immunol. 151:5261-5271(1993).  
RN [2]  
RC SEQUENCE FROM N.A.  
RP MEDLINE=95255413; PubMed=7737295;  
RX Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,  
RA Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,  
RA "Gene structure and chromosomal localization of the mouse homologue  
RT of rat OX40 protein.";  
RL Eur. J. Immunol. 25:926-930(1995).  
CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
CC  
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CC  
CC EMBL; Z21674; CAA79772.1; -.  
CC EMBL; X85214; CAA59476.1; -.  
CC HSP; P19438; LEXI.  
CC MGI; MGI:104512; Tnfrsf4.  
CC InterPro; IPR001368; TNFR\_c6.  
CC Pfam; PF00020; TNFR\_c6; 3.  
CC ProDom; PD000771; TNFR\_c6; 1.  
CC SMART; SM00208; TNFR; 3.  
CC PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
CC PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
CC Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;  
KW SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 272  
FT TUMOR NECROSIS FACTOR RECEPTOR  
FT SUPERFAMILY MEMBER 4.  
FT  
FT DOMAIN 20 211  
FT TRANSMEM 212 236  
FT DOMAIN 237 272  
FT CYTOPLASMIC (POTENTIAL).  
FT REPEAT 26 61  
FT REPEAT 61 103  
FT REPEAT 104 124  
FT REPEAT 125 165  
FT REPEAT 144 144  
FT CARBOHYD 15 15  
FT CONFLICT 15 15  
FT N-LINKED (GLCNAC... ) (POTENTIAL).  
FT A -> G (IN REF. 2).  
SQ SEQUENCE 272 AA; 30153 MW; 06E7BB4156F0D08E CRC64;

Query Match 66.1%; Score 39; DB 1; Length 272;

Best Local Similarity 66.7%; Pred. No. 3.6;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 TONTKCRCK 10  
1:|:|:|:|:|  
Db 98 TQDTVCRCR 106

RESULT 8  
ID TNR4\_HUMAN STANDARD; PRT; 277 AA.  
TNR4\_HUMAN

P43489; Q13663;  
 01-NOV-1995 (Rel. 32, Created)  
 01-NOV-1995 (Rel. 32, Last sequence update)  
 16-OCT-2001 (Rel. 40, Last annotation update)  
 Tumor necrosis factor receptor superfamily member 4 precursor (OX40L receptor) (ACT35 antigen) (TAX-transcriptionally activated glycoprotein 1 receptor) (CD134 antigen).  
 GN TNFRSF4 OR TKGPI1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94170844; PubMed=7510240;  
 RA Latza U., Duerkop H., Schnittger S., Ringeling J., Eitelbach F., Hummel M., Fonatsch C., Stein H.;  
 RT "The human OX40 homolog: cDNA structure, expression and chromosomal assignment of the ACT35 antigen.";  
 RL Eur. J. Immunol. 24:677-683(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95219871; PubMed=7704935;  
 RA Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A., Watson M.L., Seldin M.F., Clifford K.N., Grabstein K., Alderson M.R.;  
 RT "Identification of OX40 ligand and preliminary characterization of its activities on OX40 receptor.";  
 RL Circ. Shock 44:30-34(1994).  
 CC -!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD134 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd134.htm".  
 CC -----  
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 CC -----  
 DR EMBL; X75962; CAA53576.1; -;  
 DR EMBL; S76792; AAB33944.1; ALT\_INIT.  
 DR HSP; P25942; 1CDF.  
 DR MIM: 600315; -;  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00020; TNFR\_c6; 3.  
 DR ProDom: PD000771; TNFR\_c6; 1.  
 DR SMART; SM00208; TNFR; 3.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS00650; TNFR\_NGFR\_2; 2.  
 KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat; Signal.  
 FT SIGNAL  
 FT CHAIN 1 28 POTENTIAL.  
 FT CHAIN 29 277 TUMOR NECROSIS FACTOR RECEPTOR  
 FT DOMAIN 29 214 SUPRAFAMILY MEMBER 4.  
 FT TRANSMEM 215 235 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 236 277 POTENTIAL.  
 FT REPEAT 30 65 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 66 107 TNFR-CYS 1.  
 FT REPEAT 108 126 TNFR-CYS 2.  
 FT REPEAT 127 167 TNFR-CYS 3 (INCOMPLETE).  
 FT REPEAT 146 166 TNFR-CYS 4.  
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 277 AA; 29340 MW; 49F15525941550BF CRC64;  
 Query Match 66.1%; Score 39; DB 1; Length 277;  
 Best Local Similarity 66.7%; Pred. No. 3.7;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TONTKCRCK 10  
 II: I I I I I  
 DB 102 TQDTVCRCR 110  
 RESULT 9  
 ID WNT2\_MOUSE STANDARD; PRT; 360 AA.  
 AC P21552;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Wnt-2 protein precursor (IRP protein) (INT-1 related protein).  
 GN WNT2 OR WNT-2 OR IRP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90126394; PubMed=2693041;  
 RA McMahon J.A., McMahon A.P.;  
 RT "Nucleotide sequence, chromosomal localization and developmental expression of the mouse int-1-related gene.";  
 RL Development 107:643-650(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91122634; PubMed=2279700;  
 RA Gavin B.J., McMahon J.A., McMahon A.P.;  
 RT "Expression of multiple novel Wnt-1/int-1-related genes during fetal and adult mouse development.";  
 RL Genes Dev. 4:2319-2332(1990).  
 CC -!- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN TRANSMEMBRANE RECEPTORS. PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING MOLECULE WHICH AFFECTS THE DEVELOPMENT OF DISCRETE REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS.  
 CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the extracellular matrix.  
 CC -!- TISSUE SPECIFICITY: IN EMBRYOS IN THE DEVELOPING ALLANTOIS, IN PERICARDIUM HEART, AND VENTRAL-LATERAL MESODERM; IN ADULTS, IN LUNG, BRAIN, HEART AND PLACENTA.  
 CC -!- SIMILARITY: BELONGS TO THE WNT FAMILY.  
 DR PIR; B36470; B36470.  
 DR PIR; A43558; A43558.  
 DR MGI; 98954; Wnt2.  
 DR InterPro: IPR000970; Wnt1.  
 DR Pfam; PF00110; wnt; 1.  
 DR PRINTS; PR01349; WNTPROTEIN.  
 DR SMART; SM00097; WNT1; 1.  
 DR PROSITE; PS00246; WNT1; 1.  
 KW Developmental protein; Glycoprotein; Signal.  
 FT SIGNAL 1 25 POTENTIAL.  
 FT CHAIN 26 360 WNT-2 PROTEIN.  
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 360 AA; 40496 MW; 5EC265FD3815EF1D CRC64;  
 Query Match 62.7%; Score 37; DB 1; Length 360;  
 Best Local Similarity 66.7%; Pred. No. 10;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TONTKCRCK 10  
 I: I I I I I  
 DB 319 TRMTKCECK 327  
 RESULT 10  
 ID TRIA\_MOUSE STANDARD; PRT; 454 AA.  
 AC P25118;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)



DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Tumor necrosis factor receptor 1 precursor (p60) (TNF-RI) (TNF-RI)  
DE (p55).  
GN TNFRSF1A OR TNFR1 OR TNFR-1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=91187885; PubMed=1849278;  
RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,  
RA Wong G.H., Chen E.L., Goeddel D.V.;  
RT "Cloning and expression of cDNAs for two distinct murine tumor  
RT necrosis factor receptors demonstrate one receptor is species  
RT specific.";  
RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).  
RN [2]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=91246168; PubMed=1645445;  
RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,  
RA Copeland N.G., Jenkins N.A., Smith C.A.;  
RT "Molecular cloning and expression of the type 1 and type 2 murine  
RT receptors for tumor necrosis factor.";  
RL Mol. Cell. Biol. 11:3020-3026(1991).  
RN [3]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=91285014; PubMed=1647956;  
RA Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissonerghis A.M.,  
RA Gray P.W., Feldmann M., Foxwell B.M.J.;  
RT "Cloning, expression and cross-linking analysis of the murine p55  
RT tumor necrosis factor receptor.";  
RL Eur. J. Immunol. 21:1649-1656(1991).  
RN [4]  
RN SEQUENCE FROM N.A.  
RX TISSUE=Splice;  
RX MEDLINE=82039815; PubMed=1657766;  
RA Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;  
RT "Molecular cloning and expression of the mouse Tnf receptor type b.";  
RL Immunogenetics 34:338-340(1991).  
RN [5]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=94245292; PubMed=8188324;  
RA Bebo B.F., Linthicum D.S.;  
RT "Nucleotide sequence of the TNF type I receptor from a mouse  
RT endothelioma cell line.";  
RL Immunogenetics 39:450-451(1994).  
RN [6]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=93156721; PubMed=8381516;  
RA Rothe J., Bluethmann H., Gentz R., Lesslauer W., Steinmetz M.;  
RT "Genomic organization and promoter function of the murine tumor  
RT necrosis factor receptor beta gene.";  
RL Mol. Immunol. 30:165-175(1993).  
CC -I- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD  
CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING  
CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)  
CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE  
CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE  
CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).  
CC -I- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
CC HOMOMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
CC NF-KAPPA B SIGNALING (BY SIMILARITY).  
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -I- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
CC -I- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
-----  
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CC -----  
DR EMBL; M60468; AAA39751.1; -  
DR EMBL; M59377; AAA40464.1; -  
DR EMBL; X59238; CAA41922.1; -  
DR EMBL; X57796; CAA40936.1; -  
DR EMBL; L26349; AAA59361.1; -  
DR EMBL; M76656; AAA40465.1; -  
DR EMBL; M88067; AAA40465.1; JOINED.  
DR EMBL; M76655; AAA40465.1; JOINED.  
DR PIR; A38634; GOMST1.  
DR PIR; S16677; S16677.  
DR PIR; S19021; S19021.  
DR HSP; P19438; IEXT.  
DR MGD; MGI:1314884; Tnfrsfla.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00531; death; 1.  
DR Pfam; PF00020; TNFR\_c6; 4.  
DR ProDom; PD000771; TNFR\_c6; 1.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00208; TNFR; 3.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
DR PROSITE; PS00050; TNFR\_NGFR\_2; 3.  
DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 454 TUMOR NECROSIS FACTOR RECEPTOR 1.  
FT DOMAIN 22 212 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 213 235 POTENTIAL.  
FT DOMAIN 236 454 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 43 82 TNFR-CYS 1.  
FT REPEAT 83 125 TNFR-CYS 2.  
FT REPEAT 126 166 TNFR-CYS 3.  
FT REPEAT 167 196 TNFR-CYS 4.  
FT DOMAIN 339 349 N-SMASE ACTIVATION DOMAIN (NSD).  
FT DOMAIN 356 441 DEATH.  
FT DISULFID 44 58 BY SIMILARITY.  
FT DISULFID 59 72 BY SIMILARITY.  
FT DISULFID 62 81 BY SIMILARITY.  
FT DISULFID 84 99 BY SIMILARITY.  
FT DISULFID 102 117 BY SIMILARITY.  
FT DISULFID 105 125 BY SIMILARITY.  
FT DISULFID 127 143 BY SIMILARITY.  
FT DISULFID 146 158 BY SIMILARITY.  
FT DISULFID 149 166 BY SIMILARITY.  
FT DISULFID 168 179 BY SIMILARITY.  
FT DISULFID 182 191 BY SIMILARITY.  
FT DISULFID 185 195 BY SIMILARITY.  
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 394 394 R -> G (IN REF. 6).  
SQ SEQUENCE 454 AA; 50129 MW; 0710C2E8C3C2B6D9 CRC64;  
  
Query Match 62.7%; Score 37; DB 1; Length 454;  
Best Local Similarity 75.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2 TQNTKCR 9  
Db 161 TQNTVCNC 168  
-----  
RESULT 11  
SCK2\_MESMA  
ID SCK2\_MESMA STANDARD; PRT; 58 AA.

```

AC Q9NTI5; P58489;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Toxin BMTX2 precursor (Neurotoxin TX2).
OS Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthoidea; Buthidae; Buthus.
OX NCBI_TaxID=34649;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20164067; PubMed=10698710;
RA Dai L., Wu J.-J., Gu Y.H., Lan Z.D., Ling M.-H., Chi C.-W.;
RT "Genomic organization of three novel toxins from the scorpion Buthus
RT martensii Karsch that are active on potassium channels.";
RL Biochem. J. 346:805-809(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20436245; PubMed=10978761;
RA Zeng X.-C., Zhu Z.H., Li W.-X., Zhu S.-Y., Peng F., Mao X., Liu H.;
RT "Molecular cloning and genomic organization of a K(+) channel toxin
RT from the Chinese scorpion Buthus martensii Karsch.";
RL Toxicon 39:407-410(2001).
RN [3]
RP SEQUENCE OF 22-58, SYNTHESIS, AND CHARACTERIZATION.
RX PubMed=9354615;
RA Romi-Lebrun R., Lebrun B., Martin-Eauclaire M.-F., Ishiguro M.,
RA Escoubas P., Wu F.Q., Hisada M., Pongs O., Nakajima T.;
RT "Purification, characterization, and synthesis of three novel toxins
RT from the Chinese scorpion Buthus martensii, which act on K+ channels.";
RL Biochemistry 36:13473-13482(1997).
RN [4]
RP STRUCTURE BY NMR OF 22-58.
RC TISSUE=Venom;
RX MEDLINE=98400946; PubMed=9730813;
RA Blanc E., Romi-Lebrun R., Bornet O., Nakajima T., Darbon H.;
RT "Solution structure of two new toxins from the venom of the Chinese
RT scorpion Buthus martensii Karsch blockers of potassium channels.";
RL Biochemistry 37:12412-12418(1998).
CC -!- FUNCTION: Potent blocker of both large-conductance calcium-
CC activated potassium channels (BKCa channels) and voltage-gated
CC potassium channels (Kv1.3).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE SHORT SCORPION TOXIN FAMILY. POTASSIUM
CC CHANNEL INHIBITORS SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF249746; AAF87224.1; -.
DR HSP; P24662; 2KTX.
DR InterPro; IPR001947; Charybdotoxin.
DR InterPro; IPR003614; Knt1.
DR Pfam; PF00451; toxin_2; 1.
DR ProDom; PD003586; Charybdotoxin; 1.
DR SMART; SM00505; Knt1; 1.
DR PROSITE; PS01138; SCORP_SHORT_TOXIN; 1.
KW Neurotoxin; Potassium channel inhibitor; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 59 TOXIN BMTX3.
FT DISULFID 30 51 BY SIMILARITY.
FT DISULFID 36 56 BY SIMILARITY.
FT DISULFID 40 58 BY SIMILARITY.
SQ SEQUENCE 59 AA; 6429 MW; A1A1A2C415D456A7 CRC64;

Query Match 61.0%; Score 36; DB 1; Length 59;
Best Local Similarity 55.6%; Pred. No. 3.2;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTQNTKRC 9
Db 50 KCQNNQCR 58

RESULT 13
ID NOLA_BRAEL STANDARD; PRT; 219 AA.
AC P50329;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Nodulation protein nola (Fragment).

Query Match 61.0%; Score 36; DB 1; Length 58;
Best Local Similarity 55.6%; Pred. No. 3.2;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTQNTKRC 9
Db 50 KCQNNQCR 58

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTQNTKRC 9
Db 48 KCMNSKRC 56

RESULT 12
SCK3_MESMA STANDARD; PRT; 59 AA.
AC Q9NBG9;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Toxin BMTX3 precursor (Neurotoxin TX3).
OS Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthoidea; Buthidae; Buthus.
OX NCBI_TaxID=34649;
RN [1]
RP SEQUENCE FROM N.A.
RA Ye J., Li Y., Yan Y., Ji Y.;
RT "Isolation, characterization and cDNA cloning of a novel toxin from
RT the Chinese scorpion Buthus martensii Karsch, which acts on potassium
RT channel.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Blocks potassium channels.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE SHORT SCORPION TOXIN FAMILY. POTASSIUM
CC CHANNEL INHIBITORS SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF249746; AAF87224.1; -.
DR HSP; P24662; 2KTX.
DR InterPro; IPR001947; Charybdotoxin.
DR InterPro; IPR003614; Knt1.
DR Pfam; PF00451; toxin_2; 1.
DR ProDom; PD003586; Charybdotoxin; 1.
DR SMART; SM00505; Knt1; 1.
DR PROSITE; PS01138; SCORP_SHORT_TOXIN; 1.
KW Neurotoxin; Potassium channel inhibitor; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 59 TOXIN BMTX3.
FT DISULFID 30 51 BY SIMILARITY.
FT DISULFID 36 56 BY SIMILARITY.
FT DISULFID 40 58 BY SIMILARITY.
SQ SEQUENCE 59 AA; 6429 MW; A1A1A2C415D456A7 CRC64;

Query Match 61.0%; Score 36; DB 1; Length 59;
Best Local Similarity 55.6%; Pred. No. 3.2;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RTQNTKRC 9
Db 50 KCQNNQCR 58

RESULT 13
ID NOLA_BRAEL STANDARD; PRT; 219 AA.
AC P50329;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Nodulation protein nola (Fragment).

```

GN NOLA.  
OS Bradyrhizobium elkanii.  
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
OC Bradyrhizobium group; Bradyrhizobium.  
OX NCBI\_TaxID=29448;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=USDA 94;  
RX MEDLINE=95036537; PubMed=7949325;  
RA Doberf R.C., Brell B.T., Triplett E.W.;  
RT "DNA sequence of the common nodulation genes of Bradyrhizobium  
RT elkanii and their phylogenetic relationship to those of other  
RT nodulating bacteria";  
RL Mol. Plant Microbe Interact. 7:564-572(1994).  
CC -1- FUNCTION: INVOLVED IN GENOTYPE-SPECIFIC NODULATION OF SOYBEANS.  
CC -1- SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL  
CC REGULATORS.  
CC -----  
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CC -----  
DR EMBL; U04609; AAA63596.1; -;  
DR InterPro; IPR000551; HTH\_Merr.  
DR Pfam; PF00376; merr; 1.  
DR SMART; SM00422; HTH\_MERR; 1.  
DR PROSITE; PS00552; HTH\_MERR\_FAMILY; 1.  
KW Nodulation; Nitrogen fixation; DNA-binding.  
FT DNA\_BIND 13 32 H-T-H MOTIF (POTENTIAL).  
FT NON\_TER 219 219  
SQ SEQUENCE 219 AA; 24922 MW; 64EA962B8463F029 CRC64;  
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Query Match 61.08; Score 36; DB 1; Length 219;  
Best Local Similarity 50.08; Pred. No. 10;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 RTQNTKCRCK 10  
I : I : I : I : I :  
Db 137 RSQTSRCTCK 146  
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RESULT 14  
YAHB\_ECOLI  
ID YAHB\_ECOLI STANDARD; PRT; 310 AA.  
AC P77700;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical transcriptional regulator yahb.  
GN YAHB OR B0316.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12";  
RL Science 277:1453-1474(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Durcan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis K.,  
RA Federspiel N., Hyman R., Kallman S., Komp C., Kurdi O., Lew H., Lin D.,

RA Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;  
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL  
CC REGULATORS.  
CC -----  
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CC -----  
DR EMBL; AE000138; AAC73419.1; -;  
DR EMBL; U73857; AAB18042.1; -;  
DR EcoGene; EG13586; yahb.  
DR InterPro; IPR002197; HTH\_Fis.  
DR InterPro; IPR000847; HTH\_LysR.  
DR Pfam; PF00126; HTH\_1; 1.  
DR PROSITE; PS00044; HTH\_LYSR\_FAMILY; 1.  
KW Hypothetical protein; Transcription regulation; DNA-binding;  
KW Complete proteome.  
FT DNA\_BIND 22 42 H-T-H MOTIF (POTENTIAL).  
FT SEQUENCE 310 AA; 34866 MW; A3EB895E7F69D60C CRC64;  
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Query Match 61.08; Score 36; DB 1; Length 310;  
Best Local Similarity 71.48; Pred. No. 14;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 4 NTKCRCK 10  
I : I : I : I : I :  
Db 229 NTKCQCQ 235  
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RESULT 15  
VEGD\_RAT  
ID VEGD\_RAT STANDARD; PRT; 326 AA.  
AC O35251;  
DT 01-MAR-2002 (Rel. 41, Created)  
DT 01-MAR-2002 (Rel. 41, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced  
DE growth factor) (fIGF).  
GN FIGF OR VEGFD.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley;  
RA Yamada Y., Hirata Y., Nezu J., Shimane M.;  
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis  
CC and endothelial cell growth, stimulating their proliferation and  
CC migration and also has effects on the permeability of blood  
CC vessels. May function in the formation of the venous and lymphatic  
CC vascular systems during embryogenesis, and also in the maintenance  
CC of differentiated lymphatic endothelium in adults. Binds and  
CC activates VEGFR-3 (Flt4) receptor (By similarity).  
CC -1- SUBUNIT: Homodimer; non-covalent and antiparallel (By similarity).  
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).  
CC -1- PTM: Undergoes a complex proteolytic maturation which generates a  
CC variety of processed secreted forms with increased activity toward  
CC VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer  
CC linked by disulfide bonds before secretion. The fully processed  
CC VEGF-D is composed mostly of two VEGF homology domains (VHDs)  
CC bound by non-covalent interactions (By similarity).  
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.  
CC -----  
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CC -----

DR EMBL; AF014827; AAB66557.1; -  
DR HSSP; PI5692; LVPP.  
DR InterPro; IPR000072; PDGF.  
DR Pfam; PF0341; PDGF; 1.  
DR ProDom; PD001629; PDGF; 1.  
DR SMART; SM00141; PDGF; 1.  
DR PROSITE; PS00249; PDGF\_1; 1.  
DR PROSITE; PS0278; PDGF\_2; 1.  
KW Mitogen; Growth factor; Glycoprotein; Signal; Repeat;  
KW Cleavage on pair of basic residues; Multigene family.  
FT SIGNAL 1 21  
FT PROPEP 22 93  
FT CHAIN 94 210  
FT PROPEP 211 326  
FT DOMAIN 227 317  
FT REPEAT 227 242  
FT REPEAT 263 278  
FT REPEAT 282 298  
FT REPEAT 306 317  
FT DISULFID 116 158  
FT DISULFID 147 194  
FT DISULFID 151 196  
FT DISULFID 141 141  
FT DISULFID 150 150  
FT CARBOHYD 160 160  
FT CARBOHYD 190 190  
FT CARBOHYD 292 292  
SQ SEQUENCE 326 AA; 37112 MW; 1261AFA373596C00 CRC64;  
POTENTIAL.  
POTENTIAL.  
VASCULAR ENDOTHELIAL GROWTH FACTOR D.  
POTENTIAL.  
4 X 16 AA REPEATS OF C-X(10)-C-X-C-  
X(1-3)-C  
1 (APPROXIMATE).  
2.  
3.  
4 (INCOMPLETE).  
INTRACHAIN (BY SIMILARITY).  
INTRACHAIN (BY SIMILARITY).  
INTRACHAIN (BY SIMILARITY).  
INTRACHAIN (BY SIMILARITY).  
INTERCHAIN (BY SIMILARITY).  
INTERCHAIN (BY SIMILARITY).  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
N-LINKED (GLCNAC. . .) (POTENTIAL).  
N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 61.0%; Score 36; DB 1; Length 326;  
Best Local Similarity 83.3%; Pred. No. 14;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NTKCRC 9

Db 235 NTKCRC 240

Search completed: August 14, 2002, 15:23:12  
Job time: 685 sec

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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:17:02 ; Search time 82.88 Seconds  
(without alignments)  
2.947 Million cell updates/sec

Title: US-09-499-662-1  
Perfect score: 59  
Sequence: 1 RTQNTKCRCK 10

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep: \*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep: \*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep: \*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep: \*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	119	2	US-08-219-237B-3
2	59	100.0	119	4	US-08-477-347-14
3	59	100.0	119	4	US-08-476-862-5
4	59	100.0	119	4	US-08-468-560C-3
5	59	100.0	128	4	US-09-180-100-9
6	59	100.0	143	4	US-09-180-100-10
7	59	100.0	144	4	US-09-180-100-21
8	59	100.0	157	4	US-09-180-100-15
9	59	100.0	159	4	US-09-180-100-23
10	59	100.0	219	3	US-08-974-022-45
11	59	100.0	219	4	US-08-795-445A-45
12	59	100.0	219	4	US-08-795-447A-45
13	59	100.0	219	4	US-08-974-186-45
14	59	100.0	219	4	US-08-795-446B-45
15	59	100.0	281	4	US-09-527-236A-3
16	59	100.0	314	1	US-08-444-231-19
17	59	100.0	314	1	US-08-152-443A-19
18	59	100.0	314	5	PCT-US95-17083-4
19	59	100.0	331	4	US-09-086-483A-3
20	59	100.0	335	2	US-08-219-237B-2
21	59	100.0	335	2	US-08-409-338-1
22	59	100.0	335	4	US-08-815-469-6
23	59	100.0	335	4	US-09-290-640-2
24	59	100.0	335	4	US-09-006-353A-7
25	59	100.0	335	4	US-08-468-560C-2
26	59	100.0	335	4	US-09-180-100-20
27	59	100.0	335	5	PCT-US95-17083-2

28	59	100.0	360	4	US-09-180-100-11	Sequence 11, Appl
29	59	100.0	376	4	US-09-180-100-22	Sequence 22, Appl
30	59	100.0	669	4	US-09-013-895A-3	Sequence 3, Appl
31	51	86.4	327	4	US-09-290-640-66	Sequence 66, Appl
32	40	67.8	368	2	US-08-651-579-2	Sequence 2, Appl
33	40	67.8	467	4	US-09-086-483A-6	Sequence 6, Appl
34	40	67.8	468	4	US-09-013-895A-2	Sequence 2, Appl
35	39	66.1	56	4	US-08-866-545-10	Sequence 10, Appl
36	39	66.1	186	1	US-08-089-458B-6	Sequence 6, Appl
37	39	66.1	206	1	US-08-097-827-7	Sequence 7, Appl
38	39	66.1	206	1	US-08-494-574-7	Sequence 7, Appl
39	39	66.1	277	2	US-08-147-784-2	Sequence 2, Appl
40	39	66.1	277	4	US-08-195-967-2	Sequence 2, Appl
41	39	66.1	277	4	US-09-006-353A-12	Sequence 12, Appl
42	39	66.1	277	4	US-08-472-940-2	Sequence 2, Appl
43	39	66.1	416	1	US-08-117-083-61	Sequence 61, Appl
44	39	66.1	438	1	US-08-097-827-11	Sequence 11, Appl
45	39	66.1	438	1	US-08-494-574-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1  
US-08-219-237B-3  
; Sequence 3, Application US/08219237B  
; Patent No. 5874546  
; GENERAL INFORMATION:  
; APPLICANT: NAGATA, Shigekazu  
; APPLICANT: ITOH, Naoto  
; APPLICANT: YONEHARA, Shin  
; TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James W. Hellwege  
; STREET: P.O. Box 2266 Eads Station  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/219,237B  
; FILING DATE: 28-MAR-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/872,129  
; FILING DATE: 22-APR-1992  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James W. Hellwege  
; REGISTRATION NUMBER: 28,808  
; REFERENCE/DOCKET NUMBER: 516762  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-219-237B-3

Query Match 100.0%; Score 59; DB 2; Length 119;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTQNTKCRCK 10

Db 75 RTQNTKCRCK 84

RESULT 2  
US-08-477-347-14  
; Sequence 14, Application US/08477347  
; Patent No. 6232446  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; APPLICANT: BIGDA, Jacek  
; APPLICANT: BELETSKY, Igor  
; APPLICANT: METT, Igor  
; TITLE OF INVENTION: TNF LIGANDS  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,347  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/115,685  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 106271  
; FILING DATE: 08-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Townsend, G. Kevin  
; REGISTRATION NUMBER: 34,033  
; REFERENCE/DOCKET NUMBER: WALLACH=10  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-477-347-14

Query Match 100.0%; Score 59; DB 4; Length 119;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10  
Db 75 RTQNTKCRCK 84

RESULT 3  
US-08-476-862-5  
; Sequence 5, Application US/08476862  
; Patent No. 6262239  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; APPLICANT: BIGDA, Jacek  
; APPLICANT: BELETSKY, Igor  
; APPLICANT: METT, Igor  
; APPLICANT: ENGELMANN, Hartmut  
; TITLE OF INVENTION: TNF INHIBITORS

NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,862  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 107267  
FILING DATE: 12-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 94039  
FILING DATE: 06-APR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 91229  
FILING DATE: 06-AUG-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 90339  
FILING DATE: 18-MAY-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: WALLACH=12A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 119 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-476-862-5

Query Match 100.0%; Score 59; DB 4; Length 119;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10  
Db 75 RTQNTKCRCK 84

RESULT 4  
US-08-468-560C-3  
; Sequence 3, Application US/08468560C  
; Patent No. 6270998  
; GENERAL INFORMATION:  
; APPLICANT: NAGATA, Shigekazu  
; APPLICANT: ITOH, Naoto  
; APPLICANT: YONEHARA, Shin  
; TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE  
; TITLE OF INVENTION: ANTIGEN  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.  
; STREET: P.O. BOX 747  
; CITY: FALLS CHURCH  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22040-0747

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,560C
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR., GERLAD M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 20-4393P
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-560C-3

Query Match      100.0%; Score 59; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTQNTKCRCK 10
Db 75 RTQNTKCRCK 84

RESULT 5
US-09-180-100-9
; Sequence 9, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 6306395io
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-100-9

Query Match      100.0%; Score 59; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTQNTKCRCK 10
Db 76 RTQNTKCRCK 85

RESULT 6
US-09-180-100-10
; Sequence 10, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 6306395io
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-100-10

Query Match      100.0%; Score 59; DB 4; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTQNTKCRCK 10
Db 76 RTQNTKCRCK 85

RESULT 7
US-09-180-100-21
; Sequence 21, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 6306395io
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-100-21

Query Match      100.0%; Score 59; DB 4; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTQNTKCRCK 10
Db 92 RTQNTKCRCK 101

RESULT 8
US-09-180-100-15
; Sequence 15, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 6306395io
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 157
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-180-100-15

Query Match      100.0%; Score 59; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RTQNTKCRCK 10
Db      105 RTQNTKCRCK 114
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RESULT 9
US-09-180-100-23
; Sequence 23, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, NO. 630639510
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-100-23

Query Match      100.0%; Score 59; DB 4; Length 159;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RTQNTKCRCK 10
Db      92 RTQNTKCRCK 101
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RESULT 10
US-08-974-022-45
; Sequence 45, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788

Query Match      100.0%; Score 59; DB 4; Length 219;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RTQNTKCRCK 10
Db      121 RTQNTKCRCK 130
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-022-45

Query Match      100.0%; Score 59; DB 3; Length 219;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RTQNTKCRCK 10
Db      121 RTQNTKCRCK 130
|||||

RESULT 11
US-08-795-445A-45
; Sequence 45, Application US/08795445A
; Patent No. 6284485
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,445A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-445A-45

Query Match      100.0%; Score 59; DB 4; Length 219;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RTQNTKCRCK 10
Db      121 RTQNTKCRCK 130
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RESULT 12  
US-08-795-447A-45  
; Sequence 45, Application US/08795447A  
; Patent No. 6284728  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: Osteoprotegerin  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: One Amgen Center Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378D2  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 219 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-795-447A-45

Query Match 100.0%; Score 59; DB 4; Length 219;  
Best Local Similarity 100.0%; Pred. No. 0.018;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RTQNTKCRCK 10  
Db 121 RTQNTKCRCK 130

RESULT 13  
US-08-974-186-45  
; Sequence 45, Application US/08974186  
; Patent No. 6284740  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: Osteoprotegerin  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/577,788  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 219 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-974-186-45

Query Match 100.0%; Score 59; DB 4; Length 219;  
Best Local Similarity 100.0%; Pred. No. 0.018;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RTQNTKCRCK 10  
Db 121 RTQNTKCRCK 130

RESULT 14  
US-08-795-446B-45  
; Sequence 45, Application US/08795446B  
; Patent No. 6288032  
; GENERAL INFORMATION:  
; APPLICANT: Boyle, William J.  
; APPLICANT: Lacey, David L.  
; APPLICANT: Calzone, Frank J.  
; APPLICANT: Chang, Ming-Shi  
; TITLE OF INVENTION: OSTEOPROTEGERIN  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/577,788  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Winter, Robert B.  
; REFERENCE/DOCKET NUMBER: A-378  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 219 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-795-446B-45

Query Match 100.0%; Score 59; DB 4; Length 219;  
Best Local Similarity 100.0%; Pred. No. 0.018;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10  
Db 121 RTQNTKCRCK 130

## RESULT 15

US-09-527-236A-3  
; Sequence 3, Application US/09527236A  
; Patent No. 6358508  
; GENERAL INFORMATION:  
; APPLICANT: Ni, Jian  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Fan, Ping  
; APPLICANT: Gentz, Reiner L.  
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9  
; FILE REFERENCE: PF375P1  
; CURRENT APPLICATION NUMBER: US/09/527,236A  
; CURRENT FILING DATE: 2000-03-16  
; PRIOR APPLICATION NUMBER: 60/052,991  
; PRIOR FILING DATE: 1997-06-11  
; PRIOR APPLICATION NUMBER: 09/095,094  
; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: 60/126,019  
; PRIOR FILING DATE: 1999-03-24  
; PRIOR APPLICATION NUMBER: 60/134,220  
; PRIOR FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-527-236A-3

Query Match 100.0%; Score 59; DB 4; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10  
Db 121 RTQNTKCRCK 130

Search completed: August 14, 2002, 15:17:03  
Job time: 686 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:15:34 ; Search time 230.21 Seconds  
(without alignments)  
4.825 Million cell updates/sec

Title: us-09-499-662-1  
Perfect score: 59  
Sequence: 1 RTQNTKCRCK 10

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Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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22: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	10	AAW83030	Fas epitope recogn
2	59	100.0	10	AAW83030	Human Fas epitope
3	59	100.0	10	AAW83030	Human Fas extracel
4	59	100.0	20	AAW83033	Human Fas peptide
5	59	100.0	20	AAW83033	Human Fas peptide
6	59	100.0	20	AAW83033	Human Fas epitope
7	59	100.0	20	AAW83033	Human Fas extracel
8	59	100.0	144	AAW50286	Human Fas peptide
9	59	100.0	159	AAW50288	Human Fas antigen
10	59	100.0	170	AAW50288	Human Fas receptor
11	59	100.0	173	AAW50288	Human Fas receptor

12	59	100.0	219	22	AAW86978	Fas protein. Unid
13	59	100.0	281	21	AAW86982	Human Fas. Homo s
14	59	100.0	314	16	AAW76238	Fas-delta-TM. Hom
15	59	100.0	314	17	AAW99682	Human Fas soluble
16	59	100.0	314	20	AAW98070	Soluble Fas recept
17	59	100.0	331	22	AAW50893	Human Fas receptor
18	59	100.0	335	13	AAW8084	Human cell surface
19	59	100.0	335	16	AAW78606	Human Fas protein.
20	59	100.0	335	17	AAW99681	Human Fas antigen.
21	59	100.0	335	17	AAW92528	hFas from plasmid
22	59	100.0	335	18	AAW50289	Human Fas antigen.
23	59	100.0	335	19	AAW49104	Fas protein. Mamm
24	59	100.0	335	21	AAW19341	Amino acid encodin
25	59	100.0	335	21	AAW36267	Human Fas receptor
26	59	100.0	335	21	AAW01335	CD-95 (FAS/APO-1)
27	59	100.0	335	22	AAW50517	Human tumour necro
28	59	100.0	376	18	AAW50287	Human Fas antigen
29	59	100.0	376	18	AAW60037	Antigenic peptide
30	59	100.0	600	16	AAW78610	Expression vector
31	59	100.0	600	17	AAW82526	Fas antigen #1. S
32	59	100.0	669	19	AAW64484	Human TNFRI protei
33	51	86.4	169	16	AAW78612	Plasmid fragment p
34	51	86.4	327	14	AAW41688	Murine Fas. Mus m
35	51	86.4	327	16	AAW78611	Murine Fas antigen
36	51	86.4	327	17	AAW92530	mFas sequence. Sy
37	51	86.4	327	20	AAW86244	Fas ligand (FasL)
38	51	86.4	327	21	AAW19344	Amino acid sequenc
39	51	86.4	576	16	AAW78613	Expression vector
40	51	86.4	592	17	AAW92527	Fas antigen #2. S
41	44	74.6	237	21	AAW53420	Human colon cancer
42	41	69.5	771	21	AAW93336	A human interphoto
43	41	69.5	771	21	AAW57089	Human interphoto
44	40	67.8	368	19	AAW41360	tvb polypeptide.
45	40	67.8	410	20	AAW93577	Human APOBP protei

## ALIGNMENTS

RESULT 1  
AAW83030  
ID AAW83030 standard; Peptide; 10 AA.  
XX AC AAW83030;  
XX DT 15-MAR-1999 (first entry)  
XX DE Fas epitope recognised by MAb HFE7A.  
XX KW Fas; epitope; HFE7A; monoclonal antibody; humanised antibody;  
XX KW human; apoptosis; autoimmune disease; Hashimoto's disease;  
XX KW systemic lupus erythematosus; graft versus host disease;  
XX KW Sjogren syndrome; pernicious anaemia; Addison's disease;  
XX KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
XX KW rheumatoid arthritis; autoimmune haemolytic anaemia;  
XX KW myasthenia gravis; multiple sclerosis; Basedow's disease;  
XX KW thrombopenia purpura; insulin-dependent diabetes; allergy;  
XX KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
XX KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
XX KW transplant rejection; therapy.  
XX OS Homo sapiens.  
XX AU9859701-A.  
XX PD 08-OCT-1998.  
XX PF 30-MAR-1998; 98AU-0059701.  
XX PR 08-OCT-1997; 97JP-0276064.  
XX PR 01-APR-1997; 97JP-0082953.  
XX PR 25-JUN-1997; 97JP-0169088.

(SANY ) SANKYO CO LTD.  
 Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;  
 Masahiko O, Nobufusa S, Shin Y, Tohru T;  
 WPI; 1998-543440/47.  
 New antibodies and proteins bind conserved epitope of Fas antigen -  
 used to evaluate drugs in animal models and to treat Fas-associated  
 diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
 myocarditis, hepatitis and AIDS  
 Claim 20; Page 184; 292pp; English.  
 This peptide represents the human Fas epitope recognised by novel  
 murine anti-human Fas monoclonal antibody HFE7A. It was identified  
 by ELISA and competitive assays using peptides (see AAW83043-63)  
 from the extracellular domain of Fas. The epitope is conserved  
 between mouse and human Fas. The invention provides humanised  
 HFE7A antibodies (see AAW83031-37) produced by CDR grafting. These  
 antibodies bind to the Fas epitope. They are capable of inducing  
 apoptosis in abnormal cells expressing Fas, and of inhibiting  
 Fas-induced apoptosis in normal cells. They are used to evaluate,  
 in animal models, treatments of diseases that involve Fas/Fas  
 ligand interactions, and also to treat such diseases, e.g.  
 autoimmune disease (systemic lupus erythematosus, Hashimoto's  
 disease, graft versus host disease, Sjogren syndrome, pernicious  
 anaemia, Addison's disease, scleroderma, Goodpasture syndrome,  
 Crohn's disease, rheumatoid arthritis, autoimmune haemolytic  
 anaemia, sterility, myasthenia gravis, multiple sclerosis,  
 Basedow's disease, thrombopenia purpura and insulin-dependent  
 diabetes), allergies, atopy, arteriosclerosis, myocarditis,  
 cardiomyopathy, glomerular nephritis, hypoplastic anaemia,  
 hepatitis, AIDS and transplant rejection (all claimed).  
 Sequence 10 AA;  
 Query Match 100.0%; Score 59; DB 19; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0033;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RTONTKCRCK 10  
 |||||  
 Db 1 rtqtkcrck 10  
 RESULT 2  
 AAB14740  
 ID AAB14740 standard; peptide; 10 AA.  
 AC AAB14740;  
 DT 24-NOV-2000 (first entry)  
 DE Human Fas epitope, SEQ ID NO:1.  
 KW Human Fas epitope; anti-Fas antibody; murine monoclonal antibody HFE7A;  
 KW FERM-BP-5828; humanised antibody; complementarity determining region;  
 KW CDR; Fas ligand; apoptosis modulator; programmed cell death;  
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;  
 KW hepatitis; AIDS; graft rejection.  
 OS Homo sapiens.  
 XX JP2000169393-A.  
 PN 20-JUN-2000.  
 XX 30-SEP-1999; 99JP-0278301.  
 PF 30-SEP-1998; 98JP-0276883.  
 PR

(SANY ) SANKYO CO LTD.  
 WPI; 2000-485645/43.  
 Preventive or treating agent for the diseases caused by an abnormality  
 in the Fas/Fas ligand system e.g. autoimmune diseases, contains  
 anti-Fas antibody -  
 Claim 19; Page 31; 139pp; Japanese.  
 The invention relates to compositions for the prevention or treatment  
 of diseases caused by an abnormality in the Fas/Fas ligand system  
 containing an anti-Fas antibody as the active component. The anti-Fas  
 antibody is either the murine anti-human Fas monoclonal antibody HFE7A,  
 or a humanised version of HFE7A containing identical CDRs  
 (complementarity determining regions) to antibody HFE7A. Via its  
 interaction with Fas, the antibody of the invention acts as a modulator  
 of apoptosis. The composition of the invention may therefore be used in  
 the treatment or prevention of conditions such as autoimmune diseases,  
 allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,  
 glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS  
 and organ graft rejection. Sequences AAB14740 and AAB14751-B14771  
 represent human Fas epitopes.  
 Sequence 10 AA;  
 Query Match 100.0%; Score 59; DB 21; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0033;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RTONTKCRCK 10  
 |||||  
 Db 1 rtqtkcrck 10  
 RESULT 3  
 AAW90890  
 ID AAW90890 standard; peptide; 10 AA.  
 XX AAW90890;  
 AC AAW90890;  
 DT 08-AUG-2000 (first entry)  
 DE Human Fas extracellular domain peptide fragment.  
 DE  
 XX  
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;  
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;  
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
 OS Homo sapiens.  
 XX EP990663-A2.  
 PN 05-APR-2000.  
 PD 29-SEP-1999; 99EP-0307711.  
 PF 30-SEP-1998; 98JP-0276881.  
 PR 30-SEP-1998; 98JP-0276882.  
 XX (SANY ) SANKYO CO LTD.  
 PA Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 PI

XX WPI; 2000-258930/23.  
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems -  
 XX  
 XX Example reference 6; Page 97; 263pp; English.  
 PS  
 XX This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antirheumatic, nephrotropic, antinfertility, neuroprotective,  
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto's disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a human Fas extracellular domain peptide fragment described in the method  
 CC of the invention.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 59; DB 21; Length 10;  
 Best Local Similarity 100.0%; Pred. NO. 0.0033;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RTQNTKCRCK 10  
 | | | | | | | |  
 Db 1 rtqntkcrck 10  
 RESULT 4  
 AAW83053  
 ID AAW83053 standard; Peptide; 20 AA.  
 XX  
 AC AAW83053;  
 XX  
 DT 15-MAR-1999 (first entry)  
 XX  
 DE Human Fas peptide p11.  
 XX  
 XX Fas; epitope: HFE7A; monoclonal antibody; humanised antibody;  
 KW human; apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;  
 KW systemic lupus erythematosus; graft versus host disease;  
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;  
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;  
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;  
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;  
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
 KW transplant rejection; therapy.  
 XX  
 XX Synthetic.  
 OS Homo sapiens.  
 OS

XX AU9859701-A.  
 XX  
 XX 08-OCT-1998.  
 XX  
 XX 30-MAR-1998; 98AU-0059701.  
 XX  
 PR 08-OCT-1997; 97JP-0276064.  
 PR 01-APR-1997; 97JP-0082953.  
 PR 25-JUN-1997; 97JP-0169088.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;  
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;  
 DR WPI; 1998-543440/47.  
 XX  
 XX New antibodies and proteins bind conserved epitope of Fas antigen -  
 PT used to evaluate drugs in animal models and to treat Fas-associated  
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
 PT myocarditis, hepatitis and AIDS  
 XX  
 PS Reference Example 6; Page 87; 292pp; English.  
 XX  
 CC Synthetic peptides P1-P15 (see AAW83043-57) are partial sequences of  
 CC amino acids 1-157 of the extracellular domain of human Fas, with  
 CC between 9 and 11 amino acid residues overlapping one another. P16  
 CC (see AAW83059) is a negative control having no homology with human  
 CC Fas. P1-P16 were used in an ELISA, which demonstrated that novel  
 CC murine anti-human Fas monoclonal antibody HFE7A specifically binds  
 CC an amino acid sequence contained in P11. The epitope (see AAW83030)  
 CC was subsequently identified. The invention provides humanised  
 CC HFE7A antibodies (see AAW83031-37) produced by CDR grafting. These  
 CC antibodies are capable of inducing apoptosis in abnormal cells  
 CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal  
 CC cells. They are used to evaluate, in animal models, treatments of  
 CC diseases that involve Fas/Fas ligand interactions, and also to treat  
 CC such diseases.  
 XX  
 SQ Sequence 20 AA;  
 Query Match 100.0%; Score 59; DB 19; Length 20;  
 Best Local Similarity 100.0%; Pred. NO. 0.0061;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RTQNTKCRCK 10  
 | | | | | | | |  
 Db 6 rtqntkcrck 15  
 RESULT 5  
 AAB14761  
 ID AAB14761 standard; peptide; 20 AA.  
 XX  
 AC AAB14761;  
 XX  
 DT 24-NOV-2000 (first entry)  
 XX  
 XX Human Fas epitope, SEQ ID NO:36.  
 DE  
 DE Human Fas epitope; anti-Fas antibody; murine monoclonal antibody HFE7A;  
 KW FERM-pp-5828; humanised antibody; complementarity determining region;  
 KW CDR; Fas ligand; apoptosis modulator; programmed cell death;  
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;  
 KW hepatitis; AIDS; graft rejection.  
 XX  
 OS Homo sapiens.  
 XX  
 XX JP2000169393-A.  
 XX

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PD 20-JUN-2000.
XX
PF 30-SEP-1999; 99JP-0278301.
XX
PR 30-SEP-1998; 98JP-0276883.
XX
PA (SANY ) SANKYO CO LTD.
XX
XX WPI; 2000-485645/43.
DR
XX Preventive or treating agent for the diseases caused by an abnormality
PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
PT anti-Fas antibody -
XX
XX Example 6; Page 30; 139pp; Japanese.
XX
XX The invention relates to compositions for the prevention or treatment
CC or diseases caused by an abnormality in the Fas/Fas ligand system
CC containing an anti-Fas antibody as the active component. The anti-Fas
CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
CC or a humanised version of HFE7A containing identical CDRs
CC (complementarity determining regions) to antibody HFE7A. Via its
CC interaction with Fas, the antibody of the invention acts as a modulator
CC of apoptosis. The compositions of the invention may therefore be used in
CC the treatment or prevention of conditions such as autoimmune diseases,
CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
CC and organ graft rejection. Sequences AAB14740 and AAB14751-B14771
CC represent human Fas epitopes.
XX
XX Sequence 20 AA;
SQ
Query Match 100.0%; Score 59; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTQNTKCRCK 10
Db 6 rtqntkerck 15
|||||
RESULT 6
AAW90911
ID AAW90911 standard; peptide; 20 AA.
XX
AC AAW90911;
XX
DT 08-AUG-2000 (first entry)
XX
DE Human Fas extracellular domain antigenic peptide #11.
XX
KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjorgen's syndrome; anemia; Addison's disease; sterility; myasthenia gravis;
KW Goodpasture syndrome; Crohn's disease; sterility; scleroderma; sterility;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX
OS Homo sapiens.
XX
XX EP990663-A2.
PN
XX
PD 05-APR-2000.
XX
PF 29-SEP-1999; 99EP-0307711.
XX
PR 30-SEP-1998; 98JP-0276881.
XX

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PR 30-SEP-1998; 98JP-0276882.
XX
PA (SANY ) SANKYO CO LTD.
XX
PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX
XX WPI; 2000-258930/23.
DR
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems -
XX
XX Example reference 6; Page 110; 263pp; English.
XX
XX This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
CC antiarteriosclerotic, cardiac and hepatropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a human Fas extracellular domain derived antigenic peptide described in
XX the method of the invention.
XX
XX Sequence 20 AA;
SQ
Query Match 100.0%; Score 59; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTQNTKCRCK 10
Db 6 rtqntkerck 15
|||||
RESULT 7
AAW9517
ID AAW69517 standard; peptide; 20 AA.
XX
AC AAW69517;
XX
XX 10-APR-2000 (first entry)
DT
DE Human Fas peptide fragment, Fp11.
XX
XX Fp11; Fas fragment; APO-1; CD95; anti-Fas autoantibody; antibody;
KW modulator; apoptosis; proliferation.
XX
OS Homo sapiens.
XX
XX WO9965935-A2.
PN
XX
XX 23-DEC-1999.
PD
XX

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PF 15-JUN-1999; 99WO-EP04105.  
 XX 18-JUN-1998; 98GB-0013194.  
 PR 12-MAR-1999; 99GB-0005793.  
 XX (KARO-) KAROLINSKA INNOVATIONS AB.  
 PA Chiodi F;  
 XX WPI; 2000-106082/09.  
 DR Fas peptide fragments useful for the treatment of proliferative  
 PT disorders -  
 PT  
 XX Claim 3; Page 57; 71pp; English.

XX Sequences AAY69514-Y69521 represent peptide fragments of the Fas protein  
 CC (also known as APO-1 or CD95). Fas is a type I cellular receptor which  
 CC transduces an apoptotic signal on binding of its ligand, Fas ligand  
 CC (FasL). Fas autoantibodies have been isolated from the serum of healthy  
 CC blood donors - these may represent an additional mode of regulation of  
 CC Fas-mediated signals in vivo. The Fas peptides may be used to modulate  
 CC apoptosis via blocking autoantibody binding to Fas, thereby reducing or  
 CC increasing FasL binding, which results in inhibition or stimulation of  
 CC apoptosis. Fp5 (AAY69514) is thus able to induce apoptosis while Fp11  
 CC (AAY69517) and Fp17 (AAY69519) are able to block apoptosis. Fp8  
 CC (AAY69515) and Fp9 (AAY69516) comprise amino acids which are important  
 CC for binding of Fas to FasL. The Fas peptides can be used to obtain  
 CC antibodies containing a Fas binding site. The peptides and antibodies can  
 CC be used in assay methods to obtain candidate modulators of Fas-mediated  
 CC apoptosis. The candidate modulator may also modulate cellular  
 CC proliferation. The peptides, mixtures of peptides, nucleic acids or  
 CC antibodies are useful for methods of treating proliferative disorders.  
 CC The disorders that may be prevented or treated include tumours, cancer,  
 CC psoriasis, type I diabetes, multiple sclerosis, liver cirrhosis and HIV  
 CC infection.

XX Sequence 20 AA;

Query Match 100.0%; Score 59; DB 21; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.0061;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTQNTKCRCK 10  
 Db 6 rtqntkcrck 15

RESULT 8  
 AAW50286  
 ID AAW50286 standard; Protein; 144 AA.

XX AC AAW50286;

DT 16-JUL-1998 (first entry)

XX Human Fas antigen derivative.

XX Human; Fas antigen; derivative; apoptosis regulation; gene therapy;  
 KW treatment; diabetes; arthritis; lupus; hepatitis; influenza; HIV;  
 KW apoptosis modulation.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH Peptide 1..16  
 FT /label= sig\_peptide  
 FT Peptide 17..144  
 FT /label= mat\_peptide

XX WO9742319-A1.

XX

PD 13-NOV-1997.  
 XX 01-MAY-1997; 97WO-JP01502.  
 XX 02-MAY-1996; 96JP-0135760.  
 XX (MOCH) MOCHIDA PHARM CO LTD. -  
 PA (OSAB-) OSAKA BIOSCIENCE INST.  
 XX Nagata S, Nakamura N;  
 XX WPI; 1997-558981/51.  
 DR N-PSDB; AAV07003.  
 XX Fas antigen derivative containing modified extracellular region -  
 PT has low antigenicity, promotes apoptosis and is useful in treatment  
 PT of viral and other diseases  
 XX Disclosure; Fig 3; 102pp; Japanese.  
 XX The present sequence is a Fas antigen derivative, which  
 CC contain a Fas antigen extracellular region lacking one or more  
 CC amino acid residues in the region from the amino-terminal to (but  
 CC excluding) the 1st cysteine residue (preferably at least 29  
 CC residues are deleted).  
 CC The derivative is an effective regulator of apoptosis and can be  
 CC used (either by administration of the polypeptide, or by the use  
 CC of the coding DNA in gene therapy) to treat a range of diseases,  
 CC e.g. diabetes, arthritis, lupus and in particular viral diseases  
 CC such as hepatitis, influenza and HIV, by modulating apoptosis of  
 CC virus-infected cells.  
 XX Sequence 144 AA;

Query Match 100.0%; Score 59; DB 18; Length 144;  
 Best Local Similarity 100.0%; Pred. No. 0.035;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTQNTKCRCK 10  
 Db 92 rtqntkcrck 101

RESULT 9  
 AAW50288  
 ID AAW50288 standard; Protein; 159 AA.

XX AC AAW50288;

DT 16-JUL-1998 (first entry)

XX Human Fas antigen derivative/IgG1 hinge fusion.

XX Human; Fas antigen; derivative; apoptosis regulation; gene therapy;  
 KW treatment; diabetes; arthritis; lupus; hepatitis; influenza; HIV;  
 KW apoptosis modulation; immunoglobulin G1 Fc; IgG1 hinge; fusion.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH Peptide 1..16  
 FT /label= sig\_peptide  
 FT Peptide 17..159  
 FT /label= mat\_peptide

XX WO9742319-A1.

XX 13-NOV-1997.

XX 01-MAY-1997; 97WO-JP01502.

XX 02-MAY-1996; 96JP-0135760.

XX (MOCH ) MOCHIDA PHARM CO LTD.  
PA (OSAB-) OSAKA BIOSCIENCE INST.  
XX  
XX Nagata S, Nakamura N;  
XX WPI; 1997-558981/51.  
DR N-PSDB; AAV07005.  
XX  
XX Fas antigen derivative containing modified extracellular region -  
PT has low antigenicity, promotes apoptosis and is useful in treatment  
PT of viral and other diseases  
XX  
XX Disclosure; Fig 5; 102pp; Japanese.  
XX  
XX The present sequence encodes a Fas antigen derivative/IgG1 hinge  
CC fusion, which contains a Fas antigen extracellular region lacking  
CC one or more amino acid residues in the region from the  
CC amino-terminal to (but excluding) the 1st cysteine residue  
CC (preferably at least 29 residues are deleted).  
CC The derivative is an effective regulator of apoptosis and can be  
CC used (either by administration of the polypeptide, or by the use  
CC of the coding DNA in gene therapy) to treat a range of diseases,  
CC e.g. diabetes, arthritis, lupus and in particular viral diseases  
CC such as hepatitis, influenza and HIV, by modulating apoptosis of  
XX virus-infected cells.  
XX  
XX Sequence 159 AA;  
SQ

Query Match 100.0%; Score 59; DB 18; Length 159;  
Best Local Similarity 100.0%; Pred. No. 0.038;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTQNTKCRCK 10  
Db 92 rtqntkcrck 101  
|||||

RESULT 10  
AAB36228  
ID AAB36228 standard; Protein; 170 AA.  
XX  
XX AAB36228;  
XX 19-FEB-2001 (first entry)  
XX Rat Fas receptor.  
XX  
XX Rat; Fas receptor; gene therapy; vascular cell; stenosis; FGFR-1;  
KW accelerated graft arteriosclerosis; vascular occlusive disease.  
XX  
XX Rattus sp.  
XX  
XX WO200063369-A2.  
XX  
XX 26-OCT-2000.  
XX  
XX 18-APR-2000; 2000WO-EP03532.  
XX  
XX 19-APR-1999; 99US-0294176.  
XX 10-MAY-1999; 99US-0307690.  
XX  
XX (NOVS ) NOVARTIS AG.  
XX (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
XX (UYJO ) UNIV JOHNS HOPKINS.  
XX Ballermann BJ, Goldschmidt P, Movva RN, Sanfilippo A;  
XX  
XX WPI; 2000-672735/65.  
XX N-PSDB; AAC66557.  
XX  
XX Genetic modification of target cells for inhibiting excessive

PT proliferation, comprises transferring, to cells or progenitors, the DNA  
PT sequence encoding Fas antigen or receptor, or the fibroblast growth  
PT factor receptor -  
XX  
XX Disclosure; Page 33-34; 4lpp; English.  
XX  
XX The present invention describes a method of gene therapy which involves  
CC the use of RasR or FGFR-1 coding sequences to treat vascular diseases.  
CC The invention also provides vectors for use in this method. The treatable  
CC diseases include vascular occlusive diseases associated with cell  
CC proliferation, such as accelerated graft arteriosclerosis and other forms  
CC of stenosis.  
XX  
XX Sequence 170 AA;  
SQ

Query Match 100.0%; Score 59; DB 21; Length 170;  
Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RTQNTKCRCK 10  
Db 117 rtqntkcrck 126  
|||||

RESULT 11  
AAB36229  
ID AAB36229 standard; Protein; 173 AA.  
XX  
XX AAB36229;  
XX 19-FEB-2001 (first entry)  
XX Human Fas receptor.  
XX  
XX Human; Fas receptor; gene therapy; vascular cell; stenosis; FGFR-1;  
KW accelerated graft arteriosclerosis; vascular occlusive disease.  
XX  
XX Homo sapiens.  
XX  
XX WO200063369-A2.  
XX  
XX 26-OCT-2000.  
XX  
XX 18-APR-2000; 2000WO-EP03532.  
XX  
XX 19-APR-1999; 99US-0294176.  
XX 10-MAY-1999; 99US-0307690.  
XX  
XX (NOVS ) NOVARTIS AG.  
XX (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
XX (UYJO ) UNIV JOHNS HOPKINS.  
XX Ballermann BJ, Goldschmidt P, Movva RN, Sanfilippo A;  
XX  
XX WPI; 2000-672735/65.  
XX N-PSDB; AAC66558.  
XX  
XX Genetic modification of target cells for inhibiting excessive  
PT proliferation, comprises transferring, to cells or progenitors, the DNA  
PT sequence encoding Fas antigen or receptor, or the fibroblast growth  
PT factor receptor -  
XX  
XX Disclosure; Page 35; 4lpp; English.  
XX  
XX The present invention describes a method of gene therapy which involves  
CC the use of RasR or FGFR-1 coding sequences to treat vascular diseases.  
CC The invention also provides vectors for use in this method. The treatable  
CC diseases include vascular occlusive diseases associated with cell  
CC proliferation, such as accelerated graft arteriosclerosis and other forms  
CC of stenosis.  
XX  
XX Sequence 173 AA;



Query Match 100.0%; Score 59; DB 21; Length 173;  
Best Local Similarity 100.0%; Pred. No. 0.041;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10  
| | | | |  
Db 121 rtgntkerck 130

## RESULT 12

AAB66978  
ID AAB66978 standard; Protein; 219 AA.

XX AC AAB66978;

XX DT 19-APR-2001 (first entry)

XX DE Fas protein.

XX KW Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;  
XX KW multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;  
XX KW systemic lupus erythematosus; graft-versus-host disease; septic shock;  
XX KW acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;  
XX KW coronary condition; myocardial infarction; cancer; diabetes; psoriasis;  
XX KW endometrios; fever; glomerulonephritis; inflammatory bowel disease;  
XX KW ischaemia; Parkinson's disease.

XX OS Unidentified.

XX XX WO200103719-A2.

XX PD 18-JAN-2001.

XX PF 07-JUL-2000; 2000WO-US18667.

XX PR 09-JUL-1999; 99US-0350670.

XX PR 09-DEC-1999; 99US-0457647.

XX PA (AMGE-) AMGEN INC.

XX PI Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;

XX DR WPI; 2001-103031/11.

XX PT Treating conditions leading to bone loss such as rheumatoid arthritis,  
XX PT multiple sclerosis and asthma, comprises administering an  
XX PT osteoprotegerin protein in conjunction with e.g. inhibitors of  
XX PT interleukin and tumor necrosis factor alpha -

XX PS Disclosure; Fig 2; 316pp; English.

XX CC The present invention relates to a method for treating conditions leading  
XX CC to bone loss. The method comprises administering a purified and isolated  
XX CC osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976)  
XX CC in conjunction with other substances such as tumour necrosis factor-alpha  
XX CC (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE  
XX CC modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet  
XX CC activating factor (PAF) antagonists. The method is useful for treating  
XX CC conditions leading to bone loss such as rheumatoid arthritis, multiple  
XX CC sclerosis, osteoporosis, osteomyelitis and asthma. The method is also  
XX CC useful for treating inflammation, systemic lupus erythematosus (SLE) and  
XX CC graft-versus-host disease (GVHD). Other diseases that can be treated  
XX CC include acute pancreatitis, Alzheimer's disease, anorexia,  
XX CC atherosclerosis, coronary conditions (e.g. myocardial infarction),  
XX CC cancer, diabetes, endometrios, fever, glomerulonephritis, hyperalgesia,  
XX CC inflammatory bowel disease, ischaemia, pain, Parkinson's disease,  
XX CC psoriasis and septic shock. The present sequence was used in a sequence  
XX CC homology comparison.

XX SQ Sequence 219 AA;

Query Match 100.0%; Score 59; DB 22; Length 219;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10  
| | | | |  
Db 121 rtgntkerck 130

## RESULT 13

AAB26982  
ID AAB26982 standard; Protein; 281 AA.

XX AC AAB26982;

XX DT 02-FEB-2001 (first entry)

XX DE Human Fas.

XX KW Human; Fas; tumour necrosis factor; TR9 receptor; immunosuppressive;  
XX KW antiinflammatory; cardiant; antiasthmatic; antidiabetic; antiallergic;  
XX KW antiarthritic; antirheumatic; anti-HIV; anticonvulsant; cytostatic;  
XX KW neuroprotective; gene therapy; Death Domain Containing Receptor 6;  
XX KW common variable immunodeficiency; X-linked agammaglobulinaemia;  
XX KW severe combined immunodeficiency; Wiskott-Aldrich syndrome;  
XX KW autoimmune disease; rheumatoid arthritis; allergic encephalomyelitis;  
XX KW multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer;  
XX KW cardiovascular disease; neurological disease; protein coordinate data.

XX OS Homo sapiens.

XX PN WO200056862-A1.

XX PD 28-SEP-2000.

XX PF 16-MAR-2000; 2000WO-US06831.

XX PR 24-MAR-1999; 99US-0126019.

XX PR 14-MAY-1999; 99US-0134220.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ni J, Gentz RL, Yu G, Fan P;

XX DR WPI; 2000-594575/56.

XX PT Nucleic acid molecule encoding a human tumor necrosis factor receptor,  
XX PT known as TR9, useful for treating, preventing and diagnosing severe  
XX PT combined immunodeficiency, autoimmune diseases, HIV infection, epilepsy  
XX PT and cancer -

XX PS Disclosure; Fig 2; 220pp; English.

XX CC The present sequence is Fas, a member of the tumour necrosis factor  
XX CC receptor family. A novel human tumour necrosis factor receptor,  
XX CC designated TR9, has been isolated. The TR9 receptor is also known as  
XX CC Death Domain Containing Receptor 6. TR9 polypeptides, polynucleotides or  
XX CC agonists are useful for treating, preventing or diagnosing common  
XX CC variable immunodeficiency, X-linked agammaglobulinaemia, severe combined  
XX CC immunodeficiency and Wiskott-Aldrich syndrome, autoimmune diseases (such  
XX CC as rheumatoid arthritis, allergic encephalomyelitis, multiple sclerosis,  
XX CC diabetes mellitus and asthma), HIV infection, epilepsy, cancer,  
XX CC cardiovascular diseases and other neurological diseases.

XX SQ Sequence 281 AA;

Query Match 100.0%; Score 59; DB 21; Length 281;  
Best Local Similarity 100.0%; Pred. No. 0.063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10

```
Db 121 rtqntkcrck 130
|||||
RESULT 14
AAR76238 standard; Protein; 314 AA.
XX
AC AAR76238;
XX
DT 06-NOV-1995 (first entry)
XX
DE Fas-delta-TM.
XX
KW Fas-delta-TM; transmembrane deletion; apoptosis; antibody;
KW adoptive immunotherapy; transgenic animal.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..16
FT Protein 17..314
FT /label= Sig_peptide
FT /label= Mat_protein
FT /note= "soluble Fas dell antigen"
FT 17..168
FT /label= Extracellular_domain
FT /note= "the 5 C-terminal residues of the
Fas antigen extracellular domain are
deleted in Fas dell"
FT 169..314
FT /label= Cytoplasmic_domain
FT Peptide 164..173
FT /note= "preferred peptide from breakpoint region
(claim 4, page 132)"
FT Peptide 164..174
FT /note= "preferred peptide from breakpoint region"
FT Peptide 161..171
FT /note= "preferred peptide from breakpoint region"
XX
PN WO9513701-A.
PD 26-MAY-1995.
XX
XX 15-NOV-1994; 94WO-US13173.
XX
XX 15-NOV-1993; 93US-0152443.
XX
PA (LXRB-) LXR BIOTECHNOLOGY INC.
PI Barr PJ, Kiefer MC, Shapiro JP;
XX
PI WPI; 1995-200120/26.
DR N-PSDB; AAQ93879.
XX
PT New nucleic acid encoding Fas protein without its trans-membrane region
PT - and related vectors, transformed cells, transgenic animals, protein and
PT antibodies, useful for control of Fas mediated apoptosis
XX
XX Claim 9; Fig.3-1 to 3-4; 38pp; English.
XX
XX mRNA was obtd. from human lymphocytes and PCR was used to make
CC cDNA specific for Fas-delta-TM (i.e. Fas lacking the transmembrane
CC region) mRNA. The PCR product was ligated into pBluescript and the
CC recombinant plasmid was used to transfect E. coli DH5-alpha cells. The
CC insert sequence of pBluescript-Fas-delta-TM encoded the protein
CC given in AAR76238.
XX
SQ Sequence 314 AA;
Query Match 100.0%; Score 59; DB 16; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTQNTKCRCK 10
Db 121 rtqntkcrck 130
|||||
RESULT 15
AAR99682 standard; Protein; 314 AA.
XX
AC AAR99682;
XX
DT 10-OCT-1996 (first entry)
XX
DE Human Fas soluble antigen Fas dell.
XX
```

```
KW Fas antigen; autoimmune disease; systemic lupus erythematosus; SLE;
KW angioimmunoblastic lymphadenopathy; AILD.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..16
FT Protein 17..314
FT /label= Sig_peptide
FT /label= Mat_protein
FT /note= "soluble Fas dell antigen"
FT 17..168
FT /label= Extracellular_domain
FT /note= "the 5 C-terminal residues of the
Fas antigen extracellular domain are
deleted in Fas dell"
FT 169..314
FT /label= Cytoplasmic_domain
FT Peptide 164..173
FT /note= "preferred peptide from breakpoint region
(claim 4, page 132)"
FT Peptide 164..174
FT /note= "preferred peptide from breakpoint region"
FT Peptide 161..171
FT /note= "preferred peptide from breakpoint region"
XX
PN WO9620206-A1.
PD 04-JUL-1996.
XX
XX 22-DEC-1995; 95WO-US17083.
XX
XX 23-DEC-1994; 94US-0371263.
XX
PA (UABR-) UAB RES FOUND.
PI Cheng J, Liu C, Mountz JD, Zhou T;
XX
XX WPI; 1996-321796/32.
DR N-PSDB; AAT34527.
XX
PT Natural, soluble form of Fas antigen secreted by human cells is
PT result of alternative mRNA processing - used to diagnose
PT Fas-associated disease, e.g. systemic lupus erythematosus
XX
PS Claim 4; Page 114-16; 152pp; English.
XX
XX A natural, soluble Fas antigen variant (AAR99682), designated Fas
CC dell, and other Fas variants (AAR99683-85) are derived by alternative
CC splicing of Fas gene transcripts. A cDNA clone (AAT34527) coding for
CC the variant was obtd. from human peripheral blood mononuclear cells.
CC The Fas dell variant lacks the transmembrane domain of insoluble
CC Fas antigen (AAR99681). Recombinant dell variant, or fragments of
CC it, can be expressed in prokaryotic or eukaryotic (e.g. COS) cells.
CC Detection of increased levels of soluble forms of Fas antigen can
CC be used to diagnose autoimmune diseases, esp. systemic lupus
CC erythematosus and angioimmunoblastic lymphadenopathy.
XX
SQ Sequence 314 AA;
Query Match 100.0%; Score 59; DB 17; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTQNTKCRCK 10
Db 121 rtqntkcrck 130
|||||
Search completed: August 14, 2002, 15:15:34
Job time: 832 sec
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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 15:18:58 ; Search time 108.64 Seconds  
(without alignments)  
8.845 Million cell updates/sec

Title: US-09-499-662-1

Perfect score: 59

Sequence: 1 RTONTKCRCK 10

Scoring table:  
BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	59	100.0	314	2 I37383	FAS soluble protei
2	59	100.0	324	2 JC2395	Fas antigen precu
3	59	100.0	335	2 A40036	apoptosis-mediat
4	51	86.4	327	2 A46484	apoptosis-mediat
5	39	66.1	272	2 I48700	gene ox40 protein
6	39	66.1	277	2 I37552	OX40 homolog - hum
7	37	62.7	235	2 I50610	T-cell surface gly
8	37	62.7	360	2 B36470	Wnt-2 protein - mo
9	37	62.7	454	1 GOMST1	tumor necrosis fac
10	37	62.7	761	2 T09052	hypothetical prote
11	36	61.0	86	2 D90874	hypothetical prote
12	36	61.0	86	2 G85524	hypothetical prote
13	36	61.0	163	1 F81938	cytochrome c552 NM
14	36	61.0	310	1 D64758	probable transcrip
15	35	59.3	89	2 T23462	hypothetical prote
16	35	59.3	360	2 S00834	int-1-like protein
17	35	59.3	413	2 C69941	hypothetical prote
18	35	59.3	843	1 A27340	complement C7 prec
19	34	57.6	37	2 A60963	charybdotoxin 1 [v
20	34	57.6	37	2 B60963	charybdotoxin 2 -
21	34	57.6	86	1 TNLJND	trans-activating t
22	34	57.6	139	2 T28303	ORF MSV142 probabl
23	34	57.6	148	2 D49530	16k vascular endot
24	34	57.6	155	2 S51770	grain softness pro
25	34	57.6	164	2 S48186	grain softness pro
26	34	57.6	351	2 T18066	hypothetical prote
27	34	57.6	363	2 C62555	first mannosyl tra
28	34	57.6	447	2 S20711	neuraminidase - in
29	34	57.6	453	1 NMIV3	exo-alpha-sialidas

30 34 57.6 454 1 NMIV  
31 34 57.6 596 2 F88188  
32 34 57.6 633 2 T23090  
33 34 57.6 711 2 T23738  
34 34 57.6 779 1 S40382  
35 34 57.6 1191 2 B97116  
36 34 57.6 2120 2 T30243  
37 33 55.9 41 2 S19586  
38 33 55.9 41 2 S19621  
39 33 55.9 50 1 MDHB  
40 33 55.9 57 2 S59073  
41 33 55.9 124 2 S08640  
42 33 55.9 192 2 P96812  
43 33 55.9 200 2 P00245  
44 33 55.9 202 2 B45512  
45 33 55.9 206 2 T47433

exo-alpha-sialidas  
protein C18H9.7 [1  
hypothetical prote  
hypothetical prote  
box A-binding fact  
chromosome segrega  
alpha tectorin - C  
ornatin A2 - leech  
ornatin A3 - leech  
mast cell degranul  
metallothionein is  
hypothetical prote  
protein F3P9.8 [im  
polyprotein (clone  
cold-regulated pro  
hypothetical prote

ALIGNMENTS

RESULT 1

I37383

FAS soluble protein - human

C:Species: Homo sapiens (man)

C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 21-Jul-2000

C:Accession: I37383

R:Cascino, I.; Fiucci, G.; Papoff, G.; Ruberti, G.

J. Immunol. 154, 2706-2713, 1995

A:Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule

A:Reference number: I37383; MUID:95181785

A:Accession: I37383

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-314 <RES>

A:Cross-references: EMBL:Z47993; NID:q728578; PIDN:CAA88031.1; PID:q695539

Query Match 100.0%; Score 59; DB 2; Length 314;

Best Local Similarity 100.0%; Pred. No. 0.0073;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTONTKCRCK 10

|||||

Db 121 RTONTKCRCK 130

RESULT 2

JC2395

Fas antigen precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 05-Nov-1999

C:Accession: JC2395; PC2246

R:Kimura, K.; Wakatsuki, T.; Yamamoto, M.

Biochem. Biophys. Res. Commun. 198, 666-674, 1994

A:Title: A variant mRNA species encoding a truncated form of Fas antigen in the rat 1

A:Reference number: JC2395; MUID:94128114

A:Accession: JC2395

A:Molecule type: mRNA

A:Residues: 1-324 <KTM>

A:Cross-references: DBJ:D26112; NID:q468486; PIDN:BAA05108.1; PID:d1005650; PID:q468

A:Experimental source: thymus

A:Accession: PC2246

A:Molecule type: mRNA

A:Residues: 1-62, 'RFT' <K12>

A:Cross-references: DBJ:D26113; NID:q468488; PIDN:BAA05109.1; PID:d1005651; PID:q468

A:Experimental source: liver

C:Genetics:

C:Superfamily: NGF receptor repeat homology

C:Keywords: transmembrane protein

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-324/Product: Fas antigen #status predicted <MAT>

F:44-79/Domain: NGF receptor repeat homology <NGF>  
F:81-124/Domain: NGF receptor repeat homology <NG4>  
F:171-188/Domain: transmembrane #status predicted <TM>

Query Match 100.0%; Score 59; DB 2; Length 324;  
Best Local Similarity 100.0%; Pred. No. 0.0075;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10  
|||||

DB 117 RTQNTKCRCK 126

## RESULT 3

A40036  
apoptosis-mediating surface antigen Fas precursor - human  
N:Alternate names: surface antigen APO-1  
C:Species: Homo sapiens (man)

C:Date: 17-Jan-1992 #sequence\_revision 17-Jan-1992 #text\_change 21-Jul-2000  
C:Accession: A40036; S24543; A38142

R:Itoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.; Hase, Cell 56, 233-243, 1991  
A:Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can mediate apoptosis

A:Reference number: A40036; MUID:91309137

A:Accession: A40036

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-335 <ITO>

A:Cross-references: GB:M67454; NID:g182409; PIDN:AAA63174.1; PID:g182410

R:Krammer, P.H.

submitted to the EMBL Data Library, February 1992

A:Reference number: S24543

A:Accession: S24543

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-335 <KRA>

A:Cross-references: EMBL:X63717; NID:g28741; PID:g28742

R:Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.; Rich J. Biol. Chem. 267, 10709-10715, 1992

A:Title: Purification and molecular cloning of the APO-1 cell surface antigen, a member of the TNF receptor family

A:Reference number: A38142; MUID:92268122

A:Accession: A38142

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-134, 'Q', 136-335 <OE>

A:Experimental source: SKW6.4 cells

A:Note: sequence extracted from NCBI backbone (NCBIP:103810)

A:Note: in NCBI backbone the source is designated as mouse

C:Genetics:

A:Gene: GDB:AP1

A:Cross-references: GDB:132671; OMIM:134637

A:Map position: 10q24.1-10q24.1

C:Superfamily: NGF receptor repeat homology

C:Keywords: apoptosis; surface antigen; transmembrane protein

F:1-16/Domain: signal sequence #status predicted <SIG>

F:85-128/Domain: NGF receptor repeat homology <NG4>

F:174-190/Domain: transmembrane #status predicted <TM>

Query Match 100.0%; Score 59; DB 2; Length 335;  
Best Local Similarity 100.0%; Pred. No. 0.0077;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10  
|||||

DB 121 RTQNTKCRCK 130

## RESULT 4

A46484

apoptosis-mediating membrane-associated polypeptide Fas - mouse  
C:Species: Mus musculus (house mouse)

C:Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
C:Accession: A46484; A47254  
R:Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenki J. Immunol. 148, 1274-1279, 1992

A:Title: The cDNA structure, expression, and chromosomal assignment of the mouse Fas gene

A:Reference number: A46484; MUID:92148151

A:Accession: A46484

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-327 <WAY>

A:Cross-references: GB:M83649; NID:g193225; PIDN:AAA37593.1; PID:g193226

A:Experimental source: BAM3 macrophage cell line

A:Note: sequence extracted from NCBI backbone (NCBIN:81544, NCBIP:81545)

R:Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S. Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993

A:Title: Aberrant transcription caused by the insertion of an early transposable element

A:Reference number: A47254; MUID:93189576

A:Accession: A47254

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-96 <ADA>

A:Cross-references: GB:S56490; NID:g298505; PIDN:AAB25700.1; PID:g298506

A:Experimental source: MRL lpr/lpr

A:Note: sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853, NCBIN:1268

C:Superfamily: NGF receptor repeat homology

C:Keywords: transmembrane protein

F:44-79/Domain: NGF receptor repeat homology <NGF>

F:81-124/Domain: NGF receptor repeat homology <NG4>

Query Match 86.4%; Score 51; DB 2; Length 327;  
Best Local Similarity 88.9%; Pred. No. 0.17;  
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TQNTKCRCK 10  
|||||

DB 118 TQNTKCRCK 126

## RESULT 5

I48700

gene ox40 protein - mouse

N:Alternate names: OX40 antigen

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 11-Jan-2000

C:Accession: I48700; I48334; S34377

R:Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J. J. Immunol. 151, 5261-5271, 1993

A:Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell

A:Reference number: I48700; MUID:94044750

A:Accession: I48700

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-272 <RES>

A:Cross-references: EMBL:Z21674; NID:g312827; PIDN:CAA79772.1; PID:g312828

R:Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N. Eur. J. Immunol. 25, 926-930, 1995

A:Title: Gene structure and chromosomal localization of the mouse homologue of rat OX

A:Reference number: I48334; MUID:95255413

A:Accession: I48334

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-14, 'G', 16-272 <RE>

A:Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819

C:Genetics:

A:Gene: Ox40

A:Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1

C:Superfamily: CD27 antigen; NGF receptor repeat homology

## Query Match

66.1%; Score 39; DB 2; Length 272;

Best Local Similarity 66.7%; Pred. No. 16;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TQNTKCRCK 10  
 ||:| |||:  
 Db 98 TQDTVCRCK 106

RESULT 6  
 OX40 homolog - human  
 C:Species: Homo sapiens (man)  
 C>Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 11-Jan-2000  
 C:Accession: 137552  
 R:Latza, U.; Burkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat  
 Eur. J. Immunol. 24, 677-683, 1994  
 A:Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment  
 A:Reference number: 137552; MUID:94170844  
 A:Accession: 137552  
 A:Status: preliminary; translated from GB/EMBL/DBDJ  
 A:Molecule type: mRNA  
 A:Residues: 1-277 <RES>  
 A:Cross-references: EMBL:X75962; NID:9472957; PIDN:CAA53576.1; PID:9472958  
 C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 66.1%; Score 39; DB 2; Length 277;  
 Best Local Similarity 66.7%; Pred. No. 16;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TQNTKCRCK 10  
 ||:| |||:  
 Db 102 TQDTVCRCK 110

RESULT 7  
 150610  
 T-cell surface glycoprotein CD8 alpha chain - chicken  
 C:Species: Gallus gallus (chicken)  
 C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
 C:Accession: 150610; S33350  
 R:Tregaskes, C.A.; Kong, F.K.; Paramithiotis, E.; Chen, C.L.; Ratcliffe, M.J.; Davison,  
 J. Immunol. 154, 4485-4494, 1995  
 A:Title: Identification and analysis of the expression of CD8 alpha beta and CD8 alpha  
 lymphocytes.  
 A:Reference number: 150609; MUID:95238946  
 A:Accession: 150610  
 A:Status: preliminary; translated from GB/EMBL/DBDJ  
 A:Molecule type: mRNA  
 A:Residues: 1-235 <TRE>  
 A:Cross-references: EMBL:Z22726; NID:9488149; PIDN:CAA80421.1; PID:9297781  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: glycoprotein

Query Match 62.7%; Score 37; DB 2; Length 235;  
 Best Local Similarity 50.0%; Pred. No. 32;  
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTQNTKCRCK 10  
 ||:| |||:  
 Db 208 KTRRRCRCK 217

RESULT 8  
 B36470  
 Wnt-2 protein - mouse  
 N:Alternate names: int-1 related protein  
 C:Species: Mus musculus (house mouse)  
 C>Date: 19-Apr-1991 #sequence\_revision 19-Apr-1991 #text\_change 15-Jun-1996  
 C:Accession: B36470; A43558  
 R:Gavin, B.J.; McMahon, J.A.; McMahon, A.P.  
 Genes Dev. 4, 2319-2332, 1990  
 A:Title: Expression of multiple novel Wnt-1/int-1-related genes during fetal and adult m  
 A:Reference number: A36470; MUID:91122634

A:Accession: B36470  
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual  
 A:Molecule type: mRNA  
 A:Residues: 1-360 <GAV>  
 R:McMahon, J.A.; McMahon, A.P.  
 Development 107, 643-650, 1989  
 A:Title: Nucleotide sequence, chromosomal localization and developmental expression o  
 A:Reference number: A43558; MUID:90126394  
 A:Accession: A43558  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-360 <MCM>  
 C:Superfamily: int-1 transforming protein

Query Match 62.7%; Score 37; DB 2; Length 360;  
 Best Local Similarity 66.7%; Pred. No. 44;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TQNTKCRCK 10  
 ||:| |||:  
 Db 319 TRMTRCKCK 327

RESULT 9  
 GOMST1  
 tumor necrosis factor receptor 1 precursor - mouse  
 N:Alternate names: tumor necrosis factor receptor, 55K  
 C:Species: Mus musculus (house mouse)  
 C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 01-Dec-2000  
 C:Accession: A38634; B40254; S16677; S19021; I54532; I57826  
 R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen,  
 Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991  
 A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto  
 A:Reference number: A38634; MUID:91187885  
 A:Accession: A38634  
 A:Molecule type: mRNA  
 A:Residues: 1-454 <LEW>  
 A:Cross-references: GB:M60468; NID:9199825; PIDN:AAA39751.1; PID:9199826  
 R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J  
 Mol. Cell. Biol. 11, 3020-3026, 1991  
 A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f  
 A:Reference number: A40254; MUID:91246168  
 A:Accession: B40254  
 A:Molecule type: mRNA  
 A:Residues: 1-454 <GO2>  
 A:Cross-references: GB:M60468; NID:9199825; PIDN:AAA39751.1; PID:9199826  
 R:Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissoneghis, A.M.; Gray, P.W.; Fel  
 Eur. J. Immunol. 21, 1649-1656, 1991  
 A:Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necro  
 A:Reference number: S16677; MUID:91285014  
 A:Accession: S16677  
 A:Molecule type: mRNA  
 A:Residues: 1-454 <BAR>  
 A:Cross-references: EMBL:X59238; NID:953578; PIDN:CAA41922.1; PID:953579  
 R:Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.  
 Immunogenetics 34, 338-340, 1991  
 A:Title: Molecular cloning and expression of the mouse Tnf receptor type b.  
 A:Reference number: S19021; MUID:92039815  
 A:Accession: S19021  
 A:Molecule type: mRNA  
 A:Residues: 1-454 <ROT>  
 A:Cross-references: EMBL:X57796; NID:954848; PIDN:CAA40936.1; PID:954849  
 R:Bebo, B.F.  
 Immunogenetics 39, 450-451, 1994  
 A:Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cel  
 A:Reference number: I54532; MUID:94245292  
 A:Accession: I54532  
 A:Status: translated from GB/EMBL/DBDJ  
 A:Molecule type: mRNA  
 A:Residues: 1-454 <RES>  
 A:Cross-references: GB:L26349; NID:9430732; PIDN:AAA59361.1; PID:9430733  
 R:Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.

Mol. Immunol. 30, 165-176, 1993  
A:Title: Genomic organization and promoter function of the murine tumor necrosis factor  
A:Reference number: I57826; MUID:93156721  
A:Accession: I57826  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-393, G', 395-454 <R2>  
A:Cross-references: GB:M76656; NID:g202100; PIDN:AAA0465.1; PID:g202102  
C:Comment: This protein is one of two distantly related receptors for both TNF-alpha (ca  
C:Genetics:  
A:Gene: TNFR-2  
A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1  
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>  
F:30-212/Domain: extracellular #status predicted <EXT>  
F:44-82/Domain: NGF receptor repeat homology <NG1>  
F:84-126/Domain: NGF receptor repeat homology <NG2>  
F:127-167/Domain: NGF receptor repeat homology <NG3>  
F:168-204/Domain: NGF receptor repeat homology <NG4>  
F:213-235/Domain: transmembrane #status predicted <MEM>  
F:236-454/Domain: intracellular #status predicted <INT>  
F:54,151,202/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 62.7%; Score 37; DB 1; Length 454;  
Best Local Similarity 75.0%; Pred. No. 53;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TQNTKRC 9  
|||||  
Db 161 TQNTVCNC 168

RESULT 10  
TQ9052  
hypothetical protein DBCCR1 - human  
C:Species: Homo sapiens (man)  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000  
C:Accession: TQ9052  
R:Habuchi, T.; Luscombe, M.; Elder, P.A.; Knowles, M.A.  
Genomics 48, 277-288, 1998  
A:Title: Structure and methylation-based silencing of a gene (DBCCR1) within a candidate  
A:Reference number: Z16537; MUID:98207242  
A:Accession: TQ9052  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-761 <HAB>  
A:Cross-references: EMBL:AF027734; NID:g3041877; PIDN:AAC39691.1; PID:g3041877  
A:Experimental source: tissue type: brain; developmental stage: fetal and infant  
C:Genetics:  
A:Gene: DBCCR1  
A:Map position: 9q32-q33  
A:Note: IB3089A  
C:Superfamily: human hypothetical protein DBCCR1

Query Match 62.7%; Score 37; DB 2; Length 761;  
Best Local Similarity 62.5%; Pred. No. 80;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 QNTKCRCK 10  
|||||  
Db 261 QNSQCRQC 268

RESULT 11  
D90674  
hypothetical protein ECs0364 [imported] - Escherichia coli (strain O157:H7, substrain R1  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 18-Jul-2001  
C:Accession: D90674

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g  
A:Reference number: A99629, MUID:21156231; PMID:11258796  
A:Accession: D90674  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-86 <HAY>  
A:Cross-references: GB:BA000007; PIDN:BA833787.1; PID:g13359821; GSPDB:GN00154  
A:Experimental source: strain O157:H7, substrain R1MD 0509952  
C:Genetics:  
A:Gene: ECs0364

Query Match 61.0%; Score 36; DB 2; Length 86;  
Best Local Similarity 71.4%; Pred. No. 21;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 NTKCRCK 10  
|||||  
Db 5 NTKCQCQ 11

RESULT 12  
G85524  
hypothetical protein Z0404 [imported] - Escherichia coli (strain O157:H7, substrain E  
C:Species: Escherichia coli  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C:Accession: G85524  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May  
iller, L.; Grothbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: G85524  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-86 <STO>  
A:Cross-references: GB:AE005174; NID:g12513132; PIDN:AAG54659.1; GSPDB:GN00145; UWGP:  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: Z0404

Query Match 61.0%; Score 36; DB 2; Length 86;  
Best Local Similarity 71.4%; Pred. No. 21;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 NTKCRCK 10  
|||||  
Db 5 NTKCQCQ 11

RESULT 13  
F81938  
cytochrome c552 NMA0925 precursor [similarity] - Neisseria meningitidis (strain Z2491  
C:Species: Neisseria meningitidis  
C:Date: 01-Sep-2000 #sequence\_revision 01-Sep-2000 #text\_change 02-Feb-2001  
C:Accession: F81938  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo  
; Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Ouail, M.A.; Rajandre  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491  
A:Reference number: A81775; MUID:20222556  
A:Accession: F81938  
A:Molecule type: DNA  
A:Residues: 1-163 <PAR>  
A:Cross-references: GB:ALI62754; GB:ALI57959; NID:g7379424; PIDN:CAB84197.1; PID:g737  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: NMA0919; NMA0925  
C:Superfamily: T. aquaticus cytochrome c552; cytochrome c6 homology



QY 2 TQNTKCRCK 10  
||:|:|:  
Db 21 TOTSKCECO 29

Search completed: August 14, 2002, 15:18:58  
Job time: 686 sec

10

9

DB

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 15:22:14 ; Search time 187.61 Seconds  
(without alignments)  
9.221 Million cell updates/sec

Title: US-09-499-662-1  
Perfect score: 59  
Sequence: 1 RTQNTKCRCK 10

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : SPTREMBL\_19:\*
- 1: sp\_archaea:\*
  - 2: sp\_bacteria:\*
  - 3: sp\_fungi:\*
  - 4: sp\_human:\*
  - 5: sp\_invertebrate:\*
  - 6: sp\_mammal:\*
  - 7: sp\_mhc:\*
  - 8: sp\_organelle:\*
  - 9: sp\_phase:\*
  - 10: sp\_plant:\*
  - 11: sp\_rodent:\*
  - 12: sp\_virus:\*
  - 13: sp\_vertebrate:\*
  - 14: sp\_unclassified:\*
  - 15: sp\_rvirus:\*
  - 16: sp\_bacteriap:\*
  - 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	150	11	Q9R230 rattus norv
2	59	100.0	310	6	Q9GK28 macaca arc
3	59	100.0	314	4	Q14293 homo sapien
4	59	100.0	327	6	Q97491 ovis aries
5	59	100.0	328	6	Q9BDF0 Q9bdp0 aotus trivi
6	59	100.0	331	6	Q9TSN4 Q9tsn4 macaca fasc
7	59	100.0	331	6	Q9GK36 Q9gk36 macaca assa
8	59	100.0	331	6	Q9BDN4 Q9bdn4 cercopithec
9	59	100.0	331	6	Q9BDN0 Q9bdn0 macaca neme
10	59	100.0	333	6	Q9BDF2 Q9bdp2 macaca mula
11	56	94.9	334	6	Q9GL40 Q9gl40 macaca mula
12	51	86.4	327	11	Q9DCQ1 Q9dcq1 mus musculu
13	49	83.1	263	6	Q9XS60 Q9xs60 oryctolagus
14	49	83.1	319	6	Q9TV79 Q9tv79 oryctolagus
15	49	83.1	320	6	Q9XS29 Q9xs29 oryctolagus
16	45	76.3	357	13	Q9DF34 Q9df34 brachydanio

17	44	74.6	385	11	Q9JUL5	Q9jjl5 mus musculu
18	42	71.2	438	13	Q9DFV0	Q9dfv0 brachydanio
19	41	69.5	368	13	Q57408	Q57408 meleagris g
20	41	69.5	381	11	Q9JUL6	Q9jjl6 mus musculu
21	41	69.5	381	11	Q9QZM4	Q9qzm4 mus musculu
22	41	69.5	797	4	Q43686	Q43686 homo sapien
23	40	67.8	368	13	Q9PW79	Q9pw79 gallus gall
24	40	67.8	368	13	Q9IAK7	Q9iar7 gallus gall
25	40	67.8	468	4	Q9E62	Q9e62 homo sapien
26	40	67.8	567	12	Q91TQ7	Q91tg7 tupala herp
27	39	66.1	186	12	Q72735	Q72735 cowpox viru
28	39	66.1	186	12	Q9Y987	Q9yp87 cowpox viru
29	39	66.1	186	12	Q9WJB4	Q9wjb4 vaccinia vi
30	39	66.1	186	12	Q91LR5	Q91lr5 vaccinia vi
31	38	64.4	136	5	Q9XZ89	Q9xz89 plasmodium
32	38	64.4	144	13	Q73822	Q73822 brachydanio
33	38	64.4	188	13	Q73682	Q73682 brachydanio
34	38	64.4	762	10	Q9LE55	Q9le55 oryza sativ
35	38	64.4	843	6	Q9TUQ3	Q9tuq3 sus scrofa
36	38	64.4	2209	5	Q9U0G6	Q9u0g6 plasmodium
37	38	64.4	2277	5	Q9U0G5	Q9u0g5 plasmodium
38	37	62.7	72	15	Q86003	Q86003 human immun
39	37	62.7	72	15	Q75560	Q75560 human immun
40	37	62.7	72	15	F88718	F88718 human immun
41	37	62.7	86	15	Q99BV5	Q99bv5 human immun
42	37	62.7	86	15	Q99BV4	Q99bv4 human immun
43	37	62.7	86	15	Q99BV3	Q99bv3 human immun
44	37	62.7	101	15	Q9Y1Q4	Q9y1q4 human immun
45	37	62.7	101	15	Q90810	Q90810 human immun

ALIGNMENTS

RESULT 1

Q9R230	ID	Q9R230	PRELIMINARY;	PRT;	150 AA.
AC	Q9R230;				
DT	01-MAY-2000	(Tremblrel. 13, Created)			
DT	01-MAY-2000	(Tremblrel. 13, Last sequence update)			
DT	01-JUN-2001	(Tremblrel. 17, Last annotation update)			
DE	FAS RECEPTOR (FRAGMENT).				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=WISTAR; TISSUE=CORPUS LUTEUM;				
RA	Lareu R.R.; Dharmarajan A.;				
RT	"Cloning and expression of Fas and Fas Ligand in the apoptotic rat				
RT	corpus luteum."				
RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF104034; AAD20221.1; -.				
DR	HSSP; P25942; ICDF.				
DR	InterPro; IPR001368; TNFR_c6.				
DR	Pfam; PF00020; TNFR_c6; 2.				
DR	SMART; SM00208; TNFR; 2.				
DR	PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN1.				
DR	PROSITE; PS50050; TNFR_NGFR_2; 1.				
KW	Receptor.				
FT	NON_TER 1 1				
FT	NON_TER 150 150				
SQ	SEQUENCE 150 AA; 16644 MW; 7DEC76EC40A6BA4F CRC64;				

Query Match 100.0%; Score 59; DB 11; Length 150;  
Best Local Similarity 100.0%; Pred. No. 0.00026;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTQNTKCRCK 10  
Db 112 RTQNTKCRCK 121

```
RESULT 2
Q9GK28          PRELIMINARY;          PRT;    310 AA.
AC  Q9GK28;
DT  01-MAR-2001 (TrEMBLrel. 16, Created)
DT  01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  FAS ANTIGEN APO-1/CD95.
GN  FAS.
OS  Macaca arctoides (Stump-tailed macaque).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC  Cercopithecoidea; Macaca.
OX  NCBI_TaxID=9540;
RN  [1]
SEQUENCE FROM N.A.
RP  Chi L., Shui B., Jiang H., Zhang Y.R., He F.Q., Cai Y.Y.;
RT  "Cloning of fas gene in stump-tailed monkey.";
RL  Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF332357; AAG49394.1; -.
DR  HSSP; P25445; 1DDF.
DR  InterPro; IPR000488; Death.
DR  InterPro; IPR001368; TNFR_c6.
DR  Pfam; PF00531; death; 1.
DR  Pfam; PF00020; TNFR_c6; 2.
DR  SMART; SM00005; DEATH; 1.
DR  SMART; SM00208; TNFR; 2.
DR  PROSITE; PS50017; DEATH_DOMAIN; 1.
DR  PROSITE; PS00652; TNFR_NGFR_1; 1.
DR  PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ  SEQUENCE 310 AA; 34806 MW; C5C79BF1F804A419 CRC64;

Query Match          100.0%; Score 59; DB 6; Length 310;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 RTQNTKCRCK 10
    |||
Db  121 RTQNTKCRCK 130

RESULT 3
Q14293          PRELIMINARY;          PRT;    314 AA.
AC  Q14293;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  FAS SOLUBLE PROTEIN.
GN  FAS/APO 1.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
SEQUENCE FROM N.A.
RP  Cascino I., Flucci G., Papoff G., Ruberti G.;
RL  "Three functional soluble forms of the human apoptosis-inducing Fas
RT  molecule are produced by alternative splicing.";
RL  J. Immunol. 154:2706-2713(1995).
DR  EMBL; Z47993; CA88031.1; -.
DR  HSSP; P25445; 1DDF.
DR  InterPro; IPR000488; Death.
DR  InterPro; IPR001368; TNFR_c6.
DR  Pfam; PF00531; death; 1.
DR  Pfam; PF00020; TNFR_c6; 2.
DR  SMART; SM00005; DEATH; 1.
DR  SMART; SM00208; TNFR; 2.
DR  PROSITE; PS50017; DEATH_DOMAIN; 1.

RESULT 4
Q97491          PRELIMINARY;          PRT;    327 AA.
AC  Q97491;
DT  01-MAY-1999 (TrEMBLrel. 10, Created)
DT  01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT  01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE  FAS PROTEIN.
GN  FAS.
OS  Ovis aries (Sheep).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC  Bovidae; Caprinae; Ovis.
OX  NCBI_TaxID=9940;
RN  [1]
SEQUENCE FROM N.A.
RP  TISSUE-LYMPHOCYTE;
RA  Takagi M., Takahashi H., Kabeya H., Ohashi K., Sugimoto C., Onuma M.;
RT  "Cloning of sheep fas antigen.";
RL  Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AB011671; BAA37093.1; -.
DR  HSSP; P25445; 1DDF.
DR  InterPro; IPR000488; Death.
DR  InterPro; IPR001368; TNFR_c6.
DR  Pfam; PF00531; death; 1.
DR  Pfam; PF00020; TNFR_c6; 3.
DR  SMART; SM00005; DEATH; 1.
DR  SMART; SM00208; TNFR; 3.
DR  PROSITE; PS50017; DEATH_DOMAIN; 1.
DR  PROSITE; PS00652; TNFR_NGFR_1; 1.
DR  PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ  SEQUENCE 327 AA; 36928 MW; 5CFEE844B2BE387A CRC64;

Query Match          100.0%; Score 59; DB 6; Length 327;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 RTQNTKCRCK 10
    |||
Db  120 RTQNTKCRCK 129

RESULT 5
Q9BDP0          PRELIMINARY;          PRT;    328 AA.
AC  Q9BDP0;
DT  01-JUN-2001 (TrEMBLrel. 17, Created)
DT  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  FAS ANTIGEN CD95.
OS  Aotus trivirgatus (Night monkey) (Douroucoul).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotus.
OX  NCBI_TaxID=9505;
RN  [1]
SEQUENCE FROM N.A.
RP  Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.;
RX  MEDLINE=21383618; PubMed=11491535;
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RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344835; AAK37531.1; -.
DR HSSP; P25445; 1DDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
FT VARIANT 157 158 S -> T.
SQ SEQUENCE 328 AA; 37332 MW; B3DED1DAC97D6353 CRC64;

Query Match 100.0%; Score 59; DB 6; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
Db 120 RTQNTKCRCK 129

RESULT 6
Q9TSN4 PRELIMINARY; PRT; 331 AA.
AC Q9TSN4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DEATH RECEPTOR FAS (APO-1/CD95).
GN FAS.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20237686; PubMed=10773350;
RA Murayama Y., Teruo K., Inoue-Murayama M.;
RT "Molecular cloning and characterization of cynomolgus monkey Fas.";
RL Hum. Immunol. 61:474-485(2000).
DR EMBL; AB031420; BAA83551.1; -.
DR HSSP; P25445; 1DDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 331 AA; 37265 MW; OC617508081B05DF CRC64;

Query Match 100.0%; Score 59; DB 6; Length 331;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
Db 121 RTQNTKCRCK 130

RESULT 7
Q9GK36 PRELIMINARY; PRT; 331 AA.
AC Q9GK36;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE FAS ANTIGEN APO-1/CD95.
GN FAS.
OS Macaca assamensis (Assam's macaque) (Assam's monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9551;
RN [1]
RP SEQUENCE FROM N.A.
RA Chi L., Shui B., Jiang H., He F.Q., Zhang Y.R., Cai Y.Y.;
RT "Cloning and sequencing of bear monkey Fas antigen cDNA.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF326208; AAG49382.1; -.
DR HSSP; P25445; 1DDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 331 AA; 37167 MW; CE58DB046C67834F CRC64;

Query Match 100.0%; Score 59; DB 6; Length 331;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
Db 121 RTQNTKCRCK 130

RESULT 8
Q9BDN4 PRELIMINARY; PRT; 331 AA.
AC Q9BDN4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE FAS ANTIGEN CD95.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercocebus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344843; AAK37602.1; -.
DR HSSP; P25445; 1DDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
FT VARIANT 44 44 I -> V.
FT VARIANT 47 47 E -> Q.
FT VARIANT 55 55 E -> D.

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FT VARIANT 60 R -> H.
FT VARIANT 61 N -> S.
FT VARIANT 77 E -> G.
FT VARIANT 95 G -> A.
FT VARIANT 282 E -> G.
FT VARIANT 298 G -> D.
FT VARIANT 300 C -> *.
SQ SEQUENCE 331 AA; 37277 MW; 1D843C4DE1D343F4 CRC64;

Query Match 100.0%; Score 59; DB 6; Length 331;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
DB 121 RTQNTKCRCK 130

RESULT 9
ID Q9BDN0 PRELIMINARY; PRT; 331 AA.
AC Q9BDN0:
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE FAS ANTIGEN CD95.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
RT "Cloning, sequencing, and homology analysis of nonhuman primate
Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344850; AAK37610.1; -.
DR HSSP; P25445; 1DDF.
DR InterPro; IPR000488; Death.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
FT VARIANT 75 75 V -> A.
FT VARIANT 89 89 E -> K.
FT VARIANT 196 196 E -> K.
FT VARIANT 201 201 R -> H.
SQ SEQUENCE 331 AA; 37254 MW; A6CFE3DA12C94765 CRC64;

Query Match 100.0%; Score 59; DB 6; Length 331;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
DB 121 RTQNTKCRCK 130

RESULT 10
ID Q9BDP2 PRELIMINARY; PRT; 333 AA.
AC Q9BDP2:
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE FAS ANTIGEN CD95.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;

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OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
RT "Cloning, sequencing, and homology analysis of nonhuman primate
Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344833; AAK37529.1; -.
DR HSSP; P25445; 1DDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
FT VARIANT 75 75 V -> A.
FT VARIANT 89 89 E -> K.
FT VARIANT 196 196 E -> K.
FT VARIANT 201 201 R -> H.
SQ SEQUENCE 333 AA; 37468 MW; 98C17F766762F287 CRC64;

Query Match 100.0%; Score 59; DB 6; Length 333;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
DB 121 RTQNTKCRCK 130

RESULT 11
ID Q9GL40 PRELIMINARY; PRT; 334 AA.
AC Q9GL40:
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE FAS ANTIGEN.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Shui B., Chi L., Zhang Y.R.;
RT "Cloning and sequencing of Rhesus monkey Fas antigen cDNA.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY007572; AAG16762.1; -.
DR HSSP; P25445; 1DDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 334 AA; 37531 MW; 2DC5B1661C3191C6 CRC64;

Query Match 94.9%; Score 56; DB 6; Length 334;
Best Local Similarity 90.0%; Pred. No. 0.002;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10

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Db 121 RTQNTKCRCK 130

# RESULT 12

Q9DCQ1 PRELIMINARY; PRT; 327 AA.  
 AC Q9DCQ1: 2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY, MEMBER 6.  
 GN TNFRSF6.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 PC STRAIN=C57BL/6J; TISSUE=KIDNEY;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamane A. I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staehli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).  
 DR EMBL; AK002590; BAB22211.1; -  
 DR HSSP; P25445; 1DDF.  
 DR MGD; MGI:95484; Tnfrsf6.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 3.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00208; TNFR; 3.  
 DR PROSITE; PS00017; DEATH\_DOMAIN; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 SQ SEQUENCE 327 AA; 37437 MW; D8DA95CA525CED56 CRC64;

Query Match 86.4%; Score 51; DB 11; Length 327;

Best Local Similarity 88.9%; Pred. No. 0.02; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TQNTKCRCK 10

Db 118 TQNTKCRCK 126

# RESULT 13

Q9XS60 PRELIMINARY; PRT; 263 AA.  
 AC Q9XS60:  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE FAS ANTIGEN SPLICED VARIANT.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RA Isono T., Tanbe Y., Nagano Y., Seto A.;  
 RT "Splicing and allelic variation in the rabbit Fas antigen gene."  
 RL submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB021297; BAA78429.1; -  
 DR HSSP; O14763; 1D4V.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 3.  
 DR SMART; SM00208; TNFR; 3.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 SQ SEQUENCE 263 AA; 30374 MW; 6D76782ADEB1BFD7 CRC64;

Query Match 83.1%; Score 49; DB 6; Length 263;

Best Local Similarity 100.0%; Pred. No. 0.041; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QNTKCRCK 10

Db 108 QNTKCRCK 115

# RESULT 14

Q9TV79 PRELIMINARY; PRT; 319 AA.  
 AC Q9TV79:  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE B-TYPE FAS ANTIGEN.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RA Isono T., Tanbe Y., Nagano Y., Seto A.;  
 RT "Splicing and allelic variation in the rabbit Fas antigen gene."  
 RL submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB021298; BAA78430.1; -  
 DR HSSP; P25445; 1DDF.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR002885; PPR.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00531; death; 1.  
 DR Pfam; PF00020; TNFR\_c6; 3.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00208; TNFR; 3.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 SQ SEQUENCE 319 AA; 35961 MW; 06FA0033B1846591 CRC64;

Query Match 83.1%; Score 49; DB 6; Length 319;

Best Local Similarity 100.0%; Pred. No. 0.048; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QNTKCRCK 10

Db 108 QNTKCRCK 115

# RESULT 15

Q9XS29 PRELIMINARY; PRT; 320 AA.  
 AC Q9XS29:  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

Search completed: August 14, 2002, 15:22:14  
Job time: 682 sec



!!AA\_MULTIPLE\_ALIGNMENT 1.0  
Pileup of: us\*

Symbol comparison table: GenRunData:blosum62.cmp CompCheck: 1102

GapWeight: 8  
GapLengthWeight: 2

lightchain.msf MSF: 238 Type: P August 15, 2002 08:42 Check: 3138 ..

Name: us-09-499-662-127 Len: 238 Check: 7077 Weight: 1.00  
Name: us-09-499-662-131 Len: 238 Check: 6752 Weight: 1.00  
Name: us-09-499-662-129 Len: 238 Check: 7131 Weight: 1.00  
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09/499,662

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:15:33 ; Search time 230.21 Seconds  
(without alignments)  
37.634 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	205	100.0	238 19	AAW83031 Anti-Fas humanised
2	205	100.0	238 19	AAW83032 Anti-Fas humanised
3	205	100.0	238 19	AAW83033 Anti-Fas humanised
4	205	100.0	238 19	AAW83034 Anti-Fas humanised
5	205	100.0	238 19	AAW83035 Anti-Fas humanised
6	205	100.0	238 19	AAW83042 Anti-Fas MAB HFE7A
7	205	100.0	238 21	AA14748 Mouse anti-Fas ant
8	205	100.0	238 21	AA14772 Humanised anti-Fas
9	205	100.0	238 21	AA14773 Humanised anti-Fas
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12	205	100.0	238	21	AA14778 Humanised anti-Fas
13	205	100.0	238	21	AAW90898 Murine anti-Fas an
14	205	100.0	238	21	AAW90922 Humanised anti-Fas
15	205	100.0	238	21	AAW90923 Humanised anti-Fas
16	205	100.0	238	21	AAW90924 Humanised anti-Fas
17	205	100.0	238	21	AAW90927 Humanised HFE7A de
18	205	100.0	238	21	AAW90928 Humanised HFE7A de
19	205	100.0	238	21	AAW90930 Humanised anti-Fas
20	205	100.0	238	21	AAW90931 Humanised anti-Fas
21	205	100.0	238	21	AAW90932 Humanised anti-Fas
22	198	96.6	111	20	AAV23781 Light chain variab
23	198	96.6	111	20	AAV18123 Light chain sequen
24	198	96.6	131	16	AAV70202 Humanized antibody
25	198	96.6	131	20	AAV23779 Fight chain variab
26	198	96.6	131	20	AAV18126 Fight chain sequen
27	198	96.6	132	16	AAV70189 Mouse MAb 3B9 high
28	198	96.6	132	20	AAV23767 Light chain variab
29	198	96.6	132	20	AAV18120 Light chain sequen
30	197	96.1	106	14	AAV33309 MAb15 light chain.
31	197	96.1	106	14	AAV85197 Light chain amino
32	197	96.1	111	10	AAV90541 Immunoglobulin L c
33	197	96.1	111	15	AAV55123 Mouse anti-HIV mu5
34	197	96.1	111	15	AAV55127 Mouse-human chimere
35	197	96.1	111	15	AAV60302 Anti HIV antibody
36	197	96.1	111	15	AAV60306 Chimeric anti HIV
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39	197	96.1	131	10	AAV90543 Amino acids sequen
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41	197	96.1	222	18	AAV01751 MAb1 monoclonal ant
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ALIGNMENTS

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DT 15-MAR-1999 (first entry)	
DE	Anti-Fas humanised antibody HFE7A light chain HH type.
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KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;	
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;	
KW systemic lupus erythematosus; graft versus host disease;	
KW Sjogren syndrome; pernicious anaemia; Addison's disease;	
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;	
KW rheumatoid arthritis; autoimmune haemolytic anaemia;	
KW myasthenia gravis; multiple sclerosis; Basedow's disease;	
KW thrombopenia purpura; insulin-dependent diabetes; allergy;	
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;	
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;	
KW transplant rejection; therapy.	
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XX 08-OCT-1998.
XX
XX 30-MAR-1998; 98AU-0059701.
XX
XX 08-OCT-1997; 97JP-0276064.
XX 01-APR-1997; 97JP-0082953.
XX 25-JUN-1997; 97JP-0169088.
XX
XX (SANY ) SANKYO CO LTD.
XX
XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
XX Masahiko O, Nobufusa S, Shin Y, Tohru T;
XX
XX WPI; 1998-543440/47.
XX N-PSDB; AAV70074.
XX
XX New antibodies and proteins bind conserved epitope of Fas antigen -
XX used to evaluate drugs in animal models and to treat Fas-associated
XX diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
XX myocarditis, hepatitis and AIDS
XX
XX Claim 21; Page 199-199; 292pp; English.
XX
XX This is the amino acid sequence of the HH type humanised light
XX chain of murine anti-human Fas monoclonal antibody HFE7A.
XX Humanisation of the murine sequence (see AAW83042) entailed making
XX P47A, K49R, H80S, P81R, V82L, E84P, E85A, A87F and T89V amino acid
XX substitutions; these residues are conserved in the human light
XX chain (kappa chain). Host cell Escherichia coli PHSGH7 SANK 73497
XX harbors plasmid PHSGH7 carrying a fusion fragment of the humanised
XX HH type HFE7A light chain and DNA encoding the region of human
XX immunoglobulin kappa chain, and is deposited as FERM BP-6073
XX (claimed). The invention provides methods for producing humanised
XX antibodies by culturing host cells. Humanised versions of HFE7A
XX (see AAW83031-37), like native HFE7A, are capable of inducing
XX apoptosis in abnormal cells expressing Fas, and of inhibiting
XX Fas-induced apoptosis in normal cells. The humanised antibodies
XX are used to evaluate, in animal models, treatments of diseases that
XX involve Fas/Fas ligand interactions, and also to treat such
XX diseases, including autoimmune disease (e.g. systemic lupus
XX erythematosus, Hashimoto's disease, graft versus host disease,
XX Sjogren syndrome, pernicious anaemia, Addison's disease,
XX scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid
XX arthritis, autoimmune haemolytic anaemia, sterility, myasthenia
XX gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura
XX and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
XX myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
XX anaemia, hepatitis, AIDS and transplant rejection (all claimed).
XX
XX Sequence 238 AA;
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XX Query Match 100.0%; Score 205; DB 19; Length 238;
XX Best Local Similarity 39.7%; Pred. No. 1.2e-05;
XX Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;
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XX AC AAW83032;
XX
XX DT 15-MAR-1999 (first entry)
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XX DE Anti-Fas humanised antibody HFE7A light chain HM type.
XX
XX KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
XX apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
XX systemic lupus erythematosus; graft versus host disease;
XX Sjogren syndrome; pernicious anaemia; Addison's disease;
XX scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
XX rheumatoid arthritis; autoimmune haemolytic anaemia;
XX myasthenia gravis; multiple sclerosis; Basedow's disease;
XX thrombopenia purpura; insulin-dependent diabetes; allergy;
XX atopy; arteriosclerosis; myocarditis; cardiomyopathy;
XX glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
XX transplant rejection; therapy.
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XX OS Homo sapiens.
XX Synthetic.
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XX 30-MAR-1998; 98AU-0059701.
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XX 08-OCT-1997; 97JP-0276064.
XX 01-APR-1997; 97JP-0082953.
XX 25-JUN-1997; 97JP-0169088.
XX
XX (SANY ) SANKYO CO LTD.
XX
XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
XX Masahiko O, Nobufusa S, Shin Y, Tohru T;
XX
XX WPI; 1998-543440/47.
XX N-PSDB; AAV70075.
XX
XX New antibodies and proteins bind conserved epitope of Fas antigen -
XX used to evaluate drugs in animal models and to treat Fas-associated
XX diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
XX myocarditis, hepatitis and AIDS
XX
XX Claim 21; Page 200; 292pp; English.
XX

```

```
CC This is the amino acid sequence of the HM type humanised light
CC chain of murine anti-human Fas monoclonal antibody HFE7A.
CC Humanisation of the murine sequence (see AAW83042) entailed making
CC P47A and K49R amino acid substitutions; these residues are
CC conserved in the human light (kappa) chain. Host cell E. coli
CC PHSGHM17 SANK 73597 harbors plasmid PHSGHM17 carrying a fusion
CC fragment of the humanised HM type HFE7A light chain and DNA
CC encoding the region of human immunoglobulin kappa chain, and is
CC deposited as FERM BP-6072 (claimed). The invention provides
CC methods for producing humanised antibodies by culturing host
CC cells. Humanised versions of HFE7A (see AAW83031-37), like native
CC HFE7A, are capable of inducing apoptosis in abnormal cells
CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal
CC cells. The humanised antibodies are used to evaluate, in animal
CC models, treatments of diseases that involve Fas/Fas ligand
CC interactions, and also to treat such diseases, including autoimmune
CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
CC graft versus host disease, Sjogren syndrome, pernicious anaemia,
CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
CC sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
CC thrombopenia purpura and insulin-dependent diabetes), allergies,
CC atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
CC nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
CC rejection (all claimed).
XX Sequence 238 AA;

Query Match 100.0%; Score 205; DB 19; Length 238;
Best Local Similarity 39.7%; Pred. No. 1.2e-05;
Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

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Db 104 eedaatyccqgsnedprt 121

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XX AAW83033;
XX
XX 15-MAR-1999 (first entry)
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XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
KW systemic lupus erythematosus; graft versus host disease;
KW Sjogren syndrome; pernicious anaemia; Addison's disease;
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KW rheumatoid arthritis; autoimmune haemolytic anaemia;
KW myasthenia gravis; multiple sclerosis; Basedow's disease;
KW thrombopenia purpura; insulin-dependent diabetes; allergy;
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KW transplant rejection; therapy.
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XX Homo sapiens.
OS Synthetic.
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XX 08-OCT-1998.
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XX 30-MAR-1998; 98AU-0059701.
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PR 25-JUN-1997; 97JP-0169088.
XX
XX (SANY ) SANKYO CO LTD.
PA
XX
XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
XX
XX WPI: 1998-543440/47.
DR N-PSDB: AAV70076.
DR
XX
XX New antibodies and proteins bind conserved epitope of Fas antigen -
XX used to evaluate drugs in animal models and to treat Fas-associated
XX diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
XX myocarditis, hepatitis and AIDS
XX
XX Claim 21; Page 202; 292pp; English.
XX
XX This is the amino acid sequence of the MM type humanised light
XX chain of murine anti-human Fas monoclonal antibody HFE7A. E. coli
XX SANK 73697 harbors plasmid PHSGMM6 carrying a fusion fragment of the
XX humanised MM type HFE7A light chain and DNA encoding the region of
XX human kappa chain, and is deposited as FERM BP-6071 (claimed). The
XX invention provides methods for producing humanised antibodies by
XX culturing host cells. Humanised versions of HFE7A (see AAW83031-37),
XX like native HFE7A, are capable of inducing apoptosis in abnormal
XX cells expressing Fas, and of inhibiting Fas-induced apoptosis in
XX normal cells. The humanised antibodies are used to evaluate, in
XX animal models, treatments of diseases that involve Fas/Fas ligand
XX interactions, and also to treat such diseases, including autoimmune
XX disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
XX graft versus host disease, Sjogren syndrome, pernicious anaemia,
XX Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
XX disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
XX sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
XX thrombopenia purpura and insulin-dependent diabetes), allergies,
XX atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
XX nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
XX rejection (all claimed).
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Query Match 100.0%; Score 205; DB 19; Length 238;
Best Local Similarity 39.7%; Pred. No. 1.2e-05;
Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

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KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;  
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;  
KW systemic lupus erythematosus; graft versus host disease;  
KW Sjogren syndrome; pernicious anaemia; Addison's disease;  
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
KW rheumatoid arthritis; autoimmune haemolytic anaemia;  
KW myasthenia gravis; multiple sclerosis; Basedow's disease;  
KW thrombopenia purpura; insulin-dependent diabetes; allergy;  
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
KW transplant rejection; therapy.  
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OS Homo sapiens.  
OS Synthetic.

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FT Protein /label= Sig\_peptide 21..238  
FT Region /label= Mat\_protein 21..131  
FT Region /label= Variable 132..238  
FT Region /label= Constant 44..58  
FT Region /label= CDR\_L1 /note= "claim 9"  
FT Region /label= CDR\_L2 /note= "claim 9"  
FT Region /label= CDR\_L3 /note= "claim 9"  
FT Region /note= "claim 9"  
XX AU9859701-A.  
XX  
XX 08-OCT-1998.  
XX  
XX 30-MAR-1998; 98AU-0059701.  
XX  
XX 08-OCT-1997; 97JP-0276064.  
XX 01-APR-1997; 97JP-0082953.  
XX 25-JUN-1997; 97JP-0169086.  
XX  
XX (SANY ) SANKYO CO LTD.  
XX  
XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;  
XX Masahiko O, Nobufusa S, Shin Y, Tohru T;  
XX  
XX WPI; 1998-543440/47.  
XX  
XX N-PSDB; AAV70077.  
XX  
XX New antibodies and proteins bind conserved epitope of Fas antigen -  
XX used to evaluate drugs in animal models and to treat Fas-associated  
XX diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
XX myocarditis, hepatitis and AIDS  
XX  
XX Claim 21; Page 218; 292pp; English.  
XX  
XX This is the amino acid sequence of the PDHH type humanised light

CC chain of murine anti-human Fas monoclonal antibody HFE7A.  
CC Humanisation of the murine sequence (see AAW83042) entailed making  
CC D1E, P47A, K49R, H80S, P81R, V82L, E84P, T89V and R107K  
CC amino acid substitutions; these residues are conserved in the  
CC human light chain (kappa chain). Host cell Escherichia coli  
CC PHSH5 SANK 70398 harbors plasmid PHSH5 carrying a fusion  
CC fragment of the humanised PDHH type HFE7A light chain and DNA  
CC encoding the region of human immunoglobulin kappa chain, and is  
CC deposited as FERM BP-6274 (claimed). The invention provides  
CC methods for producing humanised antibodies by culturing host  
CC cells. Humanised versions of HFE7A (see AAW83031-37), like native  
CC HFE7A, are capable of inducing apoptosis in abnormal cells  
CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal  
CC cells. The humanised antibodies are used to evaluate, in animal  
CC models, treatments of diseases that involve Fas/Fas ligand  
CC interactions, and also to treat such diseases, including autoimmune  
CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,  
CC graft versus host disease, Sjogren syndrome, pernicious anaemia,  
CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,  
CC sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,  
CC thrombopenia purpura and insulin-dependent diabetes), allergies,  
CC atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular  
CC nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant  
CC rejection (all claimed).  
XX  
XX Sequence 238 AA:  
SQ

Query Match 100.0%; Score 205; DB 19; Length 238;  
Best Local Similarity 39.7%; Pred. NO. 1.2e-05;  
Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KASQSVYDGDGSMYNNKXXXXXXXXXXXXXXXXXASNLXXXXXXXXXXXXXXXXXXXXX 60  
Db 44 KASQSVYDGDGSMYNNKXXXXXXXXXXXXXXXXXASNLXXXXXXXXXXXXXXXXXXXXX 103

Oy 61 XXXXXXXXQSQSNEDPRT 78  
Db 104 pefavyyccgsnedprt 121

RESULT 5  
AAW83035  
ID AAW83035 standard; Protein; 238 AA.  
XX  
AC AAW83035;  
XX  
DT 15-MAR-1999 (first entry)  
XX  
DE Anti-Fas humanised antibody HFE7A light chain PDHH type.  
XX  
KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;  
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;  
KW systemic lupus erythematosus; graft versus host disease;  
KW Sjogren syndrome; pernicious anaemia; Addison's disease;  
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
KW rheumatoid arthritis; autoimmune haemolytic anaemia;  
KW myasthenia gravis; multiple sclerosis; Basedow's disease;  
KW thrombopenia purpura; insulin-dependent diabetes; allergy;  
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy; AIDS;  
KW transplant rejection; therapy.  
XX  
OS Homo sapiens.  
OS Synthetic.

FH Key Location/Qualifiers  
FT Peptide 1..20  
FT Protein /label= Sig\_peptide 21..238  
FT Region /label= Mat\_protein 21..131

FT                    /label= Variable  
 FT                    132...238  
 FT                    /label= Constant  
 FT                    44..58  
 FT                    /label= CDR\_L1  
 FT                    /note= "claim 9"  
 FT                    74..80  
 FT                    /label= CDR\_L2  
 FT                    /note= "claim 9"  
 FT                    113..121  
 FT                    /label= CDR\_L3  
 FT                    /note= "claim 9"

XX AU9859701-A.

XX 08-OCT-1998.

XX 30-MAR-1998; 98AU-0059701.

XX 08-OCT-1997; 97JP-0276064.

XX 01-APR-1997; 97JP-0082953.

XX 25-JUN-1997; 97JP-0169088.

XX (SANY ) SANKYO CO LTD.

XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;

XX Masahiko O, Nobufusa S, Shin Y, Tohru T;

XX WPI: 1998-543440/47.

XX N-PSDB; AAV70078.

XX New antibodies and proteins bind conserved epitope of Fas antigen -

XX used to evaluate drugs in animal models and to treat Fas-associated

XX diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,

XX myocarditis, hepatitis and AIDS

XX Claim 21; Page 220-221; 292pp; English.

XX This is the amino acid sequence of the PDHM type humanised light

XX chain of murine anti-human Fas monoclonal antibody HFE7A.

XX Humanisation of the murine sequence (see AAW83042) entailed making

XX DIE, P47A, K49R and R107K amino acid substitutions; these

XX residues are conserved in the human light (kappa) chain. Host

XX cell Escherichia coli PHSHM2 SANK 70198 harbors plasmid PHSHM2

XX carrying a fusion of the humanised PDHM type HFE7A light chain and

XX DNA encoding the region of human immunoglobulin kappa chain, and is

XX deposited as FERM BP-6272 (claimed). The invention provides

XX methods for producing humanised antibodies by culturing host

XX cells. Humanised versions of HFE7A (see AAW83031-37), like native

XX HFE7A, are capable of inducing apoptosis in abnormal cells

XX expressing Fas, and of inhibiting Fas-induced apoptosis in normal

XX cells. The humanised antibodies are used to evaluate, in animal

XX models, treatments of diseases that involve Fas/Fas ligand

XX interactions, and also to treat such diseases, including autoimmune

XX disease (e.g. systemic lupus erythematosus, Hashimoto's disease,

XX graft versus host disease, Sjogren syndrome, pernicious anaemia,

XX Addison's disease, scleroderma, Goodpasture syndrome, Crohn's

XX disease, rheumatoid arthritis, autoimmune haemolytic anaemia,

XX sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,

XX thrombopenia purpura and insulin-dependent diabetes), allergies,

XX atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular

XX nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant

XX rejection (all claimed).

XX Sequence 238 AA;

Query Match 100.0%; Score 205; DB 19; Length 238;

Best Local Similarity 39.7%; Pred. No. 1.2e-05;

Matches 31; Conservative 47; Mismatches 0; Indels 0; Caps 0;

QY 1 KASQSDYDGDGSDYMNXXXXXXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXX 60

|||||XX

Db 44 kasqsvdydgdsgymwyyqqpgqprlliyaaasnlsgipdrfsgsgsgtdftitihpve 103

QY 61 XXXXXXXXQSQSNEDPRT 78

Db 104 eedaatyycqgsnedprt 121

RESULT 6

AAW83042

ID AAW83042 standard; Protein; 238 AA.

XX AC AAW83042;

XX 15-MAR-1999 (first entry)

XX Anti-Fas MAB HFE7A light chain.

XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;  
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;  
 KW systemic lupus erythematosus; graft versus host disease;  
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;  
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;  
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;  
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;  
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
 KW transplant rejection; therapy; complementarity determining region;  
 KW CDR.

XX Mus musculus.

XX Key Location/Qualifiers

XX Peptide 1..20

XX Protein /label= Sig\_peptide

XX Region 21..238

XX Region /label= Mat\_protein

XX Region 21..131

XX Region /label= Variable

XX Region 132..238

XX Region /label= Constant

XX Region 44..58

XX Region /label= CDR\_L1

XX Region /note= "claim 9"

XX Region 74..80

XX Region /label= CDR\_L2

XX Region /note= "claim 9"

XX Region 113..121

XX Region /label= CDR\_L3

XX Region /note= "claim 9"

XX AU9859701-A.

XX 08-OCT-1998.

XX 30-MAR-1998; 98AU-0059701.

XX 08-OCT-1997; 97JP-0276064.

XX 01-APR-1997; 97JP-0082953.

XX 25-JUN-1997; 97JP-0169088.

XX (SANY ) SANKYO CO LTD.

XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;

XX Masahiko O, Nobufusa S, Shin Y, Tohru T;

XX WPI: 1998-543440/47.

XX N-PSDB; AAV70130.

XX New antibodies and proteins bind conserved epitope of Fas antigen -  
 XX used to evaluate drugs in animal models and to treat Fas-associated  
 XX diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
 XX myocarditis, hepatitis and AIDS

```
XX PS Reference Example 4; Page 189-190; 292pp; English.
XX CC This is the amino acid of the light chain of murine anti-human Fas
XX CC monoclonal antibody HFE7A. cDNA (see AAV70130) encoding the light
XX CC chain was obtained from HFE7A-secreting hybridoma (FERM BP-5828)
XX CC RNA by RT-PCR (see AAV70127-28). The invention provides humanised
XX CC HFE7A antibodies (see AAW83031-37) produced by CDR grafting. These
XX CC antibodies are capable of inducing apoptosis in abnormal cells
XX CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal
XX CC cells. They are used to evaluate, in animal models, treatments of
XX CC diseases that involve Fas/Fas ligand interactions, and also to treat
XX CC such diseases, including autoimmune disease (e.g. systemic lupus
XX CC erythematosus, Hashimoto's disease, graft versus host disease,
XX CC Sjogren syndrome, pernicious anaemia, Addison's disease,
XX CC scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid
XX CC arthritis, autoimmune haemolytic anaemia, sterility, myasthenia
XX CC gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura
XX CC and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
XX CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
XX CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
XX SQ Sequence 238 AA;

Query Match 100.0%; Score 205; DB 19; Length 238;
Best Local Similarity 39.7%; Pred. No. 1.2e-05;
Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDSYMNXNXXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXX 60
DB 44 kasqsvdydgsymnwqgkpgppklliyaaaslesgiparfsgsgtdftlnhpve 103
QY 61 XXXXXXXXQSQNEPRT 78
DB 104 eedaatyycqgsnedprt 121

RESULT 7
AAB14748
ID AAB14748 standard; Protein; 238 AA.
AC AAB14748;
XX
XX
XX 24-NOV-2000 (first entry)
DE Mouse anti-Fas antibody HFE7A light chain.
KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
KW murine; humanised antibody; complementarity determining region; CDR;
KW Fas ligand; apoptosis modulator; programmed cell death;
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancyelophthisis;
KW hepatitis; AIDS; graft rejection; light chain.
XX
XX Mus musculus.
OS
XX JP2000169393-A.
PN
XX 20-JUN-2000.
PD
XX 30-SEP-1999; 99JP-0278301.
PF
XX 30-SEP-1998; 98JP-0276883.
PR
XX (SANY ) SANKYO CO LTD.
PA
XX WPI; 2000-485645/43.
DR
XX N-PSDB; AAA72109.
PT Preventive or treating agent for the diseases caused by an abnormality
PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
anti-Fas antibody
```

```
XX PS Example 4; Page 70; 139pp; Japanese.
XX CC The invention relates to compositions for the prevention or treatment
XX CC of diseases caused by an abnormality in the Fas/Fas ligand system
XX CC containing an anti-Fas antibody as the active component. The anti-Fas
XX CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
XX CC or a humanised version of HFE7A containing identical CDRs
XX CC (complementarity determining regions) to antibody HFE7A. Via its
XX CC interaction with Fas, the antibody of the invention acts as a modulator
XX CC of apoptosis. The composition of the invention may therefore be used in
XX CC the treatment or prevention of conditions such as autoimmune diseases,
XX CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
XX CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
XX CC and organ graft rejection. The present sequence represents the
XX CC light chain of the murine anti-human Fas monoclonal antibody HFE7A,
XX CC which is produced by hybridoma HFE7A (FERM-BP-5828).
XX SQ Sequence 238 AA;

Query Match 100.0%; Score 205; DB 21; Length 238;
Best Local Similarity 39.7%; Pred. No. 1.2e-05;
Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDSYMNXNXXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXX 60
DB 44 kasqsvdydgsymnwqgkpgppklliyaaaslesgiparfsgsgtdftlnhpve 103
QY 61 XXXXXXXXQSQNEPRT 78
DB 104 eedaatyycqgsnedprt 121

RESULT 8
AAB14772
ID AAB14772 standard; Protein; 238 AA.
XX
XX
XX 24-NOV-2000 (first entry)
DE Humanised anti-Fas antibody light chain, SEQ ID NO:50.
XX
XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
KW murine; humanised antibody; complementarity determining region; CDR;
KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancyelophthisis;
KW hepatitis; AIDS; graft rejection; light chain.
XX
XX Chimeric - Mus musculus.
OS Chimeric - Homo sapiens.
XX JP2000169393-A.
PN
XX 20-JUN-2000.
PD
XX 30-SEP-1999; 99JP-0278301.
PF
XX 30-SEP-1998; 98JP-0276883.
PR
XX (SANY ) SANKYO CO LTD.
PA
XX WPI; 2000-485645/43.
DR
XX N-PSDB; AAA72124.
PT Preventive or treating agent for the diseases caused by an abnormality
PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
anti-Fas antibody
PS Claim 20; Page 78-79; 139pp; Japanese.
XX
```







CC represent the light chains of several humanised HFE7A-derived anti-Fas  
 CC antibodies.  
 XX  
 SQ Sequence 238 AA;

Query Match 100.0%; Score 205; DB 21; Length 238;  
 Best Local Similarity 39.7%; Pred. No. 1.2e-05;  
 Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSDVDGDSYMNXXXXXXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXX 60  
 DB 44 kasqsvdydgdsymwvqqpgqprlliyaaasnesgiporfsgsgtdftihpve 103  
 QY 61 XXXXXXXXQSQSNEPRT 78  
 DB 104 eedaatyccgsnedprt 121

RESULT 13  
 AAW90898  
 ID AAW90898 standard; Protein; 238 AA.  
 AC AAW90898;  
 XX  
 XX  
 DT 08-AUG-2000 (first entry)  
 XX  
 XX Murine anti-Fas antibody HFE7A light chain protein.  
 XX  
 XX Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic;  
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;  
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;  
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus; HFE7A;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
 XX  
 XX Mus musculus.  
 XX  
 XX EP990663-A2.  
 PN  
 XX  
 XX 05-APR-2000.  
 XX  
 XX 29-SEP-1999; 99EP-0307711.  
 XX  
 XX 30-SEP-1998; 98JP-0276881.  
 PR  
 XX 30-SEP-1998; 98JP-0276882.  
 XX  
 XX (SANY ) SANKYO CO LTD.  
 PA  
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 PI  
 XX WPI: 2000-258930/23.  
 DR  
 XX N-PSDB; AAA11547.  
 XX  
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems -  
 XX  
 XX Example reference 4; Page 104; 263pp; English.  
 PS  
 XX This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,

CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a murine anti-Fas monoclonal antibody HFE7A light chain described in the  
 CC method of the invention.  
 XX  
 XX Sequence 238 AA;

Query Match 100.0%; Score 205; DB 21; Length 238;  
 Best Local Similarity 39.7%; Pred. No. 1.2e-05;  
 Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSDVDGDSYMNXXXXXXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXX 60  
 DB 44 kasqsvdydgdsymwvqqpgqprlliyaaasnesgiparfsgsgtdftihpve 103  
 QY 61 XXXXXXXXQSQSNEPRT 78  
 DB 104 eedaatyccgsnedprt 121

## RESULT 14

AAW90922

ID AAW90922 standard; Protein; 238 AA.

AC AAW90922;

XX 08-AUG-2000 (first entry)

XX Humanised anti-Fas antibody HFE7A light chain HH type protein.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;  
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;  
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
 XX  
 XX Synthetic.

OS EP990663-A2.

PN 05-APR-2000.

XX 29-SEP-1999; 99EP-0307711.

XX 30-SEP-1998; 98JP-0276881.

PR 30-SEP-1998; 98JP-0276882.

XX (SANY ) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

DR WPI; 2000-258930/23.  
DR N-PSDB; AAA11562.  
XX  
PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
PT inflammatory or autoimmune disease, induces apoptosis selectively in  
PT cells with abnormal Fas-Fas ligand systems  
XX  
PS Example reference 14; Page 114-115; 263pp; English.  
XX  
XX This invention describes a novel humanized anti-Fas antibody-like  
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
CC ligand system, by binding to Fas on the cell surface, and prevents  
CC apoptosis in cells with a normal system, by inhibiting binding between  
CC Fas and its ligand. The products of the invention have anti-inflammatory,  
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
CC immunomodulatory, dermatological, immunosuppressive, thymimetic,  
CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,  
CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce  
CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
CC inhibition of ligand binding. (I) are used to treat and/or prevent  
CC diseases associated with the Fas/Fas ligand system, especially systemic  
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
CC cells. They bind to both human and murine Fas, so can be evaluated in  
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
CC the native ligand, do not induce liver disease, and have reduced risk of  
CC inducing a human anti-murine antibody response. This sequence represents  
CC a humanised anti-Fas antibody HFE7A light chain HH type which is used in  
XX the method described in the invention.

XX Sequence 238 AA;

Query Match 100.0%; Score 205; DB 21; Length 238;  
Best Local Similarity 39.7%; Pred. No. 1.2e-05;  
Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KASQSVDDGDSYMNKXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXX 60  
Db 44 KASQSVDDGDSYMNWYQKPGAPRLIIYAASNLSEGIPDRFSGSGTDTLTISRL 103  
QY 61 XXXXXXXXQSNEDPRT 78  
Db 104 PADFAVYVYCGQSGNEPRT 121

#### RESULT 15

AAW90923  
ID AAW90923 standard; Protein; 238 AA.

XX AAW90923;

XX 08-AUG-2000 (first entry)

XX Humanised anti-Fas antibody HFE7A light chain HM type protein.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;  
KW dermatological; immunosuppressive; thymimetic; antirheumatic; anti-Fas;  
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;  
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;

KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
XX Synthetic.  
XX EP990663-A2.  
XX 05-APR-2000.  
XX 29-SEP-1999; 99EP-0307711.  
XX 30-SEP-1998; 98JP-0276881.  
XX 30-SEP-1998; 98JP-0276882.  
XX (SANY ) SANKYO CO LTD.  
XX Serizawa N, Haryuyama H, Nakahara K, Tamaki I, Takahashi T;  
PI WPI; 2000-258930/23.  
XX N-PSDB; AAA11563.  
DR New humanized anti-Fas antibody, useful for treating or preventing e.g.  
DR inflammatory or autoimmune disease, induces apoptosis selectively in  
XX cells with abnormal Fas-Fas ligand systems  
XX Example reference 14; Page 117-118; 263pp; English.  
XX This invention describes a novel humanized anti-Fas antibody-like  
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
CC ligand system, by binding to Fas on the cell surface, and prevents  
CC apoptosis in cells with a normal system, by inhibiting binding between  
CC Fas and its ligand. The products of the invention have anti-inflammatory,  
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
CC immunomodulatory, dermatological, immunosuppressive, thymimetic,  
CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,  
CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce  
CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
CC inhibition of ligand binding. (I) are used to treat and/or prevent  
CC diseases associated with the Fas/Fas ligand system, especially systemic  
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
CC cells. They bind to both human and murine Fas, so can be evaluated in  
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
CC the native ligand, do not induce liver disease, and have reduced risk of  
CC inducing a human anti-murine antibody response. This sequence represents  
CC a humanised anti-Fas antibody HFE7A light chain HM type which is used in  
XX the method described in the invention.

XX Sequence 238 AA;

Query Match 100.0%; Score 205; DB 21; Length 238;  
Best Local Similarity 39.7%; Pred. No. 1.2e-05;  
Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVDDGDSYMNKXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXX 60

Db 44 KASQSVDDGDSYMNWYQKPGAPRLIIYAASNLSEGIPDRFSGSGTDTLTIHPE 103

QY 61 XXXXXXXXQSNEDPRT 78

Db 104 EEDAATYVYCGQSGNEPRT 121

Search completed: August 14, 2002, 15:15:34  
Job time: 832 sec

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09/499, 662

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.  
  
OM protein - protein search, using sw model  
  
Run on: August 14, 2002, 15:17:02 ; Search time 82.88 Seconds  
(without alignments)  
22.987 Million cell updates/sec  
  
Title: 5\_g\_6\_g\_7  
Perfect score: 205  
Sequence: 1 KASQSYDYDGSYNNXXXXX.....XXXXXXXXXXQSQSNEPDPT 78  
  
Scoring table:  
BLOSUM62DX  
Gapop 10.0 , Gapext 0.5  
  
Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
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3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					Query		Match		Length		DB		ID		Description	
Result No.	Score	Query	Match	Length	DB	ID	Score	Match	Length	DB	ID	Score	Match	Length	DB	ID
1	198	96.6	111	2	US-08-483-636-73	Sequence 73, Appl										
2	198	96.6	111	2	US-08-483-632-73	Sequence 73, Appl										
3	198	96.6	131	2	US-08-483-636-58	Sequence 58, Appl										
4	198	96.6	131	2	US-08-483-632-58	Sequence 58, Appl										
5	198	96.6	132	2	US-08-483-636-2	Sequence 2, Appl										
6	198	96.6	132	2	US-08-483-632-2	Sequence 2, Appl										
7	197	96.1	106	3	US-08-466-151-6	Sequence 6, Appl										
8	197	96.1	106	4	US-08-466-163B-6	Sequence 6, Appl										
9	197	96.1	111	1	US-08-491-845-8	Sequence 8, Appl										
10	197	96.1	111	1	US-08-491-845-16	Sequence 16, Appl										
11	197	96.1	115	3	US-08-513-968-51	Sequence 51, Appl										
12	197	96.1	131	4	US-08-579-378A-14	Sequence 14, Appl										
13	197	96.1	131	4	US-08-579-378A-18	Sequence 18, Appl										
14	197	96.1	218	5	PCT-US96-13152-2	Sequence 2, Appl										
15	195	95.1	131	2	US-08-483-636-14	Sequence 14, Appl										
16	195	95.1	131	2	US-08-483-632-14	Sequence 14, Appl										
17	184	89.8	120	1	US-08-111-080-24	Sequence 24, Appl										
18	184	89.8	120	1	US-08-211-980-24	Sequence 24, Appl										
19	184	89.8	120	5	PCT-US93-07967-24	Sequence 24, Appl										
20	182	88.8	111	2	US-08-887-352B-6	Sequence 6, Appl										
21	182	88.8	111	4	US-09-109-207C-6	Sequence 6, Appl										
22	182	88.8	111	4	US-09-296-005-6	Sequence 6, Appl										
23	182	88.8	114	2	US-08-887-352B-10	Sequence 10, Appl										
24	182	88.8	114	4	US-09-109-207C-10	Sequence 10, Appl										
25	182	88.8	114	4	US-09-296-005-10	Sequence 10, Appl										
26	182	88.8	218	2	US-08-887-352B-13	Sequence 13, Appl										
27	182	88.8	218	3	US-08-466-151-9	Sequence 9, Appl										

ALIGNMENTS

RESULT 1  
US-08-483-636-73  
; Sequence 73, Application US/08483636  
; Patent No. 5914110  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Smithline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/483,636  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117366  
; FILING DATE: 07-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/136783  
; FILING DATE: 14-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US/94/10308  
; FILING DATE: 07-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 73:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 111 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown

28 182 88.8 218 4 US-09-109-207C-13 Sequence 13, Appl  
29 182 88.8 218 4 US-09-296-005-13 Sequence 13, Appl  
30 182 88.8 218 4 US-08-466-163B-9 Sequence 9, Appl  
31 178 86.8 111 2 US-08-887-352B-5 Sequence 5, Appl  
32 178 86.8 111 3 US-08-466-151-2 Sequence 2, Appl  
33 178 86.8 111 4 US-09-109-207C-5 Sequence 5, Appl  
34 178 86.8 111 4 US-09-296-005-5 Sequence 5, Appl  
35 178 86.8 111 4 US-08-466-163B-2 Sequence 2, Appl  
36 178 86.8 114 2 US-08-887-352B-9 Sequence 9, Appl  
37 175 85.4 114 4 US-09-109-207C-9 Sequence 9, Appl  
38 175 85.4 114 4 US-09-296-005-9 Sequence 9, Appl  
39 165 80.5 239 2 US-08-553-497A-18 Sequence 18, Appl  
40 159 77.6 114 2 US-08-887-352B-8 Sequence 8, Appl  
41 159 77.6 218 4 US-09-054-255-1 Sequence 1, Appl  
42 159 77.6 218 4 US-09-109-207C-8 Sequence 8, Appl  
43 156 76.1 114 4 US-09-296-005-8 Sequence 8, Appl  
44 156 76.1 114 4 US-08-887-352B-15 Sequence 15, Appl  
45 156 76.1 218 2 US-08-887-352B-15 Sequence 15, Appl

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; MOLECULE TYPE: protein
US-08-483-636-73

Query Match          96.6%; Score 198; DB 2; Length 111;
Best Local Similarity 38.5%; Pred. No. 3.1e-08;
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSDYDGDSDYMNXXXXXXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 60
DB 24 KASQSDYDGDSDYMNWYQKPGKAPKLLIYAASNLSEGIPSRFSGSGGDTFTLTISLQ 83
QY 61 XXXXXXXXXQSQSNEDPRT 78
DB 84 PEDIATYVCQSQSNEDPPT 101

RESULT 3
US-08-483-636-58
; Sequence 58, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,636
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-636-58

Query Match          96.6%; Score 198; DB 2; Length 131;
Best Local Similarity 38.5%; Pred. No. 5.1e-08;
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSDYDGDSDYMNXXXXXXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 60
DB 43 KASQSDYDGDSDYMNWYQKPGKAPKLLIYAASNLSEGIPSRFSGSGGDTFTLTISLQ 102
QY 61 XXXXXXXXXQSQSNEDPRT 78

; MOLECULE TYPE: protein
US-08-483-632-73

Query Match          96.6%; Score 198; DB 2; Length 111;
Best Local Similarity 38.5%; Pred. No. 3.1e-08;
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSDYDGDSDYMNXXXXXXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 60
DB 24 KASQSDYDGDSDYMNWYQKPGKAPKLLIYAASNLSEGIPSRFSGSGGDTFTLTISLQ 83
QY 61 XXXXXXXXXQSQSNEDPRT 78
DB 84 PEDIATYVCQSQSNEDPPT 101

RESULT 2
US-08-483-632-73
; Sequence 73, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,632
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-483-632-73

Query Match          96.6%; Score 198; DB 2; Length 111;
Best Local Similarity 38.5%; Pred. No. 3.1e-08;
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Db 103 AEDVAVYCOQSNEDPPT 120

RESULT 4

US-08-483-632-58  
; Sequence 58, Application US/08483632  
; Patent No. 5928904  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,632  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117366  
; FILING DATE: 07-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/136783  
; FILING DATE: 14-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US/94/10308  
; FILING DATE: 07-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 58:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 131 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-483-632-58

Query Match 96.6%; Score 198; DB 2; Length 131;  
Best Local Similarity 38.5%; Pred. No. 5.1e-08;  
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSDYDGDSDYNNXXXXXXXXXXXXXXXXXAAASLNLESXXXXXXXXXXXXXXXXXXXXX 60  
Db 43 KASQSDYDGDSDYNNYQKPGQPKLLIYAASLNLESVPDRFSGSGSGTDTLTISLQ 102  
QY 61 XXXXXXXXQOQSNEDPPT 78  
Db 103 AEDVAVYCOQSNEDPPT 120

RESULT 5

US-08-483-636-2  
; Sequence 2, Application US/08483636

; Patent No. 5914110  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,636  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117366  
; FILING DATE: 07-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/136783  
; FILING DATE: 14-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US/94/10308  
; FILING DATE: 07-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028  
; REFERENCE/DOCKET NUMBER: P50186-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 270-5024  
; TELEFAX: (215) 270-5090  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 132 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-483-636-2

Query Match 96.6%; Score 198; DB 2; Length 132;  
Best Local Similarity 38.5%; Pred. No. 5.2e-08;  
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSDYDGDSDYNNXXXXXXXXXXXXXXXXXAAASLNLESXXXXXXXXXXXXXXXXXXXXX 60  
Db 44 KASQSDYDGDSDYNNYQKPGQPKLLIYAASLNLESGIPARFSGSGSGTDTLNIHPE 103  
QY 61 XXXXXXXXQOQSNEDPPT 78  
Db 104 EDAATYCOQSNEDPPT 121

RESULT 6

US-08-483-632-2  
; Sequence 2, Application US/08483632  
; Patent No. 5928904  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders

NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corp./Corporate  
ADDRESSEE: Intellectual Property  
STREET: P.O. Box 1539 / UW2220  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,632  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/117366  
FILING DATE: 07-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/136783  
FILING DATE: 14-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US/94/10308  
FILING DATE: 07-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Sutton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50186-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 270-5024  
TELEFAX: (215) 270-5090  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 132 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-483-632-2

Query Match 96.6%; Score 198; DB 2; Length 132;  
Best Local Similarity 38.5%; Pred. No. 5.2e-08;  
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSDYDGDSDYMNXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXX 60  
|||||  
Db 44 KASQSDYDGDSDYMNWYQKQPPKLLIYAASNLESIGIPARFSGSGTDTLNIHPVE 103  
QY 61 XXXXXXXXQSQSNEPPT 78  
Db 104 EEDAATYYCQSQSNEPPT 121

RESULT 7  
US-08-466-151-6  
Sequence 6, Application US/08466151  
Patent No. 6037453  
GENERAL INFORMATION:  
APPLICANT: Presta, Leonard G.  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,151  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/466163  
FILING DATE: 06-Jun-1995  
APPLICATION NUMBER: 08/405617  
FILING DATE: 15-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/185899  
FILING DATE: 26-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/879495  
FILING DATE: 07-MAY-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/744768  
FILING DATE: 14-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P07182C1D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-466-151-6

Query Match 96.1%; Score 197; DB 3; Length 106;  
Best Local Similarity 38.5%; Pred. No. 3.3e-08;  
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSDYDGDSDYMNXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXX 60  
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Db 24 KASQSDYDGDSDYMNWYQKQPPKLLIYAASNLESIGIPARFSGSGTDTLNIHPVE 83  
QY 61 XXXXXXXXQSQSNEPPT 78  
Db 84 EEDAATYYCQSQSNEPPT 101

RESULT 8  
US-08-466-163B-6  
Sequence 6, Application US/08466163B  
Patent No. 6329509  
GENERAL INFORMATION:  
APPLICANT: Jardieu, Paula M.  
TITLE OF INVENTION: Immunoglobulin Variants  
FILE REFERENCE: P07182C1D1  
CURRENT APPLICATION NUMBER: US/08/466,163B  
CURRENT FILING DATE: 1995-06-06  
PRIOR APPLICATION NUMBER: US 08/405,617  
PRIOR FILING DATE: 1995-03-15  
PRIOR APPLICATION NUMBER: US 08/185,899  
PRIOR FILING DATE: 1994-01-26  
PRIOR APPLICATION NUMBER: US 07/879,495  
PRIOR FILING DATE: 1992-05-07  
PRIOR APPLICATION NUMBER: US 07/744,768  
PRIOR FILING DATE: 1991-08-14  
NUMBER OF SEQ ID NOS: 64  
SEQ ID NO 6  
LENGTH: 106  
TYPE: PRT

RESULT 11  
US-08-513-968-51  
; Sequence 51, Application US/08513968  
; Patent No. 611413  
; GENERAL INFORMATION:

```
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: MAKIZUMI, Keiichi
; APPLICANT: SHIOSAKI, Kouichi
; APPLICANT: OSATOMI, Kiyoshi
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-HIV MONOCLONAL ANTIBODY
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,968
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 78913/1993
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: EDA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 115 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-513-968-51

Query Match 96.1%; Score 197; DB 3; Length 115;
Best Local Similarity 38.5%; Pred. No. 4.2e-08;
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDSYMNXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXX 60
Db 28 KASQSVYDGDSDSYMNWYQKPGKAPKLLIYAASNLESVPSRFGSGSGTDTFTFISSIQ 87
QY 61 XXXXXXXXQSNEDPRT 78
Db 88 PEDIATYCCQSNEDPWT 105

RESULT 12
US-08-579-378A-14
; Sequence 14, Application US/08579378A
; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
```

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; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,378A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-002220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-579-378A-14

Query Match 96.1%; Score 197; DB 4; Length 131;
Best Local Similarity 38.5%; Pred. No. 6.2e-08;
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDSYMNXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXX 60
Db 44 KASQSVYDGDSDSYMNWYQKPGKAPKLLIYAASNLESIPARFSGSGTDTFTLNHPVE 103
QY 61 XXXXXXXXQSNEDPRT 78
Db 104 EEDAATYCCQSNEDPWT 121

RESULT 13
US-08-579-378A-18
; Sequence 18, Application US/08579378A
; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/579,378A  
;; FILING DATE: 27-DEC-1995  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/160,074  
;; FILING DATE: 30-NOV-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/983,946  
;; FILING DATE: 01-DEC-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 95112895.8  
;; FILING DATE: 17-AUG-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: EP 95114696.8  
;; FILING DATE: 19-SEP-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Liebescheutz, Joe O.  
;; REGISTRATION NUMBER: 37,505  
;; REFERENCE/DOCKET NUMBER: 11823-002220  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-326-2400  
;; TELEFAX: 415-326-2422  
;; INFORMATION FOR SEQ ID NO: 18:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 131 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-579-378A-18

Query Match 96.1%; Score 197; DB 4; Length 131;  
Best Local Similarity 38.5%; Pred. No. 6.2e-08;  
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSDYDGD SYNNXXXXXXXAAASNLSEXXXXXXX 60  
Db 44 KASQSDYDGD SYNNWYQKPGKAPKLLIYAASNLSEGIPIRSGSGGDTFTLTISLQ 103

QY 61 XXXXXXXXQSQSNEPRT 78  
Db 104 PEDFATYQCQSNEPWT 121

RESULT 14  
PCT-US96-13152-2  
; Sequence 2, Application PC/TUS9613152  
; GENERAL INFORMATION:  
; APPLICANT: Martin, Ulrich, et al.  
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; ADDRESSEE: Attn: Norman D. Hanson  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Computer Disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/13152  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/578,953  
; FILING DATE: 27-Dec-95  
; APPLICATION NUMBER: EP 95 112 895.8

;; FILING DATE: 17-Aug-95  
;; APPLICATION NUMBER: EP 95 114 969.9  
;; FILING DATE: 19-Sep-95  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Norman D. Hanson  
;; REGISTRATION NUMBER: 30,946  
;; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 688-9200  
;; TELEFAX: (212) 838-3884  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 218  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
PCT-US96-13152-2

Query Match 96.1%; Score 197; DB 5; Length 218;  
Best Local Similarity 38.5%; Pred. No. 2.9e-07;  
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSDYDGD SYNNXXXXXXXAAASNLSEXXXXXXX 60  
Db 24 KASQSDYDGD SYNNWYQKPGKAPKLLIYAASNLSEGIPIRSGSGGDTFTLTISLQ 83

QY 61 XXXXXXXXQSQSNEPRT 78  
Db 84 PEDFATYQCQSNEPWT 101

RESULT 15  
US-08-483-636-14  
; Sequence 14, Application US/08483636  
; Patent No. 5914110  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Stephen D.  
; APPLICANT: Gross, Mitchell S.  
; APPLICANT: Sylvester, Daniel R.  
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in  
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corp./Corporate  
; ADDRESSEE: Intellectual Property  
; STREET: P.O. Box 1539 / UW2220  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,636  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117366  
; FILING DATE: 07-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/136783  
; FILING DATE: 14-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US/94/10308  
; FILING DATE: 07-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sutton, Jeffrey A.  
; REGISTRATION NUMBER: 34,028

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; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-636-14

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Query Match      95.1%; Score 195; DB 2; Length 131;
Best Local Similarity 38.2%; Pred. No. 9.2e-08;
Matches 29; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGD SYMNNXXXXXXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXX 60
Db 43 KASQSVYDGD SYMNNWYQQKPPKLLIYAAASNLESVDPDRFSGSGGTFTLTISLIQ 102
QY 61 XXXXXXXXXXXXQSNEDP 76
Db 103 AEDVAVIYCQSNEDP 118

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Search completed: August 14, 2002, 15:17:02  
Job time: 685 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 15:18:57 ; Search time 108.64 Seconds  
(without alignments)  
68.989 Million cell updates/sec

Title: 5\_g\_6\_g\_7  
Perfect score: 205  
Sequence: 1 KASQSDYDGSYMNXXXXX.....XXXXXXXXXXQSQSNEDPRT 78

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	198	96.6	111	1 KVM583	Ig kappa chain V r
2	197	96.1	111	1 KVM543	Ig kappa chain V r
3	197	96.1	111	1 KVM569	Ig kappa chain V r
4	193	94.1	93	2 A38601	Ig kappa chain V r
5	193	94.1	111	1 KVM508	Ig kappa chain V r
6	191	93.2	81	2 S42193	Ig kappa chain V r
7	190	92.7	112	2 S19971	Ig kappa chain V r
8	190	92.7	131	2 PH1226	Ig kappa chain pre
9	187	91.2	111	1 KVM5C1	Ig kappa chain V r
10	179	87.3	111	2 S09966	Ig kappa chain V-J
11	172.5	84.1	110	1 KVM510	Ig kappa chain V r
12	172	83.9	112	2 S19976	Ig kappa chain V r
13	162	79.0	112	2 S19972	Ig kappa chain V r
14	157	76.6	111	2 D45722	anti-glycoprotein
15	155	75.6	107	2 S26344	Ig kappa chain V r
16	155	75.6	111	1 KVM537	Ig kappa chain V r
17	154	75.1	107	2 S26343	Ig kappa chain V r
18	151	73.7	131	1 KVM5M6	Ig kappa chain pre
19	149	72.7	96	2 B49442	Ig light chain V r
20	147	71.7	115	2 S63596	Ig kappa chain V r
21	137	66.8	111	1 KVM584	Ig kappa chain V r
22	136	66.3	111	2 S09965	Ig kappa chain V-J
23	136	66.3	132	1 KVM532	Ig kappa chain pre
24	135	65.9	109	2 PH0093	Ig kappa chain V r
25	133	64.9	102	2 PH1079	Ig light chain V r
26	133	64.9	111	2 PL0081	Ig kappa chain V r
27	133	64.9	120	2 S06731	Ig kappa chain pre
28	132	64.4	111	1 KVM580	Ig kappa chain V r
29	130	63.4	108	1 KVM554	Ig kappa chain V r

30	130	63.4	111	1 KVM575	Ig kappa chain V r
31	130	63.4	111	2 S09963	Ig kappa chain V-J
32	130	63.4	111	2 E53285	Ig kappa chain V a
33	130	63.4	120	2 S06732	Ig kappa chain pre
34	129	62.9	102	2 PH1076	Ig light chain V r
35	129	62.9	111	2 S09969	Ig kappa chain V-J
36	129	62.9	210	2 A56169	Ig kappa chain V r
37	127	62.0	111	1 KVM540	Ig kappa chain V r
38	127	62.0	111	2 S37202	Ig kappa chain V r
39	127	62.0	112	2 S45715	Ig kappa chain V r
40	127	62.0	123	2 S40331	Ig kappa chain - h
41	125	61.0	111	1 KVM585	Ig kappa chain V r
42	124	60.5	218	2 JC5810	monoclonal antibody
43	123	60.0	111	1 KVM550	Ig kappa chain V r
44	121	59.0	218	2 S68241	Ig kappa chain V r
45	120	58.5	108	2 B49047	Ig kappa chain V r

ALIGNMENTS

RESULT 1  
KVM583  
Ig kappa chain V region (PC7183) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 21-Jan-2000  
C:Accession: B01937; A01937  
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
Nature 276, 785-790, 1978  
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
A:Reference number: A93204; MUID:79073152  
A:Accession: B01937  
A:Molecule type: protein  
A:Residues: 1-111 <WEI>  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-94/Domain: immunoglobulin homology <IMM>  
F:23-92/Disulfide bonds: #status predicted

Query Match 96.6%; Score 198; DB 1; Length 111;  
Best Local Similarity 38.5%; Pred. No. 2.2e-09;  
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KASQSDYDGSYMNXXXXXAAASNLESGIPARFSGSGDTFTLNHPVE 60  
DB 24 KASQSDYDGSYMNWTQKPPKLLTYAASNLESGIPARFSGSGDTFTLNHPVE 83  
QY 61 XXXXXXXXQSQSNEDPRT 78  
DB 84 EEDAATYCCQSQSNEDPLT 101

RESULT 2  
KVM543  
Ig kappa chain V region (PC7043) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 21-Jan-2000  
C:Accession: A01937; S42187; S42194; S42189; S42188; S42191; S42192  
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.  
Nature 276, 785-790, 1978  
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.  
A:Reference number: A93204; MUID:79073152  
A:Accession: A01937  
A:Molecule type: protein  
A:Residues: 1-111 <WEI>  
R:Mo, J.A.; Bona, C.A.; Holmdahl, R.  
Eur. J. Immunol. 23, 2503-2510, 1993  
A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with s  
A:Reference number: S42176; MUID:94009207  
A:Accession: S42187





Qy 1 KASQSDVDGDSYMNXXXXXXXXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXXXXXXXXX 60  
|||||  
Db 24 KASQSDVDGDSYMNWYQKPGPKLLIYTASNLESGIPARFSGSGGTDTFLNIHPVE 83  
Qy 61 XXXXXXXXQSQSNEDPRT 78  
Db 84 EEDAATYYCQSQSNEDPWT 101

RESULT 6  
S42193  
Ig kappa chain V region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 07-Oct-1994 #sequence\_revision 26-May-1995 #text\_change 23-Jul-1999  
C:Accession: S42193  
Eur. J. Immunol. 23, 2503-2510, 1993  
A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec  
A:Reference number: S42193; MUID:94009207  
A:Accession: S42193  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-81 <WQJ>  
A:Cross-references: EMBL:225456; NID:g407846; PIDN:CAA80943.1; PID:g407847  
A:Note: the authors translated the codon GTT for residue 36 as Ala  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

Query Match 93.2%; Score 191; DB 2; Length 81;  
Best Local Similarity 36.8%; Pred. No. 7e-09; Mismatches 1; Indels 0; Gaps 0;  
Matches 28; Conservative 47;

Qy 1 KASQSDVDGDSYMNXXXXXXXXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXXXXXXXXX 60  
|||||  
Db 6 KASQSDVDGDSYMNWYQKPGPKLLIYASNLESGIPARFSGSGGTDTFLNIHPVE 65  
Qy 61 XXXXXXXXQSQSNEDP 76  
Db 66 EEDAATYYCQSQSNEDP 81

RESULT 7  
S19971  
Ig kappa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C:Accession: S19971; S19973  
R:Weissenhorn, W.; Rietmueller, G.; Weiss, E.M.; Rieber, E.P.  
submitted to the EMBL Data Library, March 1992  
A:Description: Structural characterization of CD4 mAb.  
A:Reference number: S19963  
A:Accession: S19971  
A:Molecule type: mRNA  
A:Residues: 1-112 <WEI>  
A:Cross-references: EMBL:X65091; NID:g52288; PIDN:CAA46219.1; PID:g52289  
A:Experimental source: clone M-T310  
A:Accession: S19973  
A:Molecule type: mRNA  
A:Residues: 1-112 <WEW>  
A:Cross-references: EMBL:X65092; NID:g52292; PIDN:CAA46220.1; PID:g52293  
A:Experimental source: M-T404  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 92.7%; Score 190; DB 2; Length 112;  
Best Local Similarity 35.9%; Pred. No. 1.5e-08;  
Matches 28; Conservative 49; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KASQSDVDGDSYMNXXXXXXXXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXXXXXXXXX 60  
|||||  
Db 1 KASQSDVDGDSYMNWYQKPGPKLLIYASNLESGIPARFSGSGGTDTFLNIHPVE 83  
Qy 61 XXXXXXXXQSQSNEDPRT 78

Db 24 KASQSLDVGDSYMNWYQKPGPKLLIYAAASNLSEGIPARFSGSGGTDTFLNIHPVE 83  
Qy 61 XXXXXXXXQSQSNEDPRT 78  
Db 84 EEDAATYYCQSQSNEDPPT 101

RESULT 8  
PH1226  
Ig kappa chain precursor V region (M-T310) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 21-Jan-2000  
C:Accession: PH1226  
R:Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; I  
Gene 121, 271-278, 1992  
A:Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and  
A:Reference number: PH1224; MUID:93077041  
A:Accession: PH1226  
A:Molecule type: mRNA  
A:Residues: 1-131 <WEI>  
A:Cross-references: GB:S50265; NID:g260765; PIDN:AAB24320.1; PID:g260766  
A:Note: this mouse sequence was hybridized and fused with a human constant region gen  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-131/Product: Ig light chain V region #status predicted <MAT>  
F:36-114/Domain: immunoglobulin homology <IMM>

Query Match 92.7%; Score 190; DB 2; Length 131;  
Best Local Similarity 35.9%; Pred. No. 1.8e-08;  
Matches 28; Conservative 49; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KASQSDVDGDSYMNXXXXXXXXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXXXXXXXXX 60  
|||||  
Db 44 KASQSLDVGDSYMNWYQKPGPKLLIYAAASNLSEGIPARFSGSGGTDTFLNIHPVE 103  
Qy 61 XXXXXXXXQSQSNEDPRT 78  
Db 104 EEDAATYYCQSQSNEDPPT 121

RESULT 9  
KVMSCL  
Ig kappa chain V region (CBFC 101) - mouse (tentative sequence)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Nov-1980 #sequence\_revision 30-Nov-1980 #text\_change 31-Mar-2000  
C:Accession: A01936  
R:McKean, D.J.; Bell, M.; Potter, M.  
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978  
A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related  
A:Reference number: A93822; MUID:79012520  
A:Accession: A01936  
A:Molecule type: protein  
A:Residues: 1-111 <MCK>  
C:Comment: This chain was isolated from a myeloma protein.  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (   
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer  
F:16-94/Domain: immunoglobulin homology <IMM>  
F:23-92/Disulfide bonds: #status predicted

Query Match 91.2%; Score 187; DB 1; Length 111;  
Best Local Similarity 35.9%; Pred. No. 2.9e-08;  
Matches 28; Conservative 48; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KASQSDVDGDSYMNXXXXXXXXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXXXXXXXXX 60  
|||||  
Db 24 KASQSDVDGDSYMNWYQKPGPKLLIYAAASNLSEGIPARFSGSGGTDTFLNIHPVE 83  
Qy 61 XXXXXXXXQSQSNEDPRT 78

C;Species: Mus musculus (house mouse)  
C;Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C;Accession: S19976  
R;Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.  
submitted to the EMBL Data Library, March 1992  
A;Description: Structural characterization of CD4 mAb.  
A;Reference number: S19963  
A;Accession: S19976  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-112 <WEI>  
A;Cross-references: EMBL:X65093; NID:g52298; PIDN:CAA46221.1; PID:g52299  
C;Superfamily: Immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-94/Domain: immunoglobulin homology <IMM>

Query Match 83.9%; Score 172; DB 2; Length 112;  
Best Local Similarity 32.1%; Pred.No. 9.4e-07;  
Matches 25; Conservative 50; Mismatches 3; Indels 0; Gaps

Qy 1 KASQVDYDGDGYMNXXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXXXX 60  
|||||:||| ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 24 KASQLDYDADSYWHVYQQKPGRPKLLIYAASNLSEIGIPARFSGSGGTDTLTINHPVE 83  
|||||:||| ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 XXXXXXXXXQSQSNEEDPT 78  
:|||||:|||||:|||||:  
Db 84 EEDAATYYCQSIEDPYT 101  
:|||||:|||||:|||||:

RESULT 13  
S19972  
Ig kappa chain V region (M-T321) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C;Accession: S19972  
R;Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.  
submitted to the EMBL Data Library, March 1992  
A;Description: Structural characterization of CD4 mAb.  
A;Reference number: S19963  
A;Accession: S19972  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-112 <WEI>  
A;Cross-references: EMBL:X65094; NID:g52290; PIDN:CAA46222.1; PID:g52291  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-94/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 162; DB 2; Length 112;  
Best Local Similarity 29.5%; Pred.No. 9.6e-06;  
Matches 23; Conservative 52; Mismatches 3; Indels 0; Gaps

Qy 1 KASQVDYDGDGYMNXXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXXXX 60  
|||||:||| ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 24 RASQVDYNAYSIMHYVQQKPGPPKLLIYAANLESIGIPARFSGSGGTDTLTLDIHPE 83  
|||||:||| ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 XXXXXXXXXQSQSNEEDPT 78  
:|||||:|||||:|||||:  
Db 84 EEDAATYYCQSIEDPYT 101  
:|||||:|||||:|||||:

RESULT 14  
D45722  
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 10)  
C;Species: Mus musculus (house mouse)  
C;Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C;Accession: D45722  
R;Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co  
J. Virol. 67, 489-496, 1993  
A;Title: Neutralizing monoclonal antibodies that distinguish three antigenic  
A;Reference number: A45722; MUID:93100833



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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 15:23:12 ; Search time 53.64 Seconds  
(without alignments)  
56.304 Million cell updates/sec

Title: 5\_g\_6\_g\_7  
Perfect score: 205  
Sequence: 1 KASQSVDDGSDYNNXXXXX.....XXXXXXXXXXQSQSNEDPRT 78

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	198	96.6	111	1	KV3N_MOUSE
2	197	96.1	111	1	KV3M_MOUSE
3	197	96.1	111	1	KV3Q_MOUSE
4	193	94.1	111	1	KV3O_MOUSE
5	187	91.2	111	1	KV3L_MOUSE
6	172.5	84.1	110	1	KV3P_MOUSE
7	155	75.6	111	1	KV3H_MOUSE
8	152	74.1	111	1	KV3J_MOUSE
9	152	74.1	111	1	KV3K_MOUSE
10	151	73.7	131	1	KV3I_MOUSE
11	137	66.8	111	1	KV3R_MOUSE
12	136	66.3	112	1	KV3G_MOUSE
13	136	66.3	132	1	KV3F_MOUSE
14	135	65.9	111	1	KV3C_MOUSE
15	132	64.4	111	1	KV3A_MOUSE
16	130	63.4	108	1	KV3U_MOUSE
17	130	63.4	111	1	KV3S_MOUSE
18	130	63.4	112	1	KV3B_MOUSE
19	127	62.0	111	1	KV3T_MOUSE
20	125	61.0	111	1	KV3V_MOUSE
21	123	60.0	111	1	KV3D_MOUSE
22	113	55.1	108	1	KV1A_HUMAN
23	112	54.6	108	1	KV1E_HUMAN
24	110.5	53.9	113	1	KV2B_HUMAN
25	110	53.7	108	1	KV1K_HUMAN
26	110	53.7	108	1	KV1N_HUMAN
27	110	53.7	129	1	KV1W_HUMAN
28	109	53.2	112	1	KV1U_HUMAN
29	108	52.7	108	1	KV5K_MOUSE
30	108	52.7	108	1	KV5O_MOUSE
31	106	51.7	108	1	KV5L_MOUSE
32	105	51.2	109	1	KV1T_HUMAN
33	104.5	51.0	133	1	KV2F_HUMAN

ALIGNMENTS

RESULT 1																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
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P01594 homo sapien  
P01599 homo sapien  
P01598 homo sapien  
P01600 homo sapien  
P01605 homo sapien  
P01647 mus musculus  
P01657 mus musculus  
P01643 mus musculus  
P18133 homo sapien  
P01626 mus musculus  
P01628 mus musculus  
P01617 homo sapien

```
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7043.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity."
RL Nature 276:785-790(1978).
DR PIR: A01937; KVM543.
DR HSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 96.1%; Score 197; DB 1; Length 111;
Best Local Similarity 38.5%; Pred. No. 8.1e-08;
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVDDGDSYMNXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXX 60
Db 24 KASQSVDDGDSYMNWYQKQPPLIIYAASNLESIPARFSGSGTDTLNIHPVE 83

QY 61 XXXXXXXXQSQSNEDPRT 78
Db 84 EEDAATYYCQSQSNEDPWT 101

RESULT 3
KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7769.
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity."
RL Nature 276:785-790(1978).
DR PIR: A01937; KVM569.
DR HSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 96.1%; Score 197; DB 1; Length 111;
Best Local Similarity 38.5%; Pred. No. 8.1e-08;
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVDDGDSYMNXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXX 60
Db 24 KASQSVDDGDSYMNWYQKQPPLIIYAASNLESIPARFSGSGTDTLNIHPVE 83

QY 61 XXXXXXXXQSQSNEDPRT 78
Db 84 EEDAATYYCQSQSNEDPWT 101

RESULT 3
KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7769.
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity."
RL Nature 276:785-790(1978).
DR PIR: A01937; KVM569.
DR HSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;
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FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match 96.1%; Score 197; DB 1; Length 111;
Best Local Similarity 38.5%; Pred. No. 8.1e-08;
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVDDGDSYMNXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXX 60
Db 24 KASQSVDDGDSYMNWYQKQPPLIIYAASNLESIPARFSGSGTDTLNIHPVE 83

QY 61 XXXXXXXXQSQSNEDPRT 78
Db 84 EEDAATYYCQSQSNEDPWT 101

RESULT 4
KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01667;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 6308.
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity."
RL Nature 276:785-790(1978).
DR PIR: C01937; KVM508.
DR HSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 94.1%; Score 193; DB 1; Length 111;
Best Local Similarity 37.2%; Pred. No. 1.8e-07;
Matches 29; Conservative 47; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSVDDGDSYMNXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXX 60
Db 24 KASQSVDDGDSYMNWYQKQPPLIIYAASNLESIPARFSGSGTDTLNIHPVE 83

QY 61 XXXXXXXXQSQSNEDPRT 78
Db 84 EEDAATYYCQSQSNEDPWT 101
```

```
RESULT 5
KV3L_MOUSE
ID KV3L_MOUSE STANDARD; PRT; 111 AA.
AC P01664;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region CBPC 101.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR: A01936; KVMSC1.
DR HSSP: P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11964 MW; E2B1AD98AD965962 CRC64;

Query Match 91.2%; Score 187; DB 1; Length 111;
Best Local Similarity 35.9%; Pred. No. 5.8e-07;
Matches 28; Conservative 48; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KASQSDYDGDGSDYNNMXXXXXXXAAASNLESXXXXXXXKXXXXXXXXXXXX 60
Dy 24 KASQSDYDGTGSDYNNMYYQKPKLLIYAASNLESIGIPARFSGSGGTDFTLNHPVE 83
Qy 61 XXXXXXXXQGSNEDPRT 78
Dy 84 EDAATYYCQGSNEDPYT 101

RESULT 6
KV3P_MOUSE
ID KV3P_MOUSE STANDARD; PRT; 110 AA.
AC P01668;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7210.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).

Qy 1 KASQSDYDGDGSDYNNMXXXXXXXAAASNLESXXXXXXXKXXXXXXXXXXXX 60
Dy 24 KASQSDYDGTGSDYNNMYYQKPKLLIYAASNLESIGIPARFSGSGGTDFTLNHPVE 83
Qy 61 XXXXXXXXQGSNEDPRT 78
Dy 84 EDAATYYCQGSNEDPYT 101

RESULT 7
KV3H_MOUSE
ID KV3H_MOUSE STANDARD; PRT; 111 AA.
AC P01660;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 3741/TEPC 111.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (PC 3741).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
RN [2]
RP SEQUENCE (TEPC 111).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -!- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
DR PIR: A01934; KVMSC7.
DR HSSP: P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DOMAIN 103 111
FT DOMAIN 104 111
SQ SEQUENCE 110 AA; 11950 MW; 69F1A5CE886B1249 CRC64;
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```
DR PIR: D01937; KVMSC10.
DR HSSP: P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 100
FT DOMAIN 101 110
FT DISULFID 23 92
FT NON_TER 110 110
SQ SEQUENCE 110 AA; 11950 MW; 69F1A5CE886B1249 CRC64;

Query Match 84.1%; Score 172.5; DB 1; Length 110;
Best Local Similarity 34.6%; Pred. No. 9.7e-06;
Matches 27; Conservative 48; Mismatches 2; Indels 1; Gaps 1;

Qy 1 KASQSDYDGDGSDYNNMXXXXXXXAAASNLESXXXXXXXKXXXXXXXXXXXX 60
Dy 24 KASQSLDYDGDGSDYNNMYYQKPKLLIYAASNLESIGIPARFSGSGGTDFTLNHPVE 83
Qy 61 XXXXXXXXQGSNEDPRT 78
Dy 84 EDAATYYCHQS-EDPWT 100

RESULT 8
KV3L_MOUSE
ID KV3L_MOUSE STANDARD; PRT; 111 AA.
AC P01664;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 3741/TEPC 111.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (PC 3741).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
RN [2]
RP SEQUENCE (TEPC 111).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -!- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
DR PIR: A01934; KVMSC7.
DR HSSP: P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DOMAIN 103 111
FT DOMAIN 104 111
SQ SEQUENCE 110 AA; 11950 MW; 69F1A5CE886B1249 CRC64;
```

QY 61 XXXXXXXXXXQSNEDPRT 78

RA Burstein Y., Schechter I.;  
RT "Primary structures of N-terminal extra peptide segments linked to

*Mus musculus* (Mouse).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.



RT	precursors: implications on the organization and controlled
RT	expression of immunoglobulin genes.";
RL	Biochemistry 17:2392-2400(1978).
RN	[2]
RP	SEQUENCE OF 21-131.
RX	MEDLINE=73140225; PubMed=4691517;
RA	McKean D.J., Potter M., Hood L.E.;
RA	"Mouse immunoglobulin chains. Pattern of sequence variation among
RT	kappa chains with limited sequence differences.";
RL	Biochemistry 12:760-771(1973).
RN	[3]
RP	REVISIONS.
RX	MEDLINE=79012520; PubMed=99744;
RA	McKean D.J., Bell M., Potter M.;
RA	"Mechanisms of antibody diversity: multiple genes encode structurally
RT	related mouse kappa variable regions.";
RL	Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
DR	PIR; A01935; KVM5M6.
DR	HSSP; P01789; LMCP.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_V.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00406; IGV; 1.
KW	Immunoglobulin V region; Signal.
FT	SIGNAL 1 20
FT	CHAIN 21 131
FT	DOMAIN 21 43
FT	DOMAIN 44 58
FT	DOMAIN 59 73
FT	DOMAIN 74 80
FT	DOMAIN 81 112
FT	DOMAIN 113 121
FT	DOMAIN 122 131
FT	DISULFID 43 112
FT	NON_TER 131 131
SQ	SEQUENCE 131 AA; 144291 MW; D212EC9F08DC880A CRC64;

Query Match 73.7%; Score 151; DB 1; Length 131;  
Best Local Similarity 26.9%; Pred. No. 0.00092;  
Matches 21; Conservative 53; Mismatches 4; Indels 0; Gaps 0;

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QY      1 KASGVVDYDGDSTWNNXXXXXXXXXXXXXXXXXAAANLSSXXXXXXXXXXXXXXXXXXXXX 60
Db      44 RASESDVSYGNSFMHWYQORPGQPKLLIYLASNLSESGVPARPSGSGSRDFTLTIDPVE 103
QY      61 XXXXXXXXXXQOSNEDPRT 78
Db      104 ADDAATYYCQONNEDPWT 121

RESULT 11
KV3R_MOUSE
ID      KV3R_MOUSE      STANDARD;      PRT;      111 AA.
AC      P01670;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DE      15-JUL-1999 (Rel. 38, Last annotation update)
DE      IG kappa chain V-III region PC 5684.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=79073152; PubMed=1030003;
RA      Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT      "Rearrangement of genetic information may produce immunoglobulin
      diversity.";
RL      Nature 276:785-790(1978).
DR      PIR; A01938; KVM584.
DR      HSP; P01789; LMCP.
DR      InterPro; IPR003006; Iq_MHC.

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DR	InterPro; IPR003596; Ig_V.	
DR	Pfam; PF00047; Ig; 1.	
DR	SMART; SM00406; IGV; 1.	
KW	Immunoglobulin V region.	
FT	DOMAIN 1 23	FRAMEWORK-1.
FT	DOMAIN 24 38	COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN 39 53	FRAMEWORK-2.
FT	DOMAIN 54 60	COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN 61 92	FRAMEWORK-3.
FT	DOMAIN 93 101	COMPLEMENTARITY-DETERMINING-3.
FT	DOMAIN 102 111	FRAMEWORK-4.
FT	DISULFID 123 92	BY SIMILARITY.
FT	NON_TER 111 111	
SO	SEQUENCE 111 AA; 12039 MW; 1E4698834185826 CRC64;	
Query Match 66.8%; Score 137; DB 1; Length 111;		
Best Local Similarity 25.68; Pred. No. 0.01;		
Matches 20; Conservative 50; Mismatches 8; Indels 0; Gaps 0;		
Qy	1 KASGSVDYDGSVNMNXXXXXXXXXXXXXXXXXAAASLNLESXXXXXXXXXXXXXXXXXXXXXXX 60	
	:  :	
Db	24 RASKSVSTSGSYGMHWYQKQPQPKLLIYLAASLNLESGVPARFSGSGGTDTLNIHPVE 83	
Qy	61 XXXXXXXXXQSNEDPRT 78	
	:	
Db	84 EEDAATYCOHSRELPT 101	
RESULT 12		
KV3G_MOUSE		
ID	KV3G_MOUSE STANDARD; PRT; 112 AA.	
AC	P01659;	
DT	21-JUL-1986 (Rel. 01, Created)	
DT	21-JUL-1986 (Rel. 01, Last sequence update)	
DT	15-JUL-1999 (Rel. 38, Last annotation update)	
DE	Ig kappa chain V-III region TEPC 124.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE.	
RX	MEDLINE=73140225; PubMed=4691517;	
RA	McKean D.J., Potter M., Hood L.E.;	
RT	"Mouse immunoglobulin chains. Pattern of sequence variation among	
RL	kappa chains with limited sequence differences.";	
RL	Biochemistry 12:760-771(1973).	
DR	PIR: A01933; KWS32.	
DR	HSP; P01607; IREI.	
DR	InterPro; IPR003006; Ig_MHC.	
DR	InterPro; IPR003596; Ig_V.	
DR	Pfam; PF00047; Ig; 1.	
DR	SMART; SM00406; IGV; 1.	
KW	Immunoglobulin V region.	
FT	DOMAIN 1 23	FRAMEWORK-1.
FT	DOMAIN 24 38	COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN 39 53	FRAMEWORK-2.
FT	DOMAIN 54 60	COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN 61 92	FRAMEWORK-3.
FT	DOMAIN 93 101	COMPLEMENTARITY-DETERMINING-3.
FT	DOMAIN 102 111	FRAMEWORK-4.
FT	DISULFID 123 92	BY SIMILARITY.
FT	NON_TER 112 112	
SO	SEQUENCE 112 AA; 12339 MW; 7CFD328DBE9E9D71 CRC64;	

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Query Match      66.3%; Score 136; DB 1; Length 112;
Best Local Similarity 19.2%; Pred. No. 0.013;
Matches 15; Conservative 58; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KASQSDYDGDSDYWNXXXXXXXXXXXXXXXXXAASLDESXXXXXXXXXXXXXXXXXXXXX 60
      :||:||||: ||:|:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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DR HSP; P01789; IMCP.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 38  
FT DOMAIN 39 53  
FT DOMAIN 54 60  
FT DOMAIN 61 92  
FT DOMAIN 93 101  
FT DOMAIN 102 111  
FT DISULFID 23 92  
FT NON\_TER 111  
SQ SEQUENCE 111 AA; 11980 MW; AFEAC6A9D26FC12D CRC64;

FRAMEWORK-1.  
COMPLEMENTARITY-DETERMINING-1.  
FRAMEWORK-2.  
COMPLEMENTARITY-DETERMINING-2.  
FRAMEWORK-3.  
COMPLEMENTARITY-DETERMINING-3.  
FRAMEWORK-4.  
BY SIMILARITY.

Query Match 54.4%; Score 132; DB 1; Length 111;  
Best Local Similarity 25.6%; Pred. No. 0.028;  
Matches 20; Conservative 50; Mismatches 8; Indels 0; Gaps 0;

QY 1 KASQSDYDGDGYNNXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXXXXXX 60  
Db 24 RASEVDNYGISFMWFQQKPGQPKLLIYAASNOGCGVPARFSGSGGTDGSLNIHPME 83  
QY 61 XXXXXXXXXQOSNEDPRT 78  
Db 84 EDDTAMVFCQSQSKEVPWT 101

Search completed: August 14, 2002, 15:23:12  
Job time: 685 sec

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Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	135	65.9	103	11	Q9JL80	Q9JL80 mus musculus	
2	130	63.4	111	11	Q9Z0E9	Q9Z0E9 mus musculus	
3	113	55.1	107	4	Q96SA9	Q96SA9 homo sapien	
4	113	55.1	108	4	Q9UL77	Q9UL77 homo sapien	
5	110	53.7	107	4	Q9UL61	Q9UL61 homo sapien	
6	108	52.7	108	4	Q9UL70	Q9UL70 homo sapien	
7	104.5	51.0	114	4	Q9UL80	Q9UL80 homo sapien	
8	103	50.2	1299	4	Q96JM2	Q96JM2 homo sapien	
9	101	49.3	260	11	Q09004	Q09004 mus musculus	
10	101	49.3	408	16	Q9PMZ3	Q9PMZ3 campylobact	
11	101	49.3	557	10	Q9FVQ1	Q9FVQ1 arabidopsis	
12	101	49.3	608	11	Q9QU69	Q9QU69 mus musculus	
13	101	49.3	609	4	Q00538	Q00538 homo sapien	
14	101	49.3	671	4	Q9UL65	Q9UL65 homo sapien	
15	101	49.3	827	4	Q9H1B6	Q9H1B6 homo sapien	
16	100.5	49.0	97	11	Q9JL76	Q9JL76 mus musculus	

```
Qy 1 KASQSDYDGD SYMNX XXXXXXXXXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXX 60
```



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RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56269.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1 107
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 53.7%; Score 110; DB 4; Length 107;
Best Local Similarity 19.4%; Pred. No. 13;
Matches 14; Conservative 53; Mismatches 1; Indels 4; Gaps 1;

Qy 1 KASQSDVDGDSYMNXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXX 60
Db 24 RASQSI----SNLWVQKPGKAPNLLIYAASLSQSGVPSRFSGSGTDTLTISLQ 79

Qy 61 XXXXXXXXQOS 72
Db 80 AEDFATYCOQS 91

RESULT 6
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035034; AAD56270.1; -.
DR HSP; P80362; IWTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1 114
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match 51.0%; Score 104.5; DB 4; Length 114;
Best Local Similarity 16.9%; Pred. No. 43;
Matches 13; Conservative 53; Mismatches 10; Indels 1; Gaps 1;

Qy 1 KASQSDVDGDSYMNXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXX 59
Db 24 RSSQSPVSDGNTYLNWFQRPQSPRLIYKVSNRDGVDPFRFSGSGTDTLKISRV 83

Qy 60 XXXXXXXXQOSNEDP 76
Db 84 EAEDVGVIYCMQGTWP 100

RESULT 8
Q96JM2 PRELIMINARY; PRT; 1299 AA.
AC Q96JM2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE KIAA1803 PROTEIN (FRAGMENT).
GN KIAA1803.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=BRAIN;
RX MEDLINE=21245130; PubMed=11347906;
RA Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XX.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 8:85-95(2001).
DR EMBL; AB058706; BAB47432.1; -.
FT NON_TER 1 1299
FT NON_TER 1 1299
SQ SEQUENCE 1299 AA; 148675 MW; 69FFECB5868186DD CRC64;
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RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56269.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1 107
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 53.7%; Score 110; DB 4; Length 107;
Best Local Similarity 19.4%; Pred. No. 13;
Matches 14; Conservative 53; Mismatches 1; Indels 4; Gaps 1;

Qy 1 KASQSDVDGDSYMNXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXX 60
Db 24 RASQSI----SNLWVQKPGKAPNLLIYAASLSQSGVPSRFSGSGTDTLTISLQ 79

Qy 61 XXXXXXXXQOS 72
Db 80 AEDFATYCOQS 91

RESULT 6
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1 108
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3B41FCCA37 CRC64;

Query Match 52.7%; Score 108; DB 4; Length 108;
Best Local Similarity 17.9%; Pred. No. 20;
Matches 14; Conservative 53; Mismatches 7; Indels 4; Gaps 1;

Qy 1 KASQSDVDGDSYMNXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXX 60
Db 24 RASQSI----SNLWVQKPGKPKSLIYAASLTQSGVPSRFSGSGTDTLTISLQ 79

Qy 61 XXXXXXXXQOSNEDP 78
Db 80 PEDVATYCOKYNAPRT 97
```

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Query Match          50.2%; Score 103; DB 4; Length 1299;
Best Local Similarity 17.3%; Pred. No. 9.7e+03;
Matches 13; Conservative 51; Mismatches 11; Indels 0; Gaps 0;

QY 1 KASQVDYDGDGSMYNNXXXXXXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXX 60
   :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | |
Db 1169 ESSSSDDEKEEMNSKAEDRELMRFSHDGCAALNTEKRFPCFCGAFSGSEWEHVL 1228

QY 61 XXXXXXXXQQSND 75
Db 1229 HGMALNDRQVSREE 1243

RESULT 9
ID O09004 PRELIMINARY; PRT; 260 AA.
AC O09004;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE F2583.3 KINASE LIKE PROTEIN (FRAGMENT).
GN RASGRP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98001089; PubMed=9341881;
RA Kedra D., Seroussi E., Fransson I., Trifunovic J., Clark M.,
RA Lagercrantz J., Blennow E., Mehlin H., Dumanski J.;
RT "The germline centre kinase gene and a novel CDC25-like gene are
RT located in the vicinity of the PYGM gene on 11q13."
RL Hum. Genet. 100:611-619(1997).
CC -!- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
DR EMBL; Y12339; CAA73008.1; -.
DR HSSP; P28867; 1PTQ.
DR MGD; MGI:1333849; Rasgrp2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00130; DAG_PE-bind; 1.
DR Pfam; PF00036; ehand; 2.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR SMART; SM00109; Cl. 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_2.
KW Calcium-binding; Kinase.
FT NON_TER 1
FT SEQUENCE 260 AA; 29259 MW; 3C0CC2B41F64A12A CRC64;

Query Match          49.3%; Score 101; DB 11; Length 260;
Best Local Similarity 12.9%; Pred. No. 4.8e+02;
Matches 9; Conservative 55; Mismatches 6; Indels 0; Gaps 0;

QY 4 QSVVDGDSYNNXXXXXXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXX 63
   :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | |
Db 88 RNFVDGSGHISQEBFQIRNGFPYLSAFGLDQDQCGICISREIMSYFLRSSVILGRM 147

QY 64 XXXXXXXXQSN 73
Db 148 GFVHNFQESN 157

RESULT 10
ID Q9PMZ3 PRELIMINARY; PRT; 408 AA.
AC Q9PMZ3;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN CJ1306C.
```

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GN CJ1306C.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIC 11168;
RA MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences."
RL Nature 403:665-668(2000).
KW EMBL; AL139078; CAB73733.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 408 AA; 47256 MW; DD0D034E75EF7C22 CRC64;

Query Match          49.3%; Score 101; DB 16; Length 408;
Best Local Similarity 16.0%; Pred. No. 1.2e+03;
Matches 12; Conservative 49; Mismatches 14; Indels 0; Gaps 0;

QY 4 QSVVDGDSYNNXXXXXXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXX 63
   :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | |
Db 239 KSGKTNGDMYMQGDHFFVSCFLKTHWTRKNSPYFFNNENYFIRTLNKLHLQSKNK 298

QY 64 XXXXXXXXQSNEDPRT 78
Db 299 NIIVSVYHSKEDPLT 313

RESULT 11
ID Q9FVQ1 PRELIMINARY; PRT; 557 AA.
AC Q9FVQ1;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE NUM1 PROTEIN, PUTATIVE.
GN F2K7.6.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
RA Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
RA Barnstead M.F., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome 1 BAC F27K7 genomic sequence."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC084414; AAG29744.1; -.
DR InterPro; IPR000504; RRM.
DR Pfam; PF00076; rrm; 2.
DR SMART; SM00360; RRM; 2.
DR PROSITE; PS00102; RRM; 2.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
SQ SEQUENCE 557 AA; 58773 MW; F6CAA737689B4CBA CRC64;

Query Match          49.3%; Score 101; DB 10; Length 557;
Best Local Similarity 17.3%; Pred. No. 2.4e+03;
Matches 13; Conservative 50; Mismatches 12; Indels 0; Gaps 0;

QY 1 KASQVDYDGDGSMYNNXXXXXXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXX 60
   :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | | :| | |
Db 182 KDSSSSDDSDSEDEKPAKKAAPAAKAAASSDSDSDSEDESEDEKPAKKAADTKA 241
```



```
Query Match      49.38; Score 101; DB 11; Length 608;  
Best Local Similarity   12.9%; Pred. No. 2.9e+03;  
Matches          9; Conservative    55; Mismatches     6; Indels       0; Gaps        0;
```

Qy      4 QSVYDGDGVSNNXXXXXXXXXXXXAAASLNLSKXXXXXXXXXXXXXXXXXXXXXXXXXX 63  
       :: ||| :::::::::::::::::::: | : ::::::::::::::::::::

Dd      436 RNFDVDGGHLSQEFGIIRNFYLAFGLDONQDCISREMI SFI LASSV LGRM 495  
          :::~::~:

Qy      64 XXXXQQSN 73  
          :::~::~:

```
KW Calcium-binding; Phorbol-ester binding.
SQ SEQUENCE 609 AA; 69248 MW; 8B1321F864D24BC7 CRC64;

Query Match          49.3%; Score 101; DB 4; Length 609;
Best Local Similarity 12.9%; Pred. No. 2.9e+03;
Matches 9; Conservative 55; Mismatches 6; Indels 0; Gaps 0;

QY 4 QSVVDGDSYMNXXXXXXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXX 63
Db 436 RNFVDVGDHISQEEFQIIRGNFPYLSAFGLDQNDGICISREEMYSYFLRSSVVLGGRM 495

QY 64 XXXXXQOQSN 73
Db 496 GFVHNFQESN 505

RESULT 14
Q9UL65 PRELIMINARY; PRT; 671 AA.
AC Q9UL65;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE GUANINE EXCHANGE FACTOR MCG7 ISOFORM 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20493616; PubMed=10918068;
RA Clyde-Smith J., Sillins G., Gartside M., Grimmond S., Etheridge M.,
RA Apolloni A., Hayward N., Hancock J.F.;
RT "Characterization of RasGRP2, a Plasma Membrane-targeted, Dual
RT Specificity Ras/Rap Exchange Factor.";
RL J. Biol. Chem. 275:32260-32267(2000).
CC -/- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
DR EMBL; AF043722; AAF07219.1; -.
DR HSP; P28867; 1PTQ.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000651; RasGEFN.
DR InterPro; IPR001895; RasGRF_CDC25.
DR Pfam; PF00130; DAG_PE-bind; 1.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00617; RasGEF; 1.
DR SMART; SM00109; Cl; 1.
DR SMART; SM00147; RasGEF; 1.
DR SMART; SM00229; RasGEFN; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_2.
KW Calcium-binding.
SQ SEQUENCE 671 AA; 75547 MW; 67B7BD2B4F4AED4D CRC64;

Query Match          49.3%; Score 101; DB 4; Length 671;
Best Local Similarity 12.9%; Pred. No. 3.5e+03;
Matches 9; Conservative 55; Mismatches 6; Indels 0; Gaps 0;

QY 4 QSVVDGDSYMNXXXXXXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXX 63
Db 498 RNFVDVGDHISQEEFQIIRGNFPYLSAFGLDQNDGICISREEMYSYFLRSSVVLGGRM 557

QY 64 XXXXXQOQSN 73
Db 558 GFVHNFQESN 567

RESULT 15
Q9H1B6 PRELIMINARY; PRT; 827 AA.
AC Q9H1B6;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE XYLOSYLTRANSFERASE I (EC 2.4.2.26) (FRAGMENT).
GN XT-I.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20553456; PubMed=11099377;
RA Goetting C., Kuhn J., Zahn R., Brinkmann T., Kleesiek K.;
RT "Molecular cloning and expression of human UDP-D-xylose:proteoglycan
RT core protein beta-D-xylosyltransferase and its first isoform XT-II.";
RL J. Mol. Biol. 304:517-528(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Kuhn J., Goetting C., Schnoelzer M., Kempf T., Brinkmann T.,
RA Kleesiek K.;
RT "First isolation of human UDP-D-xylose:proteoglycan core protein
RT beta-D-xylosyltransferase secreted from cultured JAR choriocarcinoma
RT cells.";
RL J. Biol. Chem. 0:0-0(0).
DR EMBL; AJ277441; CAC16787.1; -.
KW Transferase; Glycosyltransferase.
FT NON_TER 1
SQ SEQUENCE 827 AA; 94490 MW; B4A96BE24F094CCF CRC64;

Query Match          49.3%; Score 101; DB 4; Length 827;
Best Local Similarity 17.3%; Pred. No. 5.5e+03;
Matches 13; Conservative 53; Mismatches 7; Indels 2; Gaps 1;

QY 1 KASQSDYDGDGS--YMNXXXXXXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXX 58
Db 174 KANKNVQWDEDSVEYMPANFVRIFAFLVYVHGRASRLQRMFKAIYHKHFYTHVDKRSN 233

QY 59 XXXXXXXXXXQOQSN 73
Db 234 YLHRQVLQVSQYSN 248

Search completed: August 14, 2002, 15:22:14
Job time: 682 sec
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:15:34 ; Search time 230.21 Seconds  
(without alignments)  
114.832 Million cell updates/sec

Title: US-09-499-662-127  
Perfect score: 1237  
Sequence: 1 METDRIILLWLLWPGSTG.....EVTHQGLSPVTKSPNRGEC 238

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1237	100.0	238	21	Humanised anti-Fas
2	1236	99.9	238	21	Humanised anti-Fas
3	1233	99.7	238	21	Humanised anti-Fas
4	1173	94.8	238	19	Anti-Fas humanised
5	1173	94.8	238	21	Humanised anti-Fas
6	1173	94.8	238	21	Humanised anti-Fas
7	1168	94.4	238	19	Humanised anti-Fas
8	1168	94.4	238	21	Humanised anti-Fas
9	1168	94.4	238	21	Humanised anti-Fas
10	1155	93.4	238	19	Anti-Fas humanised
11	1155	93.4	238	21	Humanised anti-Fas

12	1155	93.4	238	21	AAW90923	Humanised anti-Fas
13	1154	93.3	238	19	AAW83035	Anti-Fas humanised
14	1154	93.3	238	21	AAW83035	Humanised anti-Fas
15	1154	93.3	238	21	AAW90928	Humanised HFE7A de
16	1153	93.2	238	19	AAW83033	Anti-Fas humanised
17	1153	93.2	238	21	AAW83033	Humanised anti-Fas
18	1153	93.2	238	21	AAW90924	Humanised anti-Fas
19	1112	89.9	218	18	AAW13563	Humanised anti-L-s
20	1100	88.9	218	20	AAW95658	Mus musculus anti-
21	1100	88.9	218	21	AAW85200	Light chain amino
22	1100	88.9	218	22	AAW76947	Full variable ligh
23	1093	88.4	218	22	AAW833312	Humanised VaE11 Ve
24	1077	87.1	218	20	AAW50030	Human E27 anti-IgE
25	1077	87.1	218	20	AAW95660	Mus musculus anti-
26	1077	87.1	218	20	AAW95662	Mus musculus anti-
27	1077	87.1	218	21	AAW07472	Amino acid sequenc
28	1077	87.1	218	22	AAW74211	E27 anti-IgE antib
29	1074	86.8	218	20	AAW95669	Mus musculus anti-
30	1074	86.8	218	20	AAW95664	Mus musculus anti-
31	1074	86.8	218	22	AAW47087	Anti-IgE antibody,
32	1074	86.8	218	22	AAW76949	Full length light
33	1074	86.8	218	22	AAW76951	Full length light
34	1074	86.8	218	22	AAW76953	Variable light cha
35	1074	86.8	218	22	AAW76958	Variable light cha
36	1053.5	85.2	237	21	AAW96298	Human IGFAM-10 imm
37	1049.5	84.8	237	21	AAW96289	Human IGFAM-1 immu
38	1047.5	84.7	241	22	AAW82912	Human immune respo
39	1045.5	84.5	234	14	AAW38162	Sequence of the ka
40	1044	84.4	240	20	AAW50161	Human reshaped F19
41	1041.5	84.2	237	21	AAW96301	Human IGFAM-13 imm
42	1040	84.1	234	18	AAW11638	Human anti-RSV mon
43	1027	83.0	240	22	AAW63665	Amino acid sequenc
44	1023	82.7	236	16	AAW77614	Humanised 5G1.1 VL
45	1022.5	82.7	233	14	AAW30777	pH52-9.0 humanised

ALIGNMENTS

RESULT 1

AAW90930 ID AAW90930 standard; Protein; 238 AA.

AC AAW90930;

DT 08-AUG-2000 (first entry)

DE Humanised anti-Fas designed light chain Leu 1 protein.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;  
KW dermatologic; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;  
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;  
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

XX Synthetic.

OS EP990663-A2.

XX 05-APR-2000.

XX 29-SEP-1999; 99EP-0307711.

XX 30-SEP-1998; 98JP-0276881.

XX 30-SEP-1998; 98JP-0276882.

XX (SANY ) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 WI: 2000-258930/23.  
 N-PSDB; AAL1631.  
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems -  
 XX Claim 3; Page 156-157; 263pp; English.  
 XX This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antitumor,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,  
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody light chain construct designated Leu 1  
 CC which is described in the method of the invention.  
 XX Sequence 238 AA;

Query Match 100.0%; Score 1237; DB 21; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 6.7e-62;  
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 METDTLLWVLLWPGSTGDIIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSTYNNWY 60  
 Db 1 metdttllwvllwpgstgdiivltqspsslsasvgdrtvitckasqsdydgdstymwv 60  
 QY 61 QOKPKRKLIIYAASNLSEGVPSRFGSGSGTDFLTITSLQPEFATYVYCOQSNEDPR 120  
 Db 61 qkpkrgkplliyaasnlesgvpsrfgsgsgtdftltitsslqpeafatyvcqsgnedpr 120  
 QY 121 TFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVYVCLNNFYFREAKVQKVDNALQS 180  
 Db 121 tfgggtkveikrtvaapsvfifppsdeqlksgtasvyclnnfyfreakvqkvdnalqs 180  
 QY 181 GNSQSVTEQDSDSTYSLSSTLTSLKADYKHKYVACEVTHOGLSSPVTKFNREGC 238  
 Db 181 gnsqsvteqsdksdystyslsstltslkadyekhykvyacevthoglspsvtfkfnregc 238

RESULT 2  
 AAW90932  
 ID AAW90932 standard; Protein: 238 AA.  
 XX AC AAW90932;  
 XX DT 08-AUG-2000 (first entry)  
 XX DE Humanised anti-Fas designed light chain Leu 3 protein.

XX Pas: antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;  
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
 KW hepatotropic; antiinfertility; neuroprotective; antirheumatic; antidiabetic;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
 XX Synthetic.  
 OS EP990663-A2.  
 XX 05-APR-2000.  
 XX 29-SEP-1999; 99EP-0307711.  
 PR 30-SEP-1998; 98JP-0276881.  
 PR 30-SEP-1998; 98JP-0276882.  
 XX (SANY ) SANKYO CO LTD.  
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 WI: 2000-258930/23.  
 DR N-PSDB; AAL1633.  
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems -  
 XX Claim 3; Page 161-162; 263pp; English.  
 XX This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antitumor,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,  
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody light chain construct designated Leu 3  
 CC which is described in the method of the invention.  
 XX Sequence 238 AA;

Query Match 99.9%; Score 1236; DB 21; Length 238;  
 Best Local Similarity 99.6%; Pred. No. 7.6e-62;  
 Matches 237; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 METDTLLWVLLWPGSTGDIIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSTYNNWY 60

Db 1 metdtillwllwvpgstgdivltqspsslsasvsgdrvtltckasqsvdygdsmwmy 60  
Qy 61 QOKPGKAPKLLIYAASNLSESGVPSRFSGSGCTDFTLTISSLPQDPDFATYYCOQSNEDPR 120  
Db 61 qkpgkpklliyaasnlsegsiprfsqsgsgtdftltisslpqdpdfatyyccqsgnedpr 120  
Qy 121 TFGQGTKEIKRTVAAPSVFIPPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQS 180  
Db 121 tfgqgtkeikrtvaapsvfippsdeqlksgtasvcllnffypreakvqwkvdnalqs 180  
Qy 181 GNSQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238  
Db 181 gnsqsvteqdsksdystlsstltlskadyekhkyvacevthqglsspvtksfnrgec 238

RESULT 3  
ID AAW90931 standard; Protein; 238 AA.  
XX AAW90931;  
AC AAW90931;  
XX AAW90931;  
DT 08-AUG-2000 (first entry)  
XX 08-AUG-2000 (first entry)  
DE Humanised anti-Fas designed light chain Leu 2 protein.  
XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
XX anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;  
XX dermatologic; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
XX nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;  
XX hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
XX Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
XX Sjogren's syndrome; anemia; Addison's disease; sterility; myasthenia gravis;  
XX Goodpasture syndrome; Crohn's disease; scleroderma; sterility;  
XX multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
XX insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
XX cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
XX Synthetic.  
OS Synthetic.  
FN EP990663-A2.  
XX EP990663-A2.  
PD 05-APR-2000.  
XX 05-APR-2000.  
PF 29-SEP-1999; 99EP-0307711.  
XX 29-SEP-1999; 99EP-0307711.  
PR 30-SEP-1998; 98JP-0276881.  
XX 30-SEP-1998; 98JP-0276881.  
PR 30-SEP-1998; 98JP-0276882.  
XX 30-SEP-1998; 98JP-0276882.  
PA (SANY ) SANKYO CO LTD.  
XX (SANY ) SANKYO CO LTD.  
XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
PI WPI: 2000-258930/23.  
XX WPI: 2000-258930/23.  
DR N-PSDB: AAA11632.  
XX N-PSDB: AAA11632.  
PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
XX inflammatory or autoimmune disease, induces apoptosis selectively in  
XX cells with abnormal Fas-Fas ligand systems  
PS Claim 2; Page 159; 263pp; English.  
XX Claim 2; Page 159; 263pp; English.  
CC This invention describes a novel humanized anti-Fas antibody-like  
XX molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
XX ligand system, by binding to Fas on the cell surface, and prevents  
XX apoptosis in cells with a normal system, by inhibiting binding between  
XX Fas and its ligand. The products of the invention have anti-inflammatory,  
XX anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
XX immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
XX antirheumatic, nephrotropic, antinfertility, neuroprotective,  
XX antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce  
XX apoptosis by binding to cell surface Fas or inhibit it by competitive  
XX inhibition of ligand binding. (I) are used to treat and/or prevent

CC diseases associated with the Fas/Fas ligand system, especially systemic  
XX lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
XX versus host disease, Sjogren's syndrome, pernicious or hypoplastic  
XX anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
XX disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
XX multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
XX dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
XX cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
XX (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
XX inhibit apoptosis in normal cells but selectively induce it in abnormal  
XX cells. They bind to both human and murine Fas, so can be evaluated in  
XX murine disease models. (I) act on the active site of Fas, i.e. they mimic  
XX the native ligand, do not induce liver disease, or have reduced risk of  
XX inducing a human anti-murine antibody response. This sequence represents  
XX a humanised anti-Fas antibody light chain construct designated Leu 2  
XX which is described in the method of the invention.

SQ Sequence 238 AA;  
Query Match 99.7%; Score 1233; DB 21; Length 238;  
Best Local Similarity 99.6%; Pred. No. 1.1e-61;  
Matches 237; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 METDRIILLWLLWVPGSTGDIVLTQSPSSLSASVSGDRVTITCKASQSVDYDQDSIMWY 60  
Db 1 metdtillwllwvpgstgdivltqspsslsasvsgdrvtitckasqsvdygdsmwmy 60  
Qy 61 QOKPGKAPKLLIYAASNLSESGVPSRFSGSGCTDFTLTISSLPQDPDFATYYCOQSNEDPR 120  
Db 61 qkpgkpklliyaasnlsegsiprfsqsgsgtdftltisslpqdpdfatyyccqsgnedpr 120  
Qy 121 TFGQGTKEIKRTVAAPSVFIPPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQS 180  
Db 121 tfgqgtkeikrtvaapsvfippsdeqlksgtasvcllnffypreakvqwkvdnalqs 180  
Qy 181 GNSQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238  
Db 181 gnsqsvteqdsksdystlsstltlskadyekhkyvacevthqglsspvtksfnrgec 238

RESULT 4  
AAW83034  
ID AAW83034 standard; Protein; 238 AA.  
XX AAW83034;  
AC AAW83034;  
XX AAW83034;  
DT 15-MAR-1999 (first entry)  
XX 15-MAR-1999 (first entry)  
DE Anti-Fas humanised antibody HFE7A light chain PDHH type.  
XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;  
XX apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;  
XX systemic lupus erythematosus; graft versus host disease;  
XX Sjogren syndrome; pernicious anaemia; Addison's disease; sterility;  
XX scleroderma; Goodpasture syndrome; Crohn's disease; myasthenia gravis; multiple sclerosis; Basedow's disease;  
XX rheumatoid arthritis; autoimmune haemolytic anaemia;  
XX thrombopenia purpura; insulin-dependent diabetes; allergy;  
XX atopy; arteriosclerosis; myocarditis; cardiomyopathy; AIDS;  
XX glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
XX transplant rejection; therapy.  
OS Homo sapiens.  
XX Homo sapiens.  
OS Synthetic.  
XX Synthetic.  
XX Key Location/Qualifiers  
FH Peptide 1..20  
FT /label= Sig\_peptide  
FT Protein 21..238  
FT /label= Mat\_protein  
FT Region 21..131  
FT /label= Variable





Best Local Similarity 92.9%; Pred. No. 2.4e-58;  
Matches 221; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 METDTILLWVLLWVPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDVDYDGSYMNWY 60  
DB 1 metdtillwvllwvpgstgeivltqspgtlslpgeratlsckasqsdvdgdsymnw 60

QY 61 QOKPGKAPKLIYAAASNLSEGVPRFSGSGSDTFTLTISLQPEDFATYYCQSQSNEPDR 120  
DB 61 qkpgqapqlliyaaasnlsgipdrfsgsgsgtdftltisrlepedfavyyccsqsnedpr 120

QY 121 TFGOGTKVEIKRTVAAPSVFIPPSDEQLKSGTASVCLLNFFPREAKVQKVDNALQS 180  
DB 121 tfgogtkleikrtvaapsvfippsdeqlksgtasvcllnffpreakvqkvdnalqs 180

QY 181 GNSQSVTEQDSKDYSTSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238  
DB 181 gnsqsvteqdsksdstylsstltlskadyekhkvyacevthqglsspvtksfngrec 238

RESULT 6  
AAW90927  
ID AAW90927 standard; Protein: 238 AA.  
XX  
AC AAW90927;  
XX  
DT 08-AUG-2000 (first entry)  
XX  
DE Humanised HFE7A designed light chain protein.  
XX  
KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;  
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;  
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
XX  
OS Synthetic.  
XX  
PN EP990663-A2.  
XX  
PD 05-APR-2000.  
XX  
PF 29-SEP-1999; 99EP-0307711.  
XX  
PR 30-SEP-1998; 98JP-0276881.  
PR 30-SEP-1998; 98JP-0276882.  
XX  
PA (SANY ) SANKYO CO LTD.  
XX  
PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
XX  
DR WPI; 2000-258930/23.  
DR N-PSDB; AAA11614.  
XX  
PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
PT inflammatory or autoimmune disease, induces apoptosis selectively in  
PT cells with abnormal Fas-Fas ligand systems -  
XX  
PS Claim 3; Page 141-142; 263pp; English.  
XX  
CC This invention describes a novel humanized anti-Fas antibody-like  
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
CC ligand system, by binding to Fas on the cell surface, and prevents  
CC apoptosis in cells with a normal system, by inhibiting binding between  
CC Fas and its ligand. The products of the invention have anti-inflammatory,  
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,

CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,  
CC antiarteriosclerotic, cardiac and hepatropic activity. (I) induce  
CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
CC inhibition of ligand binding. (I) are used to treat and/or prevent  
CC diseases associated with the Fas/Fas ligand system, especially systemic  
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
CC cells. They bind to both human and murine Fas, so can be evaluated in  
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
CC the native ligand, do not induce liver disease, and have reduced risk of  
CC inducing a human anti-murine antibody response. This sequence represents  
CC a humanised anti-Fas antibody HFE7A designed light chain which is used in  
CC the method described in the invention.  
XX  
SQ Sequence 238 AA;

Query Match 94.8%; Score 1173; DB 21; Length 238;  
Best Local Similarity 92.9%; Pred. No. 2.4e-58;  
Matches 221; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 METDTILLWVLLWVPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDVDYDGSYMNWY 60  
DB 1 metdtillwvllwvpgstgeivltqspgtlslpgeratlsckasqsdvdgdsymnw 60

QY 61 QOKPGKAPKLIYAAASNLSEGVPRFSGSGSDTFTLTISLQPEDFATYYCQSQSNEPDR 120  
DB 61 qkpgqapqlliyaaasnlsgipdrfsgsgsgtdftltisrlepedfavyyccsqsnedpr 120

QY 121 TFGOGTKVEIKRTVAAPSVFIPPSDEQLKSGTASVCLLNFFPREAKVQKVDNALQS 180  
DB 121 tfgogtkleikrtvaapsvfippsdeqlksgtasvcllnffpreakvqkvdnalqs 180

QY 181 GNSQSVTEQDSKDYSTSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238  
DB 181 gnsqsvteqdsksdstylsstltlskadyekhkvyacevthqglsspvtksfngrec 238

RESULT 7  
AAW83031  
ID AAW83031 standard; Protein: 238 AA.  
XX  
AC AAW83031;  
XX  
DT 15-MAR-1999 (first entry)  
XX  
DE Anti-Fas humanised antibody HFE7A light chain HH type.  
XX  
KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;  
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;  
KW systemic lupus erythematosus; graft versus host disease;  
KW Sjogren syndrome; pernicious anaemia; Addison's disease;  
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
KW rheumatoid arthritis; autoimmune haemolytic anaemia;  
KW myasthenia gravis; multiple sclerosis; Basedow's disease;  
KW thrombopenia purpura; insulin-dependent diabetes; allergy;  
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
KW transplant rejection; therapy.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
ET Peptide 1..20 /label= Sig\_peptide  
FT

FT Protein 21..238  
 FT /label= Mat\_protein  
 FT Region 21..131  
 FT /label= Variable  
 FT Region 132..238  
 FT /label= Constant  
 FT Region 44..58  
 FT /label= CDR\_L1  
 FT /note= "claim 9"  
 FT Region 74..80  
 FT /label= CDR\_L2  
 FT /note= "claim 9"  
 FT Region 113..121  
 FT /label= CDR\_L3  
 FT /note= "claim 9"  
 PN AU9859701-A.  
 XX 08-OCT-1998.  
 PD 30-MAR-1998; 98AU-0059701.  
 XX 08-OCT-1997; 97JP-0276064.  
 PR 01-APR-1997; 97JP-0082953.  
 PR 25-JUN-1997; 97JP-0169088.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 PI Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;  
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;  
 XX  
 DR WPI; 1998-543440/47.  
 DR N-PSDB; AAV70074.  
 XX  
 PT New antibodies and proteins bind conserved epitope of Fas antigen -  
 PT used to evaluate drugs in animal models and to treat Fas-associated  
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
 PT myocarditis, hepatitis and AIDS  
 XX  
 PS Claim 21; Page 199-199; 292pp; English.  
 XX  
 CC This is the amino acid sequence of the HH type humanised light  
 CC chain of murine anti-human Fas monoclonal antibody HFE7A.  
 CC Humanisation of the murine sequence (see AA83042) entailed making  
 CC P47A, K49R, H80S, P81R, V82L, E84P, E85A, A87F and T89V amino acid  
 CC substitutions; these residues are conserved in the human light  
 CC chain (kappa chain). Host cell Escherichia coli pHS6HH7 SANK 73497  
 CC harbors plasmid pHS6HH7 carrying a fusion fragment of the humanised  
 CC HH type HFE7A light chain and DNA encoding the region of human  
 CC immunoglobulin kappa chain, and is deposited as FERM BP-6073  
 CC (claimed). The invention provides methods for producing humanised  
 CC antibodies by culturing host cells. Humanised versions of HFE7A  
 CC (see AA83031-37), like native HFE7A, are capable of inducing  
 CC apoptosis in abnormal cells expressing Fas, and of inhibiting  
 CC Fas-induced apoptosis in normal cells. The humanised antibodies  
 CC are used to evaluate, in animal models, treatments of diseases that  
 CC involve Fas/Fas ligand interactions, and also to treat such  
 CC diseases, including autoimmune disease (e.g. systemic lupus  
 CC erythematosus, Hashimoto's disease, graft versus host disease,  
 CC Sjogren syndrome, pernicious anaemia, Addison's disease,  
 CC scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid  
 CC arthritis, autoimmune haemolytic anaemia, sterility, myasthenia  
 CC gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura  
 CC and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,  
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic  
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).  
 XX  
 SQ Sequence 238 AA;

Query Match 94.4%; Score 1168; DB 19; Length 238;  
 Best Local Similarity 92.4%; Pred. NO. 4.6e-58;  
 Matches 220; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 1 METDTILLVLLWVPGSTGDIVLTQSPSSLSASVGRVTITCKASQSDYDGDSTYNNWY 60  
 DB 1 metdtillvllwvpgstgdivltqspgtslspgeratlsckasgsdvdgdsgymwy 60  
 QY 61 QQKPGKAPKLLIYAASNLSEGVPSRSGSGCTDFTLTITSSLOPEDFATYYCOQSNEDPR 120  
 DB 61 qqkpgqaprllyiaaenlesgipdrfsgsgtdftltisrlepafavvycqgsnedpr 120  
 QY 121 TFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180  
 DB 121 tfgggtkeikrtvaapsvfifppdsdeqlksgtasvvcillnnfybreakqwkvdnalqs 180  
 QY 181 GNSQSVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSPVYTKSNRSEC 238  
 DB 181 gnsqsvteqskdstyslsstltlskadyekhkvacevthqglsspvtksnrgsec 238  
 RESULT 8  
 AAB14772  
 ID AAB14772 standard; Protein; 238 AA.  
 XX  
 AC AAB14772;  
 XX  
 DT 24-NOV-2000 (first entry)  
 XX  
 DE Humanised anti-Fas antibody light chain, SEQ ID NO:50.  
 XX  
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;  
 KW murine; humanised antibody; complementarity determining region; CDR;  
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;  
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;  
 KW hepatitis; AIDS; graft rejection; light chain.  
 XX  
 OS Chimeric - Mus musculus.  
 OS Chimeric - Homo sapiens.  
 XX  
 PN JP2000169393-A.  
 XX  
 PD 20-JUN-2000.  
 XX  
 PF 30-SEP-1999; 99JP-0278301.  
 XX  
 PR 30-SEP-1998; 98JP-0276883.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 DR WPI; 2000-485645/43.  
 DR N-PSDB; AAA72124.  
 XX  
 PT Preventive or treating agent for the diseases caused by an abnormality  
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains  
 PT anti-Fas antibody -  
 XX  
 PS Claim 20; Page 78-79; 139pp; Japanese.  
 XX  
 CC The invention relates to compositions for the prevention or treatment  
 CC or diseases caused by an abnormality in the Fas/Fas ligand system  
 CC containing an anti-Fas antibody as the active component. The anti-Fas  
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,  
 CC or a humanised version of HFE7A containing identical CDRs  
 CC (complementarity determining regions) to antibody HFE7A. Via its  
 CC interaction with Fas, the antibody of the invention acts as a modulator  
 CC of apoptosis. The composition of the invention may therefore be used in  
 CC the treatment or prevention of conditions such as autoimmune diseases,  
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,  
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS  
 CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778  
 CC represent the light chains of several humanised HFE7A-derived anti-Fas  
 CC antibodies.  
 XX  
 SQ Sequence 238 AA;

Query Match 94.4%; Score 1168; DB 21; Length 238;  
 Best Local Similarity 92.4%; Pred. No. 4.6e-58;  
 Matches 220; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 1 METDTILLWVLLWVPGSTGDIVLTQSPSSLSASVGDRTVITCRASQSVVDGDSYNNWY 60  
 Db 1 metdtillwvllwvpgstgdivltqspsslsasvgdrtvitrkasqsvdvdgdsymnw 60  
 QY 61 QOKPGKAPKLLIYAASNLSEGVPSRFGSGSGTDTLTITSSLPQEDFATYTCQSQSNEPR 120  
 Db 61 qkpgqgprlliyaasnlsgvpsrfgsgsgtdftltitsslpqedfatvycqsgsnepr 120  
 QY 121 TFGGCTKVEIKRTVAAPSVFIFFPSDEQLKSGTASVWCLLNFPYPRKAVQWKVDNALQS 180  
 Db 121 tfggtrleikrtvaapsvfifpssdeqlksgtasvsvcllnfnfypreakvqkvdnalqs 180  
 QY 181 GNSQESVTEQDSKSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTXSFNRGEC 238  
 Db 181 gnsqesvteqdsksdstylsstltlskadyekhkvyacevthqglsspvtksfnrgec 238

RESULT 9  
 ID AAW90922 standard; Protein: 238 AA.  
 XX AC AAW90922;  
 XX DT 08-AUG-2000 (first entry)  
 XX DE Humanised anti-Fas antibody HFE7A light chain HH type protein.

Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
 anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;  
 dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
 nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;  
 hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
 Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
 XX OS Synthetic.  
 XX PN EP990663-A2.  
 XX PD 05-APR-2000.  
 XX PF 29-SEP-1999; 99EP-0307711.  
 XX PR 30-SEP-1998; 98JP-0276881.  
 XX PR 30-SEP-1998; 98JP-0276882.  
 XX PA (SANY ) SANKYO CO LTD.  
 XX PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 XX WPI: 2000-258930/23.  
 XX DR N-PSDB: AAA11562.  
 XX PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 XX PT inflammation or autoimmune disease, induces apoptosis selectively in  
 XX PT cells with abnormal Fas-Fas ligand systems -  
 XX PS Example reference 14; Page 114-115; 263pp; English.  
 XX CC This invention describes a novel humanized anti-Fas antibody-like  
 XX CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 XX CC ligand system, by binding to Fas on the cell surface, and prevents  
 XX CC apoptosis in cells with a normal system, by inhibiting binding between

CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC immunomodulatory, anti-allergic, anti-arthritis, antiviral,  
 CC immunosuppressive, dermatological, immunosuppressive, thyromimetic,  
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,  
 CC antiarteriosclerotic, cardiac and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody HFE7A light chain HH type which is used in  
 CC the method described in the invention.

XX SQ Sequence 238 AA;

Query Match 94.4%; Score 1168; DB 21; Length 238;  
 Best Local Similarity 92.4%; Pred. No. 4.6e-58;  
 Matches 220; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 1 METDTILLWVLLWVPGSTGDIVLTQSPSSLSASVGDRTVITCRASQSVVDGDSYNNWY 60  
 Db 1 metdtillwvllwvpgstgdivltqspsslsasvgdrtvitrkasqsvdvdgdsymnw 60  
 QY 61 QOKPGKAPKLLIYAASNLSEGVPSRFGSGSGTDTLTITSSLPQEDFATYTCQSQSNEPR 120  
 Db 61 qkpgqgprlliyaasnlsgvpsrfgsgsgtdftltitsslpqedfatvycqsgsnepr 120  
 QY 121 TFGGCTKVEIKRTVAAPSVFIFFPSDEQLKSGTASVWCLLNFPYPRKAVQWKVDNALQS 180  
 Db 121 tfggtrleikrtvaapsvfifpssdeqlksgtasvsvcllnfnfypreakvqkvdnalqs 180  
 QY 181 GNSQESVTEQDSKSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTXSFNRGEC 238  
 Db 181 gnsqesvteqdsksdstylsstltlskadyekhkvyacevthqglsspvtksfnrgec 238

RESULT 10  
 ID AAW83032 standard; Protein: 238 AA.  
 XX AC AAW83032;  
 XX DT 15-MAR-1999 (first entry)  
 XX DE Anti-Fas humanised antibody HFE7A light chain HM type.

XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;  
 XX apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;  
 XX systemic lupus erythematosus; graft versus host disease;  
 XX Sjogren syndrome; pernicious anaemia; Addison's disease;  
 XX scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
 XX rheumatoid arthritis; autoimmune haemolytic anaemia;  
 XX myasthenia gravis; multiple sclerosis; Basedow's disease;  
 XX thrombopenia purpura; insulin-dependent diabetes; allergy;  
 XX atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
 XX glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
 XX transplant rejection; therapy.  
 XX OS Homo sapiens.  
 XX OS Synthetic.

FH Key Location/Qualifiers  
 FT Peptide 1..20  
 FT Protein /label= Sig\_peptide  
 FT 21..238  
 FT /label= Mat\_protein  
 FT 21..131  
 FT /label= Variable  
 FT 132..238  
 FT /label= Constant  
 FT 44..58  
 FT /label= CDR\_L1  
 FT /note= "claim 9"  
 FT 74..80  
 FT /label= CDR\_L2  
 FT /note= "claim 9"  
 FT 113..121  
 FT /label= CDR\_L3  
 FT /note= "claim 9"  
 PN AU9859701-A.  
 XX  
 XX 08-OCT-1998.  
 XX  
 XX 30-MAR-1998; 98AU-0059701.  
 XX  
 XX 08-OCT-1997; 97JP-0276064.  
 PR 01-APR-1997; 97JP-0082953.  
 PR 25-JUN-1997; 97JP-0169088.  
 XX  
 XX (SANY ) SANKYO CO LTD.  
 XX  
 XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;  
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;  
 XX  
 XX WPI: 1998-543440/47.  
 DR N-PSDB; AAV70075.  
 XX  
 XX New antibodies and proteins bind conserved epitope of Fas antigen -  
 PT used to evaluate drugs in animal models and to treat Fas-associated  
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
 PT myocarditis, hepatitis and AIDS  
 PT  
 XX Claim 21; Page 200; 292pp; English.  
 PS  
 XX  
 CC This is the amino acid sequence of the HM type humanised light  
 CC chain of murine anti-human Fas monoclonal antibody HFE7A.  
 CC Humanisation of the murine sequence (see AA83042) entailed making  
 CC P47A and K49R amino acid substitutions; these residues are  
 CC conserved in the human light (kappa) chain. Host cell E. coli  
 CC PHSGHM17 SANK 73597 harbors plasmid PHSGHM17 carrying a fusion  
 CC fragment of the humanised HM type HFE7A light chain and DNA  
 CC encoding the region of human immunoglobulin kappa chain, and is  
 CC deposited as FERM BP-6072 (claimed). The invention provides  
 CC methods for producing humanised antibodies by culturing host  
 CC cells. Humanised versions of HFE7A (see AA83031-37), like native  
 CC HFE7A, are capable of inducing apoptosis in abnormal cells  
 CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal  
 CC cells. The humanised antibodies are used to evaluate, in animal  
 CC models, treatments of diseases that involve Fas/Fas ligand  
 CC interactions, and also to treat such diseases, including autoimmune  
 CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,  
 CC graft versus host disease, Sjogren syndrome, pernicious anaemia,  
 CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,  
 CC sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,  
 CC thrombopenia purpura and insulin-dependent diabetes), allergies,  
 CC atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular  
 CC nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant  
 CC rejection (all claimed).  
 XX Sequence 238 AA;

Query Match 93.4%; Score 1155; DB 19; Length 238;  
 Best Local Similarity 91.6%; Pred. No. 2.4e-57;  
 Matches 218; Conservative 11; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 METDTILLWVLLWPGSTGDIVLTQSPSSLSASVGDRTITCKASQSDYDGDSTNNWY 60  
 Db 1 metdtillwvllwpgstgdivltqspgtlsipgeratlsckasgsdydgdssymwy 60  
 QY 61 QOKPGKAPKLLIYAASNLSESGVPSRESGSGTDFLTITSSLOPEDFANTYCOOSNEDPR 120  
 Db 61 qkpgqaprlllyaaanlesgipdrfsgsggtdfcflthpveeadaatyccqsgnedpr 120  
 QY 121 TFGQGTKEIKRTVAAPSFIFFPPSDEQLKSGTASVVLNNFYPREAKYQWKVDNALOS 180  
 Db 121 tfggtrleiktvaapsvfifppsdeqlksgtasvvlennfypreakvqkvdnalqs 180  
 QY 181 GNSQESVTEQDSKDSSTYSLSSTLTSLKADYEHKHVYACEVTHQGLSSPVTKSFNRSEC 238  
 Db 181 gnsqesvteqgskdstyslsstltlskadyekhkvacevthqglsspvtksfnrgsec 238  
 RESULT 11  
 AAB14773  
 ID AAB14773 standard; Protein; 238 AA.  
 XX  
 XX AAB14773;  
 XX  
 DT 24-NOV-2000 (first entry)  
 XX  
 DE Humanised anti-Fas antibody light chain, SEQ ID NO:52.  
 XX  
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;  
 KW murine; humanised antibody; complementarity determining region; CDR;  
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;  
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;  
 KW hepatitis; AIDS; graft rejection; light chain.  
 XX  
 OS Chimeric - Mus musculus.  
 OS Chimeric - Homo sapiens.  
 XX  
 PN JP2000169393-A.  
 XX  
 PD 20-JUN-2000.  
 XX  
 PF 30-SEP-1999; 99JP-0278301.  
 XX  
 PR 30-SEP-1998; 98JP-0276883.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 DR WPI: 2000-485645/43.  
 DR N-PSDB; AAA72125.  
 XX  
 PT Preventive or treating agent for the diseases caused by an abnormality  
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains  
 PT anti-Fas antibody -  
 PS  
 PS Claim 20; Page 80-81; 139pp; Japanese.  
 CC The invention relates to compositions for the prevention or treatment  
 CC of diseases caused by an abnormality in the Fas/Fas ligand system  
 CC containing an anti-Fas antibody as the active component. The anti-Fas  
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,  
 CC or a humanised version of HFE7A containing identical CDRs  
 CC (complementarity determining regions) to antibody HFE7A. Via its  
 CC interaction with Fas, the antibody of the invention acts as a modulator  
 CC of apoptosis. The compositions of the invention may therefore be used in  
 CC the treatment or prevention of conditions such as autoimmune diseases,  
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,  
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS  
 CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778  
 CC represent the light chains of several humanised HFE7A-derived anti-Fas

CC antibodies.  
 XX Sequence 238 AA;  
 SQ

Query Match 93.4%; Score 1155; DB 21; Length 238;  
 Best Local Similarity 91.6%; Pred. No. 2.4e-57;  
 Matches 218; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 METDTILLWLLVPGSTGDIVLTQSPSSLSASVGRVTTTCASQSDVDGDSYNNWY 60  
 DQ 1 metdtillwllvpgstgdivltqspgtlsispggeratlsckasqsdvdgdsynmwy 60

QY 61 QOKPGKAPKLLIYAASNLSEGVPSRFGSGSGTDTFTLTISSLOPEDFATYCCQSNEDPR 120  
 DQ 61 qokpggaprlliyaasnlsgvpsrfsgsgsgtdftltihpveeedaatyccqsgnedpr 120

QY 121 TFGOGTKVEIKRTVAAPSVFFPPSDQLKSGTASVVCVLLNNFYPRCAKQVQKVDNALQS 180  
 DQ 121 tfgogtgleikrtvaapsvffppsdqlksgtasvvcvllnnfyprcakvqkvdnalqs 180

QY 181 GNSQESVTEQDSKDYSLSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 238  
 DQ 181 gnsqesvteqdsksdystlslstltlskadyekhkvyacevthqglsspvtksfnrgec 238

RESULT 12  
 AA090923  
 ID AA090923 standard; Protein; 238 AA.  
 AC AA090923;  
 XX  
 XX 08-AUG-2000 (first entry)  
 DT  
 XX Humanised anti-Fas antibody HFE7A light chain HM type protein.  
 DE  
 XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
 KW dermatological; anti-arthritis; antiviral; immunomodulatory; cardiac;  
 KW dermatologic; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
 KW nephrotropic; antinfertility; neuroprotective; antiartherosclerotic;  
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
 XX  
 OS Synthetic.  
 XX  
 PN EP990663-A2.  
 XX  
 XX 05-APR-2000.  
 PD  
 XX 29-SEP-1999; 99EP-0307711.  
 PF  
 XX 30-SEP-1998; 98JP-0276881.  
 PR  
 XX 30-SEP-1998; 98JP-0276882.  
 XX  
 XX (SANY ) SANKYO CO LTD.  
 PA  
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 PI WPI: 2000-258930/23.  
 XX  
 DR N-PSDB: AAA11563.  
 DR  
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems  
 PT  
 XX Example reference 14; Page 117-118; 263pp; English.  
 PS  
 XX This invention describes a novel humanized anti-Fas antibody-like  
 XX

CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antirheumatic, nephrotropic, antinfertility, neuroprotective,  
 CC antiartherosclerotic, cardiac and hepatotropic activity. (I) induce  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody HFE7A light chain HM type which is used in  
 CC the method described in the invention.  
 XX  
 SQ Sequence 238 AA;

Query Match 93.4%; Score 1155; DB 21; Length 238;  
 Best Local Similarity 91.6%; Pred. No. 2.4e-57;  
 Matches 218; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 METDTILLWLLVPGSTGDIVLTQSPSSLSASVGRVTTTCASQSDVDGDSYNNWY 60  
 DQ 1 metdtillwllvpgstgdivltqspgtlsispggeratlsckasqsdvdgdsynmwy 60

QY 61 QOKPGKAPKLLIYAASNLSEGVPSRFGSGSGTDTFTLTISSLOPEDFATYCCQSNEDPR 120  
 DQ 61 qokpggaprlliyaasnlsgvpsrfsgsgsgtdftltihpveeedaatyccqsgnedpr 120

QY 121 TFGOGTKVEIKRTVAAPSVFFPPSDQLKSGTASVVCVLLNNFYPRCAKQVQKVDNALQS 180  
 DQ 121 tfgogtgleikrtvaapsvffppsdqlksgtasvvcvllnnfyprcakvqkvdnalqs 180

QY 181 GNSQESVTEQDSKDYSLSTLTLSKADYEKHKYACEVTHQGLSSPVTKSFNRGEC 238  
 DQ 181 gnsqesvteqdsksdystlslstltlskadyekhkvyacevthqglsspvtksfnrgec 238

RESULT 13  
 AA083035  
 ID AA083035 standard; Protein; 238 AA.  
 AC AA083035;  
 XX  
 XX 15-MAR-1999 (first entry)  
 DT  
 XX Anti-Fas humanised antibody HFE7A light chain PDHM type.  
 DE  
 XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;  
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;  
 KW systemic lupus erythematosus; graft versus host disease;  
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;  
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;  
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;  
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;  
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
 KW transplant rejection; therapy.  
 XX



CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS  
CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778  
CC represent the light chains of several humanised HFE7A-derived anti-Fas  
XX antibodies.  
SQ Sequence 238 AA;

Query Match 93.3%; Score 1154; DB 21; Length 238;  
Best Local Similarity 91.6%; Pred. No. 2.7e-57;  
Matches 218; Conservative 11; Mismatches 9; Indels 0; Gaps 0;  
QY 1 METDTILLWLLVPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDVDGDSYNNWY 60  
DB 1 metdtillwllwpstgdivltqspgtlslspgeratlsckasqsdvdygdsymnw 60  
QY 61 QOKPGKAPKLLIYAASNLGSGVPSRFGSGSGTDTFTLTISLQPEDFATYCCQSNEDPR 120  
DB 61 qqkpgqprlliyaasnlsgipdrfsgsgtdftltihpveedaatyccqsgnedpr 120  
QY 121 TFGOGTKVEIKRTVAAPSVFIFFPSDQLKSGTASVCLLNFFYPRAKQVOMKVDNALQS 180  
DB 121 tfgggtkleikrtvaapsvfifpssdeqlksgtasvcllnnfyreakvqkvdnalqs 180  
QY 181 GNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
DB 181 gnsqesvteqdsksdystlsstltlskadyekkhkvyacevthqglsspvtksfnrgec 238

RESULT 15  
AAW90928  
ID AAW90928 standard; Protein; 238 AA.  
AC AAW90928;  
XX XX  
DT 08-AUG-2000 (first entry)  
XX XX  
DE Humanised HFE7A designed light chain protein #2.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;  
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
KW nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;  
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
KW Sjorgen's syndrome; anemia; Addison's disease; sterility;  
KW Goodpasture syndrome; Crohn's disease; scleroderma; sterility;  
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

XX Synthetic.  
XX XX  
PN EF990663-A2.  
XX XX  
XX 05-APR-2000.  
XX XX  
PF 29-SEP-1999; 99EP-0307711.  
XX XX  
PR 30-SEP-1998; 98JP-0276881.  
PR 30-SEP-1998; 98JP-0276882.  
XX XX  
XX (SANY ) SANKYO CO LTD.  
XX XX  
XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
PI WPI: 2000-258930/23.  
XX N-PSDB; AAA11615.  
DR XX

XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
PT inflammatory or autoimmune disease, induces apoptosis selectively in  
PT cells with abnormal Fas-Fas ligand systems  
XX

PS  
XX

Example reference 21; Page 144-145; 263pp; English.

XX This invention describes a novel humanized anti-Fas antibody-like  
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
CC ligand system, by binding to Fas on the cell surface, and prevents  
CC apoptosis in cells with a normal system, by inhibiting binding between  
CC Fas and its ligand. The products of the invention have anti-inflammatory,  
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
CC antirheumatic, nephrotropic, antinfertility, neuroprotective,  
CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce  
CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
CC inhibition of ligand binding. (I) are used to treat and/or prevent  
CC diseases associated with the Fas/Fas ligand system, especially systemic  
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
CC versus host disease, Sjorgen's syndrome, Goodpasture syndrome, Crohn's  
CC anemia, Addison's disease, scleroderma, myasthenia gravis,  
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
CC cells. They bind to both human and murine Fas, so can be evaluated in  
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
CC the native ligand, do not induce liver disease, and have reduced risk of  
CC inducing a human anti-murine antibody response. This sequence represents  
CC a humanised anti-Fas antibody HFE7A designed light chain which is used in  
CC the method described in the invention.

XX Sequence 238 AA;

Query Match 93.3%; Score 1154; DB 21; Length 238;  
Best Local Similarity 91.6%; Pred. No. 2.7e-57;  
Matches 218; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 METDTILLWLLVPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDVDGDSYNNWY 60  
DB 1 metdtillwllwpstgdivltqspgtlslspgeratlsckasqsdvdygdsymnw 60  
QY 61 QOKPGKAPKLLIYAASNLGSGVPSRFGSGSGTDTFTLTISLQPEDFATYCCQSNEDPR 120  
DB 61 qqkpgqprlliyaasnlsgipdrfsgsgtdftltihpveedaatyccqsgnedpr 120  
QY 121 TFGOGTKVEIKRTVAAPSVFIFFPSDQLKSGTASVCLLNFFYPRAKQVOMKVDNALQS 180  
DB 121 tfgggtkleikrtvaapsvfifpssdeqlksgtasvcllnnfyreakvqkvdnalqs 180  
QY 181 GNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
DB 181 gnsqesvteqdsksdystlsstltlskadyekkhkvyacevthqglsspvtksfnrgec 238

Search completed: August 14, 2002, 15:15:34  
Job time: 832 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:17:03 ; Search time 82.88 Seconds  
(without alignments)  
70.141 Million cell updates/sec

Title: US-09-499-662-127  
Perfect score: 1237  
Sequence: 1 MTDTILLWLLWPGSTG.....EVTHQGLSPVTKSPNRGEC 238

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
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2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1112	89.9	218	5	PCT-US96-13152-2
2	1100	88.9	218	2	US-08-887-352B-13
3	1100	88.9	218	3	US-08-466-151-9
4	1100	88.9	218	4	US-09-109-207C-13
5	1100	88.9	218	4	US-09-296-005-13
6	1100	88.9	218	4	US-08-466-163B-9
7	1077	87.1	218	4	US-09-282-505-1
8	1077	87.1	218	4	US-09-054-255-1
9	1074	86.8	218	2	US-08-887-352B-15
10	1074	86.8	218	2	US-08-887-352B-17
11	1074	86.8	218	2	US-08-887-352B-19
12	1074	86.8	218	2	US-08-887-352B-24
13	1074	86.8	218	4	US-09-109-207C-15
14	1074	86.8	218	4	US-09-109-207C-17
15	1074	86.8	218	4	US-09-109-207C-19
16	1074	86.8	218	4	US-09-109-207C-24
17	1074	86.8	218	4	US-09-296-005-15
18	1074	86.8	218	4	US-09-296-005-17
19	1074	86.8	218	4	US-09-296-005-19
20	1074	86.8	218	4	US-09-296-005-24
21	1022.5	82.7	233	2	US-07-934-373C-25
22	1022.5	82.7	233	3	US-08-437-642B-25
23	1022.5	82.7	233	5	PCT-US93-07832-25
24	1019	82.4	214	2	US-07-934-373C-39
25	1019	82.4	214	3	US-08-437-642B-39
26	1019	82.4	214	5	PCT-US93-07832-39
27	1014	82.0	214	2	US-07-934-373C-40

28	1014	82.0	214	2	US-08-788-800-11	Sequence 11, Appl
29	1014	82.0	214	3	US-08-437-642B-40	Sequence 40, Appl
30	1014	82.0	214	3	US-09-097-309-2	Sequence 2, Appl
31	1014	82.0	214	4	US-09-097-171A-2	Sequence 2, Appl
32	1014	82.0	214	5	PCT-US93-07832-40	Sequence 40, Appl
33	1014	82.0	237	3	US-09-097-309-6	Sequence 6, Appl
34	1014	82.0	237	4	US-09-097-171A-10	Sequence 10, Appl
35	1014	82.0	237	4	US-09-422-712B-2	Sequence 2, Appl
36	1014	82.0	237	4	US-09-607-756-2	Sequence 2, Appl
37	1010.5	81.7	242	3	US-09-027-449-62	Sequence 62, Appl
38	1010.5	81.7	242	4	US-09-026-985-62	Sequence 62, Appl
39	1009.5	81.6	235	4	US-09-171-945-97	Sequence 97, Appl
40	1009.5	81.6	242	3	US-09-027-449-51	Sequence 51, Appl
41	1009.5	81.6	242	3	US-08-804-444A-51	Sequence 51, Appl
42	1009.5	81.6	242	4	US-09-026-985-51	Sequence 51, Appl
43	1006.5	81.4	219	3	US-09-027-449-72	Sequence 72, Appl
44	1006.5	81.4	219	4	US-09-026-985-72	Sequence 72, Appl
45	1006.5	81.4	242	3	US-09-027-449-56	Sequence 56, Appl

ALIGNMENTS

RESULT 1  
PCT-US96-13152-2  
; Sequence 2, Application PC/TUS9613152  
; GENERAL INFORMATION:  
; APPLICANT: Martin, Ulrich, et al.  
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ f  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; ADDRESSEE: Attn: Norman D. Hanson  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Computer Disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/13152  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/578,953  
; FILING DATE: 27-Dec-95  
; APPLICATION NUMBER: EP 95 112 895.8  
; FILING DATE: 17-Aug-95  
; APPLICATION NUMBER: EP 95 114 969.9  
; FILING DATE: 19-Sep-95  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Norman D. Hanson  
; REGISTRATION NUMBER: 30,946  
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 688-9200  
; TELEFAX: (212) 638-3884  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 218  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US96-13152-2

Query Match 89.9%; Score 1112; DB 5; Length 218;  
Best Local Similarity 98.2%; Pred. No. 1.6e-87;



Qy 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 200  
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180  
Qy 201 STLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
Db 181 STLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

## RESULT 4

US-09-109-207C-13  
; Sequence 13, Application US/09109207C  
; Patent No. 6172213  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide  
; FILE REFERENCE: P1123R1  
; CURRENT APPLICATION NUMBER: US/09/109,207C  
; CURRENT FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/051,554  
; PRIOR FILING DATE: 1997-07-03  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 13  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; NAME/KEY: Artificial  
; LOCATION: 1-218  
; OTHER INFORMATION: Light chain sequence derived from MAE11  
US-09-109-207C-13

Query Match 88.9%; Score 1100; DB 4; Length 218;  
Best Local Similarity 97.7%; Pred. No. 1.7e-86;  
Matches 213; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 21 DIVLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYMMWYQKPGKAPKLLIYAASNLES 80  
Db 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYMMWYQKPGKAPKLLIYAASYLE 60  
Qy 81 GVPFRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKEIKRTVAAPSVF 140  
Db 61 GVPFRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKEIKRTVAAPSV 120  
Qy 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 200  
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180  
Qy 201 STLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
Db 181 STLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

## RESULT 5

US-09-296-005-13  
; Sequence 13, Application US/09296005  
; Patent No. 6290957  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides  
; FILE REFERENCE: P1123C1r  
; CURRENT APPLICATION NUMBER: US/09/296,005  
; CURRENT FILING DATE: 1999-04-21  
; EARLIER APPLICATION NUMBER: US 08/887,352  
; EARLIER FILING DATE: 1997-07-02  
; NUMBER OF SEQ ID NOS: 26  
; SEQ ID NO 13  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; NAME/KEY: Artificial

; LOCATION: 1-218  
; OTHER INFORMATION: Light chain sequence derived from MAE11  
US-09-296-005-13

Query Match 88.9%; Score 1100; DB 4; Length 218;  
Best Local Similarity 97.7%; Pred. No. 1.7e-86;  
Matches 213; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 21 DIVLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYMMWYQKPGKAPKLLIYAASNLES 80  
Db 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYMMWYQKPGKAPKLLIYAASYLE 60  
Qy 81 GVPFRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKEIKRTVAAPSVF 140  
Db 61 GVPFRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKEIKRTVAAPSV 120  
Qy 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 200  
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180  
Qy 201 STLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
Db 181 STLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

## RESULT 6

US-08-466-163B-9  
; Sequence 9, Application US/08466163B  
; Patent No. 6329509  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; TITLE OF INVENTION: Immunoglobulin Variants  
; FILE REFERENCE: P0718P2C1D1  
; CURRENT APPLICATION NUMBER: US/08/466,163B  
; CURRENT FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: US 08/405,617  
; PRIOR FILING DATE: 1995-03-15  
; PRIOR APPLICATION NUMBER: US 08/185,899  
; PRIOR FILING DATE: 1994-01-26  
; PRIOR APPLICATION NUMBER: US 07/879,495  
; PRIOR FILING DATE: 1992-05-07  
; PRIOR APPLICATION NUMBER: US 07/744,768  
; PRIOR FILING DATE: 1991-08-14  
; NUMBER OF SEQ ID NOS: 64  
; SEQ ID NO 9  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: humanized maell, version 1, light chain  
US-08-466-163B-9

Query Match 88.9%; Score 1100; DB 4; Length 218;  
Best Local Similarity 97.7%; Pred. No. 1.7e-86;  
Matches 213; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 21 DIVLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYMMWYQKPGKAPKLLIYAASNLES 80  
Db 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYMMWYQKPGKAPKLLIYAASYLE 60  
Qy 81 GVPFRFSGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTFGQGTKEIKRTVAAPSVF 140  
Db 61 GVPFRFSGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGQGTKEIKRTVAAPSV 120  
Qy 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 200  
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180  
Qy 201 STLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
Db 181 STLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

Db 181 STLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 7  
US-09-282-505-1  
; Sequence 1, Application US/09282505A  
; Patent No. 6194551  
; GENERAL INFORMATION:  
; APPLICANT: Eschoe Ekinaduese Idusogie et al.  
; TITLE OF INVENTION: Polypeptide Variants  
; FILE REFERENCE: P1266R1  
; CURRENT APPLICATION NUMBER: US/09/282,505A  
; CURRENT FILING DATE: 1999-03-31  
; NUMBER OF SEQ ID NOS: 2  
; SEQ ID NO 1  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: Artificial Sequence  
; LOCATION: 1-218  
; OTHER INFORMATION: Sequence is completely synthesized  
; Patent No. 6194551  
US-09-282-505-1

Query Match 87.1%; Score 1077; DB 4; Length 218;  
Best Local Similarity 95.9%; Pred. No. 1.6e-84;  
Matches 209; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSDSYNNWYQKPGKAPKLLIYAASVLS 80  
|||  
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYNNWYQKPGKAPKLLIYAASVLS 60  
QY 81 GVPFRSGSGSGDTFTLTISLSLOPEDFATYCCQSNEDPRTFGQGTVEIKRTVAAPSVF 140  
|||  
Db 61 GVPFRSGSGSGDTFTLTISLSLOPEDFATYCCQSNEDPRTFGQGTVEIKRTVAAPSVF 120  
QY 141 IFPPSDEQLKSGTASVVCLLNFPYQKQVQKVDNALQSGNSQESVTEQDSKDSYLS 200  
|||  
Db 121 IFPPSDEQLKSGTASVVCLLNFPYQKQVQKVDNALQSGNSQESVTEQDSKDSYLS 180  
QY 201 STLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
|||  
Db 181 STLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 8  
US-09-054-255-1  
; Sequence 1, Application US/09054255  
; Patent No. 6242195  
; GENERAL INFORMATION:  
; APPLICANT: Eschoe Ekinaduese Idusogie et al.  
; TITLE OF INVENTION: Polypeptide Variants  
; FILE REFERENCE: P1266  
; CURRENT APPLICATION NUMBER: US/09/054,255  
; CURRENT FILING DATE: 1998-04-02  
; NUMBER OF SEQ ID NOS: 2  
; SEQ ID NO 1  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: E27 anti-IgE antibody light chain  
US-09-054-255-1

Query Match 87.1%; Score 1077; DB 4; Length 218;  
Best Local Similarity 95.9%; Pred. No. 1.6e-84;  
Matches 209; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSDSYNNWYQKPGKAPKLLIYAASVLS 80  
|||

Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYNNWYQKPGKAPKLLIYAASVLS 60  
QY 81 GVPFRSGSGSGDTFTLTISLSLOPEDFATYCCQSNEDPRTFGQGTVEIKRTVAAPSVF 140  
|||  
Db 61 GVPFRSGSGSGDTFTLTISLSLOPEDFATYCCQSNEDPRTFGQGTVEIKRTVAAPSVF 120  
QY 141 IFPPSDEQLKSGTASVVCLLNFPYQKQVQKVDNALQSGNSQESVTEQDSKDSYLS 200  
|||  
Db 121 IFPPSDEQLKSGTASVVCLLNFPYQKQVQKVDNALQSGNSQESVTEQDSKDSYLS 180  
QY 201 STLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
|||  
Db 181 STLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 9  
US-08-887-352B-15  
; Sequence 15, Application US/08887352B  
; Patent No. 5994511  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
; TITLE OF INVENTION: Improving Polypeptides  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,352B  
; FILING DATE: 03-Jul-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P1123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 218 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-887-352B-15

Query Match 86.8%; Score 1074; DB 2; Length 218;  
Best Local Similarity 95.4%; Pred. No. 2.8e-84;  
Matches 208; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSDSYNNWYQKPGKAPKLLIYAASVLS 80  
|||  
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYNNWYQKPGKAPKLLIYAASVLS 60  
QY 81 GVPFRSGSGSGDTFTLTISLSLOPEDFATYCCQSNEDPRTFGQGTVEIKRTVAAPSVF 140  
|||  
Db 61 GVPFRSGSGSGDTFTLTISLSLOPEDFATYCCQSNEDPRTFGQGTVEIKRTVAAPSVF 120  
QY 141 IFPPSDEQLKSGTASVVCLLNFPYQKQVQKVDNALQSGNSQESVTEQDSKDSYLS 200  
|||  
Db 121 IFPPSDEQLKSGTASVVCLLNFPYQKQVQKVDNALQSGNSQESVTEQDSKDSYLS 180  
QY 201 STLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
|||



; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,352B  
; FILING DATE: 03-Jul-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P1123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 218 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-887-352B-24

Query Match 86.8%; Score 1074; DB 2; Length 218;  
Best Local Similarity 95.4%; Pred. No. 2.8e-84;  
Matches 208; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGKAPKLLIYAASNLES 80  
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGEGDSYLNWYQKPGKAPKLLIYAASYLE 60  
QY 81 GVPFRFSGSGSGTDFTLTITSSLPQEDFATYYCQSNEDPRFTGQGTKEIKRTVAAPSVF 140  
Db 61 GVPFRFSGSGSGTDFTLTITSSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120  
QY 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 200  
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180  
QY 201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
Db 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 13  
US-09-109-207C-15  
; Sequence 15, Application US/09109207C  
; Patent No. 6172213  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiue, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide  
; FILE REFERENCE: P1123R1  
; CURRENT APPLICATION NUMBER: US/09/109,207C  
; CURRENT FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/051,554  
; PRIOR FILING DATE: 1997-07-03  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 15  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; NAME/KEY: Artificial  
; LOCATION: 1-218  
; OTHER INFORMATION: Light chain sequence derived from MAE11  
US-09-109-207C-15

Query Match 86.8%; Score 1074; DB 4; Length 218;  
Best Local Similarity 95.4%; Pred. No. 2.8e-84;  
Matches 208; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGKAPKLLIYAASNLES 80  
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGEGDSYLNWYQKPGKAPKLLIYAASYLE 60  
QY 81 GVPFRFSGSGSGTDFTLTITSSLPQEDFATYYCQSNEDPRFTGQGTKEIKRTVAAPSVF 140

Db 61 GVPFRFSGSGSGTDFTLTITSSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120  
QY 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 200  
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180  
QY 201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
Db 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 14  
US-09-109-207C-17  
; Sequence 17, Application US/09109207C  
; Patent No. 6172213  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiue, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept  
; FILE REFERENCE: P1123R1  
; CURRENT APPLICATION NUMBER: US/09/109,207C  
; CURRENT FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/051,554  
; PRIOR FILING DATE: 1997-07-03  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 17  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; NAME/KEY: Artificial  
; LOCATION: 1-218  
; OTHER INFORMATION: Light chain sequence derived from MAE11  
US-09-109-207C-17

Query Match 86.8%; Score 1074; DB 4; Length 218;  
Best Local Similarity 95.4%; Pred. No. 2.8e-84;  
Matches 208; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGKAPKLLIYAASNLES 80  
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGEGDSYLNWYQKPGKAPKLLIYAASYLE 60  
QY 81 GVPFRFSGSGSGTDFTLTITSSLPQEDFATYYCQSNEDPRFTGQGTKEIKRTVAAPSVF 140  
Db 61 GVPFRFSGSGSGTDFTLTITSSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120  
QY 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 200  
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180  
QY 201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
Db 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 15  
US-09-109-207C-19  
; Sequence 19, Application US/09109207C  
; Patent No. 6172213  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiue, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept  
; FILE REFERENCE: P1123R1  
; CURRENT APPLICATION NUMBER: US/09/109,207C  
; CURRENT FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/051,554  
; PRIOR FILING DATE: 1997-07-03  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 19  
; LENGTH: 218  
; TYPE: PRT

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; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain F(ab) sequence derived from MAE11
US-09-109-207C-19

Query Match      86.8%; Score 1074; DB 4; Length 218;
Best Local Similarity 95.4%; Pred. No. 2.8e-84;
Matches 208; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 21 DIVLTQSPSSLSASVGRVTITCKASQSVYDGDSDYNNWYQQKPKAPKLLIYAASNLES 80
Db 1 DIQLTQSPSSLSASVGRVTITCKASQSVYDGDSDYNNWYQQKPKAPKLLIYAASNLES 60

Qy 81 GVPFRFGSGSGTDFTLTISSLQPEDFATYYCQQSNEDPRTEGOGTKVEIKRTVAAPSVF 140
Db 61 GVPFRFGSGSGTDFTLTISSLQPEDFATYYCQQSHEDPYTFGGGTKEIKRTVAAPSVF 120

Qy 141 IFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 200
Db 121 IFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180

Qy 201 STLTLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
```

Search completed: August 14, 2002, 15:17:03  
Job time: 686 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:18:58 ; Search time 108.64 Seconds  
(without alignments)  
210.505 Million cell updates/sec

Title: US-09-499-662-127  
Perfect score: 1237  
Sequence: 1 METDRIILLWVLLLMVPGSTG.....EVTHQGLSPVTKSFNRGEC 238

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 283138 segs, 96089334 residues  
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	945.5	76.4	215	2 JE0242	Ig kappa chain NIG
2	926.5	74.9	215	2 JE0244	Ig kappa chain NIG
3	903.5	73.0	215	2 JE0243	Ig kappa chain NIG
4	885.5	71.6	215	2 A23746	Ig kappa chain V-I
5	877	70.9	216	2 JE0241	Ig kappa chain Am3
6	809	65.4	240	2 S06084	Ig kappa chain pre
7	756	61.1	234	2 S14237	Ig kappa chain pre
8	749	60.5	218	2 S68241	Ig kappa chain V r
9	748.5	60.5	230	2 S33161	Ig kappa chain - s
10	747	60.4	218	2 JC5810	monoclonal antibod
11	729	58.9	224	2 S01320	Ig kappa chain pre
12	726	58.7	220	2 A31790	Ig kappa chain V r
13	718	58.0	210	2 A56169	Ig kappa chain V r
14	716.5	57.9	225	2 S37484	Ig kappa chain - m
15	709.5	57.4	219	2 PC4203	Ig kappa chain (mo
16	706.5	57.1	219	2 S38865	Ig kappa chain - m
17	706.5	57.1	235	2 S25058	Ig kappa chain - m
18	703.5	56.9	219	2 S52028	Ig kappa chain - m
19	697	56.3	214	2 S68212	Ig kappa chain (Ma
20	693.5	56.1	217	2 S42772	Ig kappa chain V r
21	687.5	55.6	219	2 S16112	Ig kappa chain pre
22	676.5	54.7	225	2 JL0029	Ig kappa chain pre
23	613.5	49.6	229	2 A20969	Ig kappa chain pre
24	608.5	49.2	135	2 S52059	JC-kappa protein -
25	608	49.2	178	2 PT0219	Ig kappa chain V-C
26	582.5	47.1	197	2 S29593	Ig kappa chain (WM
27	579	46.8	131	2 PH1226	Ig kappa chain pre
28	568.5	46.0	238	2 A49633	Ig lambda-like cha
29	548	44.3	106	1 K3HU	Ig kappa chain C r

30	547	44.2	144	2 PL0106	Ig kappa chain pre
31	532	43.0	131	1 KVMSM6	Ig kappa chain pre
32	522	42.2	123	2 S40331	Ig kappa chain - h
33	521	42.1	127	2 S40367	Ig kappa chain V-J
34	520	42.0	233	2 S29577	Ig light chain - r
35	519	42.0	132	1 KVMS32	Ig kappa chain pre
36	518	41.9	141	2 A49134	Ig kappa chain V-I
37	513	41.5	99	2 A37927	Ig kappa chain C r
38	511	41.3	139	2 S40365	Ig kappa chain - h
39	507	41.0	99	2 S26653	Ig kappa chain C r
40	505.5	40.9	145	2 S20631	Ig kappa chain - h
41	504	40.7	122	2 S40370	Ig kappa chain - h
42	504	40.7	140	2 PN0446	Ig kappa chain pre
43	503	40.7	132	2 S40334	Ig kappa chain - h
44	499	40.3	131	2 S55027	Ig light chain pre
45	499	40.3	131	2 S40352	Ig kappa chain V-J

ALIGNMENTS

RESULT 1

JE0242  
Ig kappa chain NIG26 precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0242  
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda  
submitted to JIPID, November 1998  
A:Description: Structure relationship of kappa type light chains with AL amyloidosis:  
A:Reference number: JE0241  
A:Accession: JE0242  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
C:Superfamily: immunoglobulin V region: immunoglobulin homology  
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 76.4% ; Score 945.5 ; DB 2 ; Length 215 ;  
Best Local Similarity 83.5% ; Pred. No. 1.2e-54 ;  
Matches 182 ; Conservative 15 ; Mismatches 18 ; Indels 3 ; Gaps 1 ;

Qy	21	DIVITQSPSSLSASVGDRTTTCRASQSDYDGDSDYMWYQKPKGKAPKLLIYASNL	80
Db	1	EIVLTQSPGTLISLSPGERATLISCRASQSV---SNNLAWYQKPKGQAPSLIYDASSR	57
Qy	81	GVPSRFGSGSGTDFTLFISSLOPEDFATYYCQSNEDPRTFGGGTKEIKRTVAAPSVF	140
Db	58	GIPDRFSGSGGTDFILFIISGLEPEDFAFYVYCCQYDRPPTFGGTKEIKRTVAAPSVF	117
Qy	141	IFPPSDEQLKSGTASVGVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSTYSLS	200
Db	118	IFPPSDEQLKSGTASVGVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSTYSLS	177
Qy	201	STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	238
Db	178	STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	215

RESULT 2

JE0244  
Ig kappa chain NIG2 precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0244  
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.  
submitted to JIPID, November 1998  
A:Description: A new subgroup of k type light chains (Vkv) identified in cases of AL  
A:Reference number: JE0243  
A:Accession: JE0244  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match	74.9%;	Score 926.5;	DB 2;	Length 215;
Best Local Similarity	83.1%;	Pred. No. 2.1e-53;		
Matches 182;	Conservative 14;	Mismatches 18;	Indels 5;	Gaps 2;

QY	21	DIVLTQSPSLSASGDRVTITCKASQSVVDYDGDSTMNMYQQPKAPKLLIYASNLNES	80
Db	1	EVLTQSPATLSVSPGERATLSCRASQSV---HSLAWYQQKPGAPRLIIYRASTRAT	56
QY	81	GVPSRSGSGSGTDFTLTITSSIQPEDFATYYCOQSNEDPRFTFGGTKKVEIKRTVAASPVS	139
Db	57	GIFARSQSGSGGDFLITLTSSIQSEDFALYYCQQYNTWPTLFTGGTKKVEIKRTVAASPVS	116
QY	140	FIFPPSDEQLKSGTASVWCILLNNFNPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSYL	199
Db	117	FIFPPSDEQLKSGTASVWCILLNNFNPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSYL	176
QY	200	SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	238
Db	177	SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	215

```

RESULT      3
JE0243
Ig kappa chain NIG93 precursor - human
CrSpecies: Homo sapiens (man)
C.Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C.Accession: JE0243
R:Alin, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.
A.Description: A new subgroup of k type light chains (Vk $\kappa$ ) identified in ca
A.Reference number: JE0243
A.Accession: JE0243
A.Molecule type: protein
A.Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F16-90/Domain: immunoglobulin homology <IMM>

```

Query Match 73.0%; Score 903.5; DB 2; Length 215;  
Best Local Similarity 81.7%; Pred. No. 6.5e-52;  
Matches 179; Conservative 16; Mismatches 19; Indels 5; Gaps 2;

Qy	21	DIVLTGSPSSLASVGSDRVITTCCKASQSVDYDGDSYMNVYQQPKGAPKLLIYAASNLES	80
Db	1	EIVMTQSPATLSVGPGERATLSCRASQSV---ATNVVMYMQKGAPRLIIYDASTRAT	56
Qy	81	GVPRESGGSGTDFTLTISSLPQEDFAIYYCQSQSNEDPRTFGQTKVEIK-RTVAAPS	139
Db	57	GVPA RESGGSGTEFTLTISSEDSDFAIYYCOHNAMPPTFGQTKVETKRRTVAAPS	116
Qy	140	FIFPPSDEQLKGTASVCLLNFPYPREAKVQWYDNALQSGNSQESTVEDSKDSTYS	199
Db	117	FIFPPSDEQLKGTASVCLLNFPYPREAKVQWYDNALQSGNSQESTVEDSKDSTYS	176
Qy	200	SSTLTLSKADYEKKHYACAEVTHQGLSSPVTKSFNRGEC	238
Db	177	SSTLTLSKADYEKKHYACAEVTHQGLSSPVTKSFNRGEC	215

RESULT 4  
A: Accession: A23746  
Ig kappa chain V-III (KAU cold agglutinin) - human  
C: Species: Homo sapiens (man)  
C: Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 21-Jan-2000  
C: Accession: A23746  
R: Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.  
J. Biol. Chem. 266, 2836-2842, 1991  
A: Title: The primary structure of the Fab fragment of protein KAU, a monoclonal antibody that recognizes the human Ig kappa chain V-III.  
A: Reference number: A23746; MUID: 91131575  
A: Accession: A23746

A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-215 <LEO>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match	71.6%	Score	885.5	DB 2	Length	215	
Best Local Similarity	81.6%	Pred.	No. 9.5e-51				
Matches	177	Conservative	14	Mismatches	23	Indels	3
						Gaps	1

[illegible]

```

RESULT      5
JE0241
Ig kappa chain Am37 precursor - human
C:Species: Homo sapiens (man)
C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0241
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I
submitted to JIPID, November 1998
A:Description: Structure relationship of kappatype light chains with AL any
A:Reference number: JE0241
A:Accession: JE0241
A:Molecule type: protein
A:Residues: 1-216 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-92/Domain: immunoglobulin homology<IMM>

```

Query Match	70.98;	Score 877;	DB 2;	Length 216;
Best Local Similarity	79.8%;	Pred. No. 3.4e-50;		
Matches 174;	Conservative 15;	Mismatches 27;	Indels 2;	Gaps 2;

QY	21	DIVLTQSPSSLSASVGDRVTITCKAQSDVDYDGDSYNNYYQQKPKAPKLLIYAASNLGS	80
Db	1	DIVLTQSPDFLAVSLGERATINCKSSQSVLYNSKNFLAWYQKPQG-PRLLIW-ANVRES	58
QY	81	GVPSRSGSGSGTDFLTITSSLQPEDFAFYCYCOOSNEDPRTFCQTKEIKTKVAAPSVF	140
Db	59	GVDPDRFGSGVGDTLTISNQAEALVAYICYOYYSTPYFSGGGRLEIKTKVAAPSVF	118
QY	141	IFFPDEQLKSGTASVVCLLNNEYPREAKVQWKVDNALQSGNSQESVTEPDQSKDSTYSLS	200
Db	119	IFFPDEQLKSGTASVVCVLNNEYPREAKVQWKVDNALQSGNSQESVTEPDQSKDSTYSLS	178
QY	201	STITLTKADYEKKHKVYACEVTHOGLSSPVTKSFNRGEC	238
Db	179	STITLTKADYEKKHKVYACEVTHOGLSSPVTKSFNRGEC	216

RESULT 6  
S06084  
Ig kappa chain precursor - rat  
C: Species: Rattus norvegicus (Norway rat)  
C: Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #  
C: Accession: S06084

C:Species: Rattus norvegicus (Norway rat)  
C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 21-Jan-2000  
C:Accession: S06084



Best Local Similarity 62.2%; Pred. No. 7.9e-42;  
Matches 145; Conservative 36; Mismatches 47; Indels 5; Gaps 2;

QY 7 LLVLLW-VPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSYDYDGSYMNWYQKPG 65  
Db 2 LIGLLLLLPAGRCDIQVOTQSPSSLSALTERVSTRTSOSV-----SNLYNWYQKPG 57

QY 66 KAPKLLIYAASNLSEGVSRFSGSGSTDTLTITISLQPEDFATYQCQSNEDPRTFGG 125  
Db 58 QAPKLLIYATRLHTDVPFRFSGSGSTDTLTISNLEANDATYCYCLOYESTPLAFGG 117

QY 126 TVTEKRTVAAPSVFIFPPSDEQLKSGTASVYVCLLNNFYPREAKYQWVDNALQSGNSE 185  
Db 118 TNVEIKRSDAQPVSFLFKPEQELRTGTGVVCLVNDVFPKDNVKKVGDVQTQNSFN 177

QY 186 SVTEQDSKDYSLSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 238  
Db 178 SFTQDSKSKYSTLSLTLSSEYQSHNAYACEVSHKSLPTALVKSFNRNEC 230

RESULT 10  
JC5810  
monoclonal antibody 13-1 light chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 04-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jan-2000  
C:Accession: JC5810  
R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.  
Biochem. Biophys. Res. Commun. 240, 566-572, 1997  
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin  
A:Reference number: JC5810; MUID:98063277  
A:Accession: JC5810  
A:Molecule type: protein  
A:Residues: 1-218 <AKA>  
C:Comment: This catalytic antibody has peroxidase oxidase. It is directed against a porphyrin  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 60.4%; Score 747; DB 2; Length 218;  
Best Local Similarity 64.7%; Pred. No. 9.3e-42;  
Matches 141; Conservative 29; Mismatches 48; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYDGSYMNWYQKPGKAPKLLIYAASNL 80  
Db 1 NIVLTQSPASLASVGLQRTATISCRASKSVASGYIYMHYQKPGPPKLLISLASNL 60

QY 81 GYPSRFSGSGSTDTLTITISLQPEDFATYQCQSNEDPRTFGGTKVEIKRTVAAPSV 140  
Db 61 GVPARFSGSGSTDTLTINHPVEEDVAIYQHSRELPLTFGAGTKLEKLRADRAPTVS 120

QY 141 IFPPSDEQLKSGTASVYVCLLNNFYPREAKYQWVDNALQSGNSESVTQDSKDYSL 200  
Db 121 IFPPSDEQLTSGGASVYVCLNFPKDIYKWKIDGSRQNGVLSWTQDSKDYSL 180

QY 201 STLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 238  
Db 181 STLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNNEC 218

RESULT 11  
S01320  
Ig kappa chain precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 21-Jan-2000  
C:Accession: S01320  
R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.  
Eur. J. Biochem. 176, 287-295, 1988  
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a  
A:Reference number: S01320; MUID:88329081  
A:Accession: S01320  
A:Molecule type: mRNA  
A:Residues: 1-234 <DEL>  
A:Cross-references: EMBL:X13187; NID:g51784; PIDN:CAA31579.1; PID:g51785

A:Note: this sequence was determined from the differentiated gene  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-234/Product: Ig kappa chain #status predicted <MAT>  
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 58.9%; Score 729; DB 2; Length 234;  
Best Local Similarity 58.3%; Pred. No. 1.5e-40;  
Matches 140; Conservative 37; Mismatches 55; Indels 8; Gaps 2;

QY 1 METDITLLVLLWVPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSYDYDGSYMN-- 58  
Db 1 MSVPTQVLGLLLLTARCDIQGTQSPASLSVSGESVITCRASENI-----YSNLA 54

QY 59 WYQKPGKAPKLLIYAASNLSEGVSRFSGSGSTDTLTITISLQPEDFATYQCQSNED 118  
Db 55 WYQKQKSPQLLVYVATKLVDPVSRFSGSGSTQYSLKINSLOQSEDFGYSYQHFWD 114

QY 119 PRTEGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVYVCLLNNFYPREAKYQWVDNAL 178  
Db 115 PTFGSGTKLEKRRADAPTIVFPPSSQLTSGGASVYVCLNFPKDIYKWKIDGSE 174

QY 179 QSGNSQESVTEQDSKDYSLSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 238  
Db 175 RQGVLSNWTQDSKDYSLSTLTITKDEYERHNSYTCETHKTSTSPIVKSFNNEC 234

RESULT 12  
A31790  
Ig kappa chain V region (17/9) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 21-Jan-2000  
C:Accession: A31790  
R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, J.A.  
J. Biol. Chem. 263, 17100-17105, 1988  
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an  
A:Reference number: A92686; MUID:89034213  
A:Accession: A31790  
A:Molecule type: mRNA  
A:Residues: 1-220 <SCH>  
A:Cross-references: GB:M23626; GB:J04061; NID:g533234; PIDN:AAA39162.1; PID:g533235  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 58.7%; Score 726; DB 2; Length 220;  
Best Local Similarity 61.8%; Pred. No. 2.2e-40;  
Matches 136; Conservative 33; Mismatches 49; Indels 2; Gaps 1;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYDG--DSYMNWYQKPGKAPKLLIYAASNL 78  
Db 1 DIVMTQSPSSLTAVTAGEKVTMSCTSSQSLFNSGKQKNLYLTWYQKPGQPKVLIYASR 60

QY 79 ESGVPSRFSGSGSTDTLTITISLQPEDFATYQCQSNEDPRTFGGTKVEIKRTVAAP 138  
Db 61 ESGVPDRFTGSGSGTDTLTITISSVQAEADLVAVYCYQNDYSNPLTFGGGTKLEKLRADAAPT 120

QY 139 VFIFPPSDEQLKSGTASVYVCLLNNFYPREAKYQWVDNALQSGNSESVTEQDSKDYSL 198  
Db 121 VSIFPPSSQLTSGGASVYVCLNFPKDIYKWKIDGSRQNGVLSWTQDSKDYSL 180

QY 199 LSSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 238  
Db 181 MSSTLTITKDEYERHNSYTCETHKTSTSPIVKSFNNEC 220

RESULT 13  
A56169  
Ig kappa chain V region (clone 23.2) - mouse (fragment)  
C:Species: Mus musculus (house mouse)

C;Date: 19-Oct-1995 #sequence\_revision 19-Oct-1995 #text\_change 11-Jan-2000  
C;Accession: A56169  
R;Monfardini, C.; Kieber-Emmons, T.; VonFeldt, J.M.; O'Malley, B.; Rosenbaum  
J. Biol. Chem. 270, 6628-6638, 1995  
C;A>Title: Recombinant antibodies in bioactive peptide design.  
A;Reference number: A56169; MUID:95204454  
A;Accession: A56169  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-210 <MON>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

[illegible]

RESULT 14  
S37484  
Ig kappa chain - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 11-Jan-2000  
C:Accession: S37484  
R:Ducancel, F.F.D.  
submitted to the EMBL Data Library, February 1993  
A:Reference number: S37483  
A:Accession: S37484  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-225 <DUC>  
A:Cross-references: EMBL:X70424; NID:g406254; PIDN:CAA49869.1; PID:g406255  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C:Keywords: heterotetramer; Immunoglobulin

Query Match	57.9%	Score 716.5;	DB 2;	Length 225;
Best Local Similarity	61.8%;	Pred. No. 9.2e-40;		
Matches 141; Conservative	29;	Mismatches 53;	Indels 5;	Gaps 2;
<hr/>				
Qy	11	LLLVPGSTGDIVLTQPSSLSASVGDRTTTCRASQSVDYDGSYMNWYOOKPKGAKPL	70	
		:   :   :   :                     :           :		
Db	3	LLLCVSGAHGISIVMTQPKFLLLARGDRVTITCRASQSVSND---	VAMYQOKKFGQSFKL	58
		:   :   :   :                     :           :		
<hr/>				
Qy	71	LIYAASNLESCVPFRFSGSGGTDTFTLTISSLPEDFAITYYCQOSNEDPRTFGOGTKVEI	130	
		:       :                 :         :		
Db	59	LIYYASSRYTCVPPRFTGSGYGCTDFTFTISTVAQEDLAIFYECQQ--DYSSYTFGGGTKLEI	117	
		:       :                 :         :		
<hr/>				
Qy	131	KRTVAAPSVETFPSPDEOLKSGTSVVYCLLNFFYPREAKVOMKDVALQNSQESVTEQ	190	
		:       :                 :         :		
Db	118	KRAADAATVSIFPPSSSEOLTSGGSAVVCFLNNFTPDKINVAWKIDGSRQNGVLNSWT	177	
		:       :                 :         :		
<hr/>				
Qy	191	DSKOSTYSLSSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC	238	
		:       :                 :         :		
Db	178	DSKOSTYSMSSTLTLDKDEYRHNSYTCATHKTSTSPIVKSFNRRNC	225	
		:       :                 :         :		

RESULT 15

E; Monfardini, C.; Kieber-Emmons, T.; Von Feldt, J.M.; O'Malley, B.; Rosenbaum, H.; Goddill, J. *Biol. Chem.* **270**, 6628-6638, 1995

A; Title: Recombinant antibodies in bioactive peptide design.

A; Reference number: A56169; MUID:95204454

A; Accession: A56169

A; Status: preliminary; not compared with conceptual translation

A; Molecule type: mRNA

A; Residues: 1-210 <MON>

C; Superfamily: immunoglobulin V region; immunoglobulin homology

C; Keywords: heterotetramer; immunoglobulin

A; Residues: 1-219 <NNA>  
A; Cross-references: GB:U9147; NID:g1594225; PID:AAC52821.1; PID:g1594226  
C; Comment: This protein is specific for human plasma apolipoprotein A-I of high-density lipoprotein (HDL) particles.  
C; Superfamily: immunoglobulin V region; immunoglobulin homology  
F; 1-112/Domain: V region #status predicted <VRG>  
F; 113-219/Domain: C region #status predicted <CRG>

Query Match	57.4%	Score	709.5	DB 2	Length	219			
Best Local Similarity	59.8%	Pred. No.	2.5e-39						
Matches	131	Conservative	37	Mismatches	50	Indels	1	Gaps	1
Qy	21	DIVLTQSPSSLSASVGDRVTITCKASQSDY-DGDSYMNWYQOKPGKAPKLLIYAASNLE	79						
Db	1	DVLTQTPSLFVSLGDAQSISCKSSOSIVTNGNTYLEWLQKPGSPKLLIYKVSNRF	60						
Qy	80	SGVPSRFSGSGSGTDFTLTITSSLPQEDFATYVYCOQSNEDPRFTGGTKVEIKRTVAAPSV	139						
Db	61	SGVPDRFSGSGSGTDFTLKISRVEAEDLQVYFCFGSHVPRFTGGTKLEIKRAADAAPT	120						
Qy	140	FIFPPSDEQLKSGTASVVCLLNNKYPREAKVQWKVDNALQSGNSQESVTEODSKDSTYSL	199						
Db	121	SIFPPSDEQLTSGGASVVCFLNNKYPDKINVKWIDGDSNGVLSWTDQDSKDSITYSM	180						
Qy	200	SSTLTSLKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	238						
Db	181	SSTLTSLKADYERINSSYTCETHRTSTSPVTKSFNRNEC	219						

Search completed: August 14, 2002, 15:18:58  
Job time: 686 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:23:12 ; Search time 53.64 Seconds  
(without alignments)  
171.798 Million cell updates/sec

Title: US-09-499-662-127

Perfect score: 1237

Sequence: 1 METDTILLWLLLVPGSTG.....EVTHQGLSPVTKSFNRGEC 238

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	548	44.3	106	1 KAC_HUMAN	P01834 homo sapien
2	532	43.0	131	1 KV3J_MOUSE	P01661 mus musculus
3	519	42.0	132	1 KV3F_MOUSE	P01658 mus musculus
4	483	39.0	111	1 KV3M_MOUSE	P01665 mus musculus
5	481	38.9	111	1 KV3N_MOUSE	P01666 mus musculus
6	480	38.8	129	1 KV1W_HUMAN	P04431 homo sapien
7	479	38.7	111	1 KV3O_MOUSE	P01667 mus musculus
8	478.5	38.7	129	1 KV3L_HUMAN	P18135 homo sapien
9	476	38.5	111	1 KV3Q_MOUSE	P01689 mus musculus
10	468	37.8	111	1 KV3L_MOUSE	P01684 mus musculus
11	461	37.3	108	1 KV1H_HUMAN	P01600 homo sapien
12	458.5	37.1	110	1 KV3P_MOUSE	P01668 mus musculus
13	456.5	36.9	129	1 KV3M_HUMAN	P18136 homo sapien
14	452	36.5	108	1 KV1G_HUMAN	P01599 homo sapien
15	449	36.3	108	1 KV1M_HUMAN	P01605 homo sapien
16	448	36.2	108	1 KV1K_HUMAN	P01603 homo sapien
17	448	36.2	134	1 KV4C_HUMAN	P06314 homo sapien
18	446	36.1	108	1 KV1B_HUMAN	P01594 homo sapien
19	445	36.0	108	1 KV1E_HUMAN	P01597 homo sapien
20	445	36.0	108	1 KV1F_HUMAN	P01598 homo sapien
21	445	36.0	108	1 KV1N_HUMAN	P01606 homo sapien
22	442	35.7	108	1 KV1V_HUMAN	P04430 homo sapien
23	441	35.7	108	1 KV1A_HUMAN	P01593 homo sapien
24	441	35.7	117	1 KV1J_HUMAN	P01602 homo sapien
25	436	35.2	111	1 KV3H_MOUSE	P01660 mus musculus
26	435	35.2	108	1 KV1O_HUMAN	P01607 homo sapien
27	434	35.1	108	1 KV1P_HUMAN	P01608 homo sapien
28	432.5	35.0	133	1 KV4B_HUMAN	P06313 homo sapien
29	431.5	34.9	129	1 KV3H_HUMAN	P04207 homo sapien
30	430	34.8	108	1 KV1Y_HUMAN	P80362 homo sapien
31	429	34.7	108	1 KV1R_HUMAN	P01610 homo sapien
32	429	34.7	108	1 KV1S_HUMAN	P01611 homo sapien
33	429	34.7	129	1 KV1X_HUMAN	P04432 homo sapien

#### RESULT 1

ID	KAC_HUMAN	STANDARD;	PRT;	106 AA.
AC	P01834;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	ig kappa chain C region.			
GN	IGKC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064023; PubMed=5489770;			
RA	Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";			
RL	Biochemistry 9:3155-3161(1970).			
RN	[2]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";			
RL	Biochemistry 9:3188-3196(1970).			
RN	[3]			
RP	SEQUENCE (BENCE-JONES PROTEIN TI).			
RX	MEDLINE=72188439; PubMed=5027703;			
RA	Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;			
RT	"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein TI). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81042304; PubMed=6775818;			
RA	Hietzer P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;			
RT	"Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments.";			
RL	Cell 22:197-207(1980).			
RN	[5]			
RP	SEQUENCE (BENCE-JONES PROTEIN ROY).			
RA	Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,			
RA	Steinmetz-Kayne M., Suter L., Watanabe S.;			
RL	(In) Fraenk F., Shugar D. (eds.);			
RL	Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).			
RN	[6]			
RP	SEQUENCE (BENCE-JONES PROTEIN CUM).			
RX	MEDLINE=68242259; PubMed=5586923;			
RA	Hilschmann N.;			
RT	"The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";			

34	427	34.5	111	1	KV3J_MOUSE	P01662 mus musculus
35	426	34.4	111	1	KV3K_MOUSE	P01663 mus musculus
36	425.5	34.4	109	1	KV1T_HUMAN	P01612 homo sapien
37	425	34.4	128	1	KV3K_HUMAN	P06311 homo sapien
38	422	34.1	108	1	KV1L_HUMAN	P01604 homo sapien
39	422	34.1	111	1	KV3R_MOUSE	P01670 mus musculus
40	420	34.0	108	1	KV1Q_HUMAN	P01609 homo sapien
41	419.5	33.9	107	1	KV1D_HUMAN	P01596 homo sapien
42	419	33.9	117	1	KV1I_HUMAN	P01601 homo sapien
43	416.5	33.7	133	1	KV2F_HUMAN	P06310 homo sapien
44	416	33.6	115	1	KV3I_HUMAN	P04433 homo sapien
45	415	33.5	128	1	KV5E_MOUSE	P01637 mus musculus

#### ALIGNMENTS

```
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [7]
RP SEQUENCE (BENCE-JONES PROTEIN AG).
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969).
RN [8]
RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains.";
RL Science 169:56-59(1970).
CC -I- MISCELLANEOUS; THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
CC MARKER, 45-ALA AND 83-LEU.
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CC -----
DR EMBL; J00241; AAA58989.1; -.
DR EMBL; V00557; CAA23823.1; -.
DR PIR; A02116; K3HU.
DR HSP; P01842; 7FAB.
DR MIM; 147200; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00407; Igc1; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 26 86
FT VARIANT 83 83 INTERCHAIN (WITH A HEAVY CHAIN).
FT V -> L (IN INV(1,2) MARKER).
FT /FTID=VAR_003897.
FT CONFLICT 14 14 D -> N (IN REF. 7 AND 8).
FT CONFLICT 57 57 E -> O (IN REF. 5 AND 6).
FT SEQUENCE 106 AA; 11609 MW; 51984D1FDD372CE8 CRC64;
SQ
Query Match 44.3%; Score 548; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.8e-37;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 133 TVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRAKWKQVDNALQSGNSQESVTEQDS 192
DB 1 TVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRAKWKQVDNALQSGNSQESVTEQDS 60
QY 193 KDSYLSLSTLRSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
DB 61 KDSYLSLSTLRSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 106
RESULT 2
KV3I_MOUSE
ID KV3I_MOUSE STANDARD; PRT; 131 AA.
AC P01661;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region MOPC 63 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
```

```
RN [1]
RP SEQUENCE OF 1-35.
RX MEDLINE=78235887; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: Implications on the organization and controlled
RT expression of immunoglobulin genes.";
RL Biochemistry 17:2392-2400(1978).
RN [2]
RP SEQUENCE OF 21-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences.";
RL Biochemistry 12:760-771(1973).
RN [3]
RP REVISIONS.
RX MEDLINE=79019520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
DR PIR; A01935; KVM5M6.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin v region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 131 IG KAPPA CHAIN V-III REGION MOPC 63.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 59 73 FRAMEWORK-2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 81 112 FRAMEWORK-3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 122 131 FRAMEWORK-4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;
Query Match 43.0%; Score 532; DB 1; Length 131;
Best Local Similarity 75.6%; Pred. No. 4.6e-36;
Matches 99; Conservative 18; Mismatches 14; Indels 0; Gaps 0;
QY 1 METDTLLWVLLWVPGSTGDIVLTQSPSSLSASVGRVITTCASQSYDYDSDYMNWY 60
DB 1 METDTLLWVLLWVPGSTGDIVLTQSPSSLSASVGRVITTCASQSYDYDSDYMNWY 60
QY 61 QOKPKAKPLLIYAASNLSESGVPSRFSGSGSTDTFTLTITSLQPEDFATYYCQSNEDPR 120
DB 61 QOKPKAKPLLIYAASNLSESGVPSRFSGSGSTDTFTLTITSLQPEDFATYYCQSNEDPR 120
QY 121 TFGGKTKVEIK 131
DB 121 TFGGKTKLEIK 131
RESULT 3
KV3F_MOUSE
ID KV3F_MOUSE STANDARD; PRT; 132 AA.
AC P01658;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region MOPC 321 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
```



[illegible]

Query Match 38.9%; Score 481; DB 1; Length 111;  
Best Local Similarity 80.2%; Pred. No. 4.5e-32;  
Matches 89; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNLES 80  
DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNLES 60

QY 81 GVPFRFSGSGGTDFTLTISLQPEDFATYYCQSNEDPRTFGQGTKEIK 131  
DB 61 GIPARFSGSGGTDFTLTINHPVEEDATYYCQSNEDPRTFGAGTKLEIK 111

## RESULT 6

ID KV1W\_HUMAN STANDARD; PRT; 129 AA.  
AC P04431;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region Walker precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=85014148; PubMed=6091049;  
RA Klobeck H.G., Combratio G., Zachau H.G.;  
RT "Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines are closely related.";  
RL Nucleic Acids Res. 12:6995-7006(1984).

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CC -----  
CC EMBL; X00965; CAA25477.1; ALT\_TERM.

DR PIR; A01883; KIHUWK.  
DR HSSP; P01607; IREI.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; Igv; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 22  
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.  
FT DOMAIN 23 45 FRAMEWORK-1.  
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 57 71 FRAMEWORK-2.  
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 79 110 FRAMEWORK-3.  
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 120 129 FRAMEWORK-4.  
FT DISULFID 45 110 BY SIMILARITY.  
FT NON\_TER 129 129  
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 38.8%; Score 480; DB 1; Length 129;  
Best Local Similarity 74.0%; Pred. No. 6.5e-32;  
Matches 97; Conservative 12; Mismatches 18; Indels 4; Gaps 1;

QY 1 METDTILLVLLIWPVSGDILVLTQSPSSLSASVGDRTVITCKASQSDYDGDSDYNNWY 60  
DB 3 MRVPAQLGLLLWLRGARDIQMTQSPSSLSASVGDRTVITCKASQSI----SNVLNMY 58  
QY 61 QOKPGKAPKLLIYAASNLESVPSRFSGSGGTDFTLTISLQPEDFATYYCQSNEDPR 120

Db 59 QOKPGKAPKLLIYAASNLSQSGVTSRFSGSGGTDFTLTISLQPEDSATYYCQSYSTLI 118  
QY 121 TFGQGTKEIK 131  
DB 119 TFGQGTLEIK 129

## RESULT 7

KV3O\_MOUSE STANDARD; PRT; 111 AA.  
ID KV3O\_MOUSE  
AC P01667;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-III region PC 6308.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]

RP SEQUENCE.  
RX MEDLINE=79073152; PubMed=103003;

RA Weigert M., Gamaitan L., Loh E., Schilling J., Hood L.E.;  
RT "Rearrangement of genetic information may produce immunoglobulin RT diversity.";  
RL Nature 276:785-790(1978).

DR PIR; C01937; KVM508.  
DR HSSP; P01789; LMCP.

DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; Igv; 1.

KW Immunoglobulin V region.

FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 39 53 FRAMEWORK-2.  
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 61 92 FRAMEWORK-3.  
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 102 111 FRAMEWORK-4.  
FT DISULFID 23 92 BY SIMILARITY.  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 38.7%; Score 479; DB 1; Length 111;  
Best Local Similarity 80.2%; Pred. No. 6.4e-32;  
Matches 89; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNLES 80  
DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNLES 60

QY 81 GVPFRFSGSGGTDFTLTISLQPEDFATYYCQSNEDPRTFGQGTKEIK 131  
DB 61 GIPARFSGSGGTDFTLTINHPVEEDATYYCQSNEDPRTFGSGTKLEIK 111

## RESULT 8

KV3L\_HUMAN STANDARD; PRT; 129 AA.  
ID KV3L\_HUMAN  
AC P18135;

DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-III region HAH precursor.

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP SEQUENCE FROM N.A.

```
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Antibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
CC PIR: PLO022; K3HUHA.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C5529272774D0 CRC64;

Query Match 38.7%; Score 478.5; DB 1; Length 129;
Best Local Similarity 68.9%; Pred. No. 8.5e-32;
Matches 91; Conservative 17; Mismatches 21; Indels 3; Gaps 1;

Qy 1 METDTLLWLLVPGSTGDIVLTQSPSSLSASVGRVITITCRASQSDVDYDGSYMNWY 60
Db 1 METPAQLLFLLLLWLPDPTGEIVLTQSPGTLISLSPGERATISCRASQSV---SSSYLAWY 57

Qy 61 QOKPGKAPKLIYAAASLESVPSRFGSGSGTDTFTLTISLQPEDFATYYCQOSNEDPR 120
Db 58 QOKPGQAPRLIYGAASSRATGIPDRFGSGSGTDTFTLTISRLEPEDFATYYCQVGTSPR 117

Qy 121 TFGQGTKEIKR 132
Db 118 TFGQGTKEIKR 129

RESULT 9
KV3Q_MOUSE
ID KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7769.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; E01937; KVM569.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region.

Query Match 37.8%; Score 468; DB 1; Length 111;
Best Local Similarity 78.4%; Pred. No. 4.9e-31;
Matches 87; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

Qy 21 DIVLTQSPSSLSASVGRVITITCRASQSDVDYDGSYMNWYQOKPGKAPKLIYAAASLES 80
Db 1 DIVLTQSPASLAVSLGQRATISCRASQSDVDYDGSYMNWYQOKPGKPLIFAAASLES 60

Qy 81 GVPSPRFGSGSGTDTFTLTISLQPEDFATYYCQOSNEDPRTFGQGTKEIK 131
Db 61 GIPARFGSGSGTDTFTLTINHPVEEEDATYYCQOSNEDPWTFGSGTKLEIK 111

RESULT 10
KV3L_MOUSE
ID KV3L_MOUSE STANDARD; PRT; 111 AA.
AC P01664;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region CBPC 101.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01936; KVM5C1.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11964 MW; E2B1AD98AD965962 CRC64;
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Db 61 GIPARFSGSGGDTFTLNHPVEEEDAAATYYCQSNEDPYTFGGTKLEIK 111
      ||:|||||
RESULT 11
KV3P_HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
chain of subgroup I (Bence-Jones Protein Hau): subdivision within
subgroups.";
RT Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -|- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -|- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01868; K1HUHU.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
FT SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 37.3%; Score 461; DB 1; Length 108;
Best Local Similarity 80.4%; Pred. No. 1.7e-30;
Matches 90; Conservative 11; Mismatches 7; Indels 4; Gaps 1;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGKAPKLLIYAASNL 80
Db 1 DIQMTQSPSSLSASVGDRTVITCKASQSI-----SSYLSWYQKPGKAPQVLIYAASL 56

QY 81 GVPSRFSGSGGTFTLTITSSLPQEDFATYYCQSNEDPRTFGQGTKVEIKR 132
Db 57 GVPSRFSGSGGTFTLTITSSLPQEDFATYYCQNYITPTSFQGTGRVEIKR 108

RESULT 12
KV3P_MOUSE STANDARD; PRT; 110 AA.
ID KV3P_MOUSE
AC P01668;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7210.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
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RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR; D01937; KVM510.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 100
FT DOMAIN 101 110
FT DISULFID 23 92
FT NON_TER 110 110
FT SEQUENCE 110 AA; 11950 MW; 69F1A5CE886B1249 CRC64;

Query Match 37.1%; Score 458.5; DB 1; Length 110;
Best Local Similarity 78.4%; Pred. No. 2.8e-30;
Matches 87; Conservative 11; Mismatches 12; Indels 1; Gaps 1;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGKAPKLLIYAASNL 80
Db 1 DIVLTQSPASLAVSLGQRATISCKASLDYDGSYMNWYQKPGKAPKLLIYAASNL 60

QY 81 GVPSRFSGSGGTFTLTITSSLPQEDFATYYCQSNEDPRTFGQGTKVEIK 131
Db 61 GIPARFSGSGGTFTLNHPVEEEDAAATYYCHQS-EDPWTFGSGTKLEIK 110

RESULT 13
KV3M_HUMAN STANDARD; PRT; 129 AA.
ID KV3M_HUMAN
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kippes T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -|- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
LEUKEMIA.
DR PIR; PLO021; K3HUH1.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129
FT DOMAIN 21 43
FT DOMAIN 44 55
FT DOMAIN 56 70
FT DOMAIN 71 77
FT DOMAIN 78 109
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FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BE74D6 CRC64;

Query Match 36.9%; Score 456.5; DB 1; Length 129;
Best Local Similarity 67.4%; Pred. No. 4.9e-30;
Matches 89; Conservative 17; Mismatches 23; Indels 3; Gaps 1;

Qy 1 METDTILWLVLLVPVSGTGVITQSPSSLSASVGDRTVTITCKASQSDVDGDSYNNWY 60
Db 1 METPAQLLFLLWLPDFTGIVITQSPCTLSLSPGERATLSCRASQSV---SSSYLAWY 57

Qy 61 QOKPKGAPKLLIYAASNLQSGVPRFSGSGTDFTLTIISSLPQEDFATYYCQSNEDPR 120
Db 58 QOKPQAPRLIYGASSRATGIPRFSGSGTDFTLTIISSLPQEDFATYYCQSNEDPR 117

Qy 121 TFGQGTKEIKR 132
Db 118 TFGQGTKEIKR 129

RESULT 14
KVIG_HUMAN STANDARD; PRT; 108 AA.
ID KVIG_HUMAN AC P01599;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region GAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059122; PubMed=4215718;
RA Laure C.J., Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
RT (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
RT kappa-type, subgroup I."
RL Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
DR PIR: A01867; KIHUGL.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGv; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11814 MW; CIAD3CB0F600FF73 CRC64;

Query Match 36.5%; Score 452; DB 1; Length 108;
Best Local Similarity 79.5%; Pred. No. 9e-30;
Matches 89; Conservative 8; Mismatches 11; Indels 4; Gaps 1;

Qy 21 DIVLTQSPSSLSASVGDRTVTITCKASQSDVDGDSYNNWYQOKPKGAPKLLIYAASNLQ 80
Db 1 DIQMTQSPSSLSASVGDRTVTITCKASQSDVDGDSYNNWYQOKPKGAPKLLIYAASNLQ 56
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Qy 81 GVPFRFSGSGGTDFTLTIISSLPQEDFATYYCQSNEDPRFTFGQGTKEIKR 132
Db 57 GVPFRFSGSGGTDFTLTIISSLPQEDFATYYCQSNEDPRFTFGQGTKEIKR 108

RESULT 15
KVIM_HUMAN STANDARD; PRT; 108 AA.
ID KVIM_HUMAN AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human
RT IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT specificities."
RL Scand. J. Immunol. 5:677-684(1976).
CC -!- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR: A01871; KIHULY.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGv; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 36.3%; Score 449; DB 1; Length 108;
Best Local Similarity 78.6%; Pred. No. 1.6e-29;
Matches 88; Conservative 8; Mismatches 12; Indels 4; Gaps 1;

Qy 21 DIVLTQSPSSLSASVGDRTVTITCKASQSDVDGDSYNNWYQOKPKGAPKLLIYAASNLQ 80
Db 1 DIQMTQSPSSLSASVGDRTVTITCKASQSDVDGDSYNNWYQOKPKGAPKLLIYGASTREA 56

Qy 81 GVPFRFSGSGGTDFTLTIISSLPQEDFATYYCQSNEDPRFTFGQGTKEIKR 132
Db 57 GVPFRFSGSGGTDFTLTIISSLPQEDFATYYCQSNEDPRFTFGQGTKEIKR 108
```

Search completed: August 14, 2002, 15:23:13  
Job time: 686 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 15:22:14 ; Search time 187.61 Seconds  
(without alignments)  
219.459 Million cell updates/sec

Title: US-09-499-662-127  
Perfect score: 1237  
Sequence: 1 METDRIILWVLLWVPGSTG.....EVTHQGLSPVTKSFNRGEC 238

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_19:\*\*

- 1: sp\_archaea:\*\*
- 2: sp\_bacteria:\*\*
- 3: sp\_fungi:\*\*
- 4: sp\_human:\*\*
- 5: sp\_invertebrate:\*\*
- 6: sp\_mammal:\*\*
- 7: sp\_mmc:\*\*
- 8: sp\_organelle:\*\*
- 9: sp\_phase:\*\*
- 10: sp\_plant:\*\*
- 11: sp\_rodent:\*\*
- 12: sp\_virus:\*\*
- 13: sp\_vertebrate:\*\*
- 14: sp\_unclassified:\*\*
- 15: sp\_rvirus:\*\*
- 16: sp\_bacteriap:\*\*
- 17: sp\_archaeap:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	746.5	60.3	238	11 Q99M37	Q99M37 mus musculus
2	739	59.7	234	11 Q91WF8	Q91WF8 mus musculus
3	738	59.7	233	11 Q91WS9	Q91WS9 mus musculus
4	725	58.6	214	11 Q91IA5	Q91IA5 mus musculus
5	705.5	57.0	235	11 Q91W12	Q91W12 mus musculus
6	704	56.9	211	11 Q91XL0	Q91XL0 mus musculus
7	471	38.1	108	4 Q9UL77	Q9UL77 homo sapien
8	463.5	37.5	107	4 Q96SA9	Q96SA9 homo sapien
9	450	36.4	108	4 Q9UL70	Q9UL70 homo sapien
10	438.5	35.4	107	4 Q9UL81	Q9UL81 homo sapien
11	437	35.3	108	4 Q9UL79	Q9UL79 homo sapien
12	433	35.0	116	4 Q96EF6	Q96EF6 homo sapien
13	431.5	34.9	235	11 Q99M11	Q99M11 mus musculus
14	429	34.7	236	4 Q96E61	Q96E61 homo sapien
15	415	33.5	111	11 Q920E9	Q920E9 mus musculus
16	394.5	31.9	109	4 Q9UL78	Q9UL78 homo sapien

17	382.5	30.9	233	4 Q96I69	Q96I69 homo sapien
18	380	30.7	108	4 Q9UL83	Q9UL83 homo sapien
19	379	30.6	298	11 Q9QYF0	Q9QYF0 mus musculus
20	377	30.5	233	11 Q91V32	Q91V32 m adult mal
21	371.5	30.0	109	4 Q9UL86	Q9UL86 homo sapien
22	371.5	30.0	109	4 Q9UL85	Q9UL85 homo sapien
23	366	29.6	103	11 Q9JL80	Q9JL80 mus musculus
24	365	29.5	109	11 Q920E6	Q920E6 mus musculus
25	351	28.4	127	11 Q925S9	Q925S9 mus musculus
26	350	28.3	114	4 Q9UL80	Q9UL80 homo sapien
27	346.5	28.0	106	5 Q9U410	Q9U410 schistosoma
28	346	28.0	107	11 Q9ER29	Q9ER29 mus musculus
29	345	27.9	99	11 Q9JL74	Q9JL74 mus musculus
30	335	27.1	101	11 Q9JL78	Q9JL78 mus musculus
31	328.5	26.6	241	11 Q921A6	Q921A6 mus musculus
32	328	26.5	97	11 Q9JL76	Q9JL76 mus musculus
33	321.5	26.0	104	11 Q9JL82	Q9JL82 mus musculus
34	306	24.7	109	6 Q9N0W5	Q9N0W5 oryctolagus
35	297	24.0	107	11 Q9JL84	Q9JL84 mus musculus
36	275.5	22.3	218	11 Q925S1	Q925S1 mus musculus
37	243	19.6	107	4 Q9JL82	Q9JL82 homo sapien
38	238.5	19.3	107	4 Q9NSD6	Q9NSD6 homo sapien
39	236.5	19.1	108	4 Q96SB0	Q96SB0 homo sapien
40	232	18.8	130	4 Q9NP29	Q9NP29 homo sapien
41	225	18.2	130	11 Q9D8W4	Q9D8W4 mus musculus
42	215	17.4	112	4 Q96JD1	Q96JD1 homo sapien
43	212	17.1	267	13 Q90529	Q90529 ginglymosto
44	208.5	16.9	112	4 Q96JD2	Q96JD2 homo sapien
45	207.5	16.8	116	4 Q96JD0	Q96JD0 homo sapien

# ALIGNMENTS

RESULT	1				
Q99M37	Q99M37	PRELIMINARY;	PRT;	238 AA.	
AC	Q99M37;				
DT	01-JUN-2001 (TREMBLrel. 17, Created)				
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	HYPOTHETICAL 26.3 KDA PROTEIN.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS				
RC	TISSUE.;				
RA	Strausberg R.;				
RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC002035; AAH02035.1; -				
DR	HSSP; P01679; 2FBJ				
DR	InterPro; IPR003599; Ig.				
DR	InterPro; IPR003597; Ig-cl.				
DR	InterPro; IPR003600; Ig-like.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR003596; Ig_v.				
DR	Pfam; PF00047; Ig; 2.				
DR	SMART; SM00409; IG; 2.				
DR	SMART; SM00407; IGC1; 1.				
DR	SMART; SM00406; IGV; 1.				
DR	SMART; SM00410; IG_Like; 1.				
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.				
KW	Hypothetical protein				
SQ	SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;				

Query Match 60.3%; Score 746.5; DB 11; Length 238;  
Best Local Similarity 58.5%; Pred. No. 1.5e-57;  
Matches 137; Conservative 40; Mismatches 56; Indels 1; Gaps 1;

Qy	6	ILLWVLLWPVGSTGDIIVLTQSPSLASVGDRTVITCKASQSDVDY-DGDSYMNNYQQKP	64
Dt	01-DEC-2001	(TrEMBLrel. 19, Created)	
Dt	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)	
Dt	01-DEC-2001	(TrEMBLrel. 19, Last annotation update)	
Dt	DE	HYPOTHETICAL 25.9 KDA PROTEIN.	
Dt	OS	Mus musculus (Mouse).	
Dt	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Dt	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
Dt	NCBI_TaxID=10090;	[1]	
RN	SEQUENCE FROM N.A.		
RP	TISSUE-COLON:		
RC	TISSUE-COLON:		
RA	Strausberg R.;		
RL	Submitted (Oct-2001) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; BC015292; AAH15292.1; -		
KW	Hypothetical protein.		
SQ	SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;		
Query Match 59.7%; Score 739; DB 11; Length 234;			
Best Local Similarity 60.1%; Pred. No. 6.6e-57;			
Matches 143; Conservative 33; Mismatches 58; Indels 4; Gaps 1;			
Qy	1	METDTILLWLVLPVGSTGDIIVLTQSPSLASVGDRTVITCKASQSDVDYDGDSYMNNY	60
Dt	01-DEC-2001	(TrEMBLrel. 19, Created)	
Dt	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)	
Dt	01-DEC-2001	(TrEMBLrel. 19, Last annotation update)	
Dt	DE	HYPOTHETICAL 25.9 KDA PROTEIN.	
Dt	OS	Mus musculus (Mouse).	
Dt	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Dt	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
Dt	NCBI_TaxID=10090;	[1]	
RN	SEQUENCE FROM N.A.		
RP	TISSUE-COLON:		
RC	TISSUE-COLON:		
RA	Strausberg R.;		
RL	Submitted (Oct-2001) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; BC015292; AAH15292.1; -		
KW	Hypothetical protein.		
SQ	SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;		
Query Match 59.7%; Score 739; DB 11; Length 234;			
Best Local Similarity 60.1%; Pred. No. 6.6e-57;			
Matches 143; Conservative 33; Mismatches 58; Indels 4; Gaps 1;			
Qy	1	METDTILLWLVLPVGSTGDIIVLTQSPSLASVGDRTVITCKASQSDVDYDGDSYMNNY	60
Dt	01-DEC-2001	(TrEMBLrel. 19, Created)	
Dt	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)	
Dt	01-DEC-2001	(TrEMBLrel. 19, Last annotation update)	
Dt	DE	HYPOTHETICAL 25.9 KDA PROTEIN.	
Dt	OS	Mus musculus (Mouse).	
Dt	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Dt	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
Dt	NCBI_TaxID=10090;	[1]	
RN	SEQUENCE FROM N.A.		
RP	TISSUE-COLON:		
RC	TISSUE-COLON:		
RA	Strausberg R.;		
RL	Submitted (Oct-2001) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; BC015292; AAH15292.1; -		
KW	Hypothetical protein.		
SQ	SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;		
Query Match 59.7%; Score 739; DB 11; Length 234;			
Best Local Similarity 60.1%; Pred. No. 6.6e-57;			
Matches 143; Conservative 33; Mismatches 58; Indels 4; Gaps 1;			
Qy	1	METDTILLWLVLPVGSTGDIIVLTQSPSLASVGDRTVITCKASQSDVDYDGDSYMNNY	60
Dt	01-DEC-2001	(TrEMBLrel. 19, Created)	
Dt	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)	
Dt	01-DEC-2001	(TrEMBLrel. 19, Last annotation update)	
Dt	DE	HYPOTHETICAL 25.9 KDA PROTEIN.	
Dt	OS	Mus musculus (Mouse).	
Dt	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Dt	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
Dt	NCBI_TaxID=10090;	[1]	
RN	SEQUENCE FROM N.A.		
RP	TISSUE-COLON:		
RC	TISSUE-COLON:		
RA	Strausberg R.;		
RL	Submitted (Oct-2001) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; BC015292; AAH15292.1; -		
KW	Hypothetical protein.		
SQ	SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;		
Query Match 59.7%; Score 739; DB 11; Length 234;			
Best Local Similarity 60.1%; Pred. No. 6.6e-57;			
Matches 143; Conservative 33; Mismatches 58; Indels 4; Gaps 1;			
Qy	1	METDTILLWLVLPVGSTGDIIVLTQSPSLASVGDRTVITCKASQSDVDYDGDSYMNNY	60
Dt	01-DEC-2001	(TrEMBLrel. 19, Created)	
Dt	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)	
Dt	01-DEC-2001	(TrEMBLrel. 19, Last annotation update)	
Dt	DE	HYPOTHETICAL 25.9 KDA PROTEIN.	
Dt	OS	Mus musculus (Mouse).	
Dt	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Dt	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
Dt	NCBI_TaxID=10090;	[1]	
RN	SEQUENCE FROM N.A.		
RP	TISSUE-COLON:		
RC	TISSUE-COLON:		
RA	Strausberg R.;		
RL	Submitted (Oct-2001) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; BC015292; AAH15292.1; -		
KW	Hypothetical protein.		
SQ	SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;		
Query Match 59.7%; Score 739; DB 11; Length 234;			
Best Local Similarity 60.1%; Pred. No. 6.6e-57;			

[illegible]



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Db 57 GVPFRSGSGQDYSITISSEYEDMGIIYCLQYDEFFTFGGTGLKLEIKRADAAPTVS 116
Qy 141 IFPPSDEQLKSGTASVCLLNFFPREAKVQWVDNALQSGNSQESVTEQDSKDSYSL 200
Db 117 IFPPSSQLSGGASVVCFLNFFPKDINKWKIDGSRQGVLSWTDQDSKDSYSMS 176
Qy 201 STLTLKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 238
Db 177 TLTLTKDEYERHNSYTCEATHKTSTSPIVKCFNRNEC 214

RESULT 5
ID Q91W12 PRELIMINARY; PRT; 235 AA.
AC Q91W12;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE UNKNOWN (PROTEIN FOR MGC:6582).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=BREAST TUMOR;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC006643; AA006643.1; -.
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;

Query Match 57.0%; Score 705.5; DB 11; Length 235;
Best Local Similarity 61.8%; Pred. No. 5.7e-54;
Matches 135; Conservative 31; Mismatches 50; Indels 5; Gaps 1;

Qy 18 STGDIVLTQSPSSLSASVGRVITTCASQSDYDGSYNNWYQKPGKAPKLLIYAASN 77
Db 20 SRGQIVLTQSPAIMSASGPERVITTCASQSDYDGSYNNWYQKPGKAPKLLIYAASN 74
Qy 78 LESGVPFRSGSGGTDTLTITSSLPQDFATYQCQSNEDPRTFGQGTKEIKRTVAAP 137
Db 75 LTSGVPRFRSGSGGTQYSLKINSLSQSEDFSGYFCQHFQWGTPTFGGTTKLEIKRADAAP 134
Qy 138 SVFIFFPSDEQLKSGTASVCLLNFFPREAKVQWVDNALQSGNSQESVTEQDSKDSY 197
Db 135 TVSIFPPSSEQLTSGGASVVCFLNFFPKDINKWKIDGSRQGVLSWTDQDSKDSY 194
Qy 198 SLSTLTLKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 238
Db 195 SMSSTLTLTDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 235

RESULT 6
ID Q91XL0 PRELIMINARY; PRT; 211 AA.
AC Q91XL0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE ADULT MALE KIDNEY CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE CLONE:0610010P20, FULL INSERT SEQUENCE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
RA Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Horii F.,
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RA Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y.,
RA Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T.,
RA Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D.,
RA Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y.,
RA Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y.,
RA Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kizama M., Nishino T., Harada A.,
RA Sumi N., Ishii Y., Nakamura S., Katsumoto H., Ikegami T., Kashiwagi K.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Iizawa M., Ohara E., Watahiki M.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
DR EMBL: AK002514; BAB22154.1; -.
SQ SEQUENCE 211 AA; 23182 MW; 1A5FFA0F8BA50163 CRC64;

Query Match 56.9%; Score 704; DB 11; Length 211;
Best Local Similarity 61.8%; Pred. No. 6.7e-54;
Matches 134; Conservative 32; Mismatches 43; Indels 8; Gaps 2;

Qy 24 LTQSPSSLSASVGRVITTCASQSDYDGSYNNWYQKPGKAPKLLIYAASNLSG 81
Db 1 MTQSPASLSVSGVETVITCRASENI-----YNSLAWYQKQKSPQLLYAATNLADG 54
Qy 82 VPSRFSGSGGTDTLTITSSLPQDFATYQCQSNEDPRTFGQGTKEIKRTVAAPSVEI 141
Db 55 VPSRFSGSGGTQYSLKINSLSQSEDFSGYFCQHFQWGTPTFGGTTKLEIKRADAAPTYSI 114
Qy 142 FPPSDEQLKSGTASVCLLNFFPREAKVQWVDNALQSGNSQESVTEQDSKDSYSL 201
Db 115 FPPSSEQLTSGGASVVCFLNFFPKDINKWKIDGSRQGVLSWTDQDSKDSYSMS 174
Qy 202 TLTLTKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 238
Db 175 TLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 211

RESULT 7
Q9UL77
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ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003396; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 38.1%; Score 471; DB 4; Length 108;
Best Local Similarity 83.0%; Pred. No. 6.8e-34;
Matches 93; Conservative 7; Mismatches 8; Indels 4; Gaps 1;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPKAPKLLIYAASNL 80
Db 1 DIQMTQSPSSLSASVGDRTVITCKASQSI-----SSYLNWYQKPKAPKLLIYAAS 56
QY 81 GVPFRFSGSGGTDFLTITSSLPQEDFATYQQSNEDPRTFGQGTKEIKR 132
Db 57 GVPFRFSGSGGTDFLTITSSLPQEDFATYQQS-YSTLTFGGKTKVEIKR 108

RESULT 8
Q96SA9 PRELIMINARY; PRT; 107 AA.
ID Q96SA9;
AC Q96SA9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes.";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 37.5%; Score 463.5; DB 4; Length 107;
Best Local Similarity 83.9%; Pred. No. 3e-33;
Matches 94; Conservative 6; Mismatches 7; Indels 5; Gaps 2;

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QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPKAPKLLIYAASNL 80
Db 1 DIQMTQSPSSLSASVGDRTVITCKASQSI-----SSYLNWYQKPKAPKLLIYAAS 56
QY 81 GVPFRFSGSGGTDFLTITSSLPQEDFATYQQSNEDPRTFGQGTKEIKR 132
Db 57 GVPFRFSGSGGTDFLTITSSLPQEDFATYQQS-YSTLTFGGKTKVEIKR 107

RESULT 9
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70;
AC Q9UL70;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003396; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 36.4%; Score 450; DB 4; Length 108;
Best Local Similarity 78.6%; Pred. No. 4.7e-32;
Matches 88; Conservative 8; Mismatches 12; Indels 4; Gaps 1;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPKAPKLLIYAASNL 80
Db 1 DIQMTQSPSSLSASVGDRTVITCKASQGI-----SNYLNWYQKPKAPKLLIYAAS 56
QY 81 GVPFRFSGSGGTDFLTITSSLPQEDFATYQQSNEDPRTFGQGTKEIKR 132
Db 57 GVPFRFSGSGGTDFLTITSSLPQEDVATYQKYNAPRTFGPGTKLEIKR 108

RESULT 10
Q9UL81 PRELIMINARY; PRT; 107 AA.
ID Q9UL81;
AC Q9UL81;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;

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RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035033; AAD56269.1; -.  
DR HSP; P01607; IREI.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR NON\_TER 1  
FT NON\_TER 107  
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 35.4%; Score 438.5; DB 4; Length 107;  
Best Local Similarity 78.6%; Pred. No. 4.7e-31;  
Matches 88; Conservative 9; Mismatches 10; Indels 5; Gaps 2;  
QY 21 DIVLTQSPSSLSASVGRVITTCRASQSDYDGSYMNWYQKPKAPKLLIYAASNL 80  
Db 1 DIQMTQSPSSLSASVGRVITTCRASQSI----SNLYNWKYQKPKAPNLLIYAASLQ 56  
QY 81 GVPFRFSGSGGTDTLTITISLQPEDFATYYCQSNEDPRTFGGKTVEIKR 132  
Db 57 GVPFRFSGSGGTDTLTITISLQPEDFATYYCQSS-YSALTFGGKTVDIRR 107

RESULT 11  
Q9UL79 PRELIMINARY; PRT; 108 AA.  
AC Q9UL79  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION  
DE (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035035; AAD56271.1; -.  
DR HSP; P01607; IREI.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR NON\_TER 1  
FT NON\_TER 108  
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 35.3%; Score 437; DB 4; Length 108;  
Best Local Similarity 77.7%; Pred. No. 6.4e-31;  
Matches 87; Conservative 7; Mismatches 14; Indels 4; Gaps 1;  
QY 21 DIVLTQSPSSLSASVGRVITTCRASQSDYDGSYMNWYQKPKAPKLLIYAASNL 80  
Db 1 DIVMTQSPSSLSASVGRVITTCRASQSI----SSLYLWYQKPKAPPELLIYAASLQ 56  
QY 81 GVPFRFSGSGGTDTLTITISLQPEDFATYYCQSNEDPRTFGGKTVEIKR 132  
Db 57 GVPFRFSGSGGTDTLTITISLQPEDFATYYCQSYFFPPTFGGKTVEIKR 108

RESULT 12

Q96PF6 PRELIMINARY; PRT; 116 AA.  
AC Q96PF6  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE KAPPA 1 LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
GN SDNK1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=21361171; PubMed=11468171;  
RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;  
RT "The tropism of organ involvement in primary systemic amyloidosis:  
contributions of Ig V(L) germ line gene use and clonal plasma cell  
burden.";  
RL Blood 98:714-720(2001).  
DR EMBL; AF361758; AAK51465.1; -.  
FT NON\_TER 1  
FT NON\_TER 116  
SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;

Query Match 35.0%; Score 433; DB 4; Length 116;  
Best Local Similarity 70.8%; Pred. No. 1.6e-30;  
Matches 85; Conservative 14; Mismatches 17; Indels 4; Gaps 1;  
QY 21 DIVLTQSPSSLSASVGRVITTCRASQSDYDGSYMNWYQKPKAPKLLIYAASNL 80  
Db 1 DIQMTQSPSSLSASVGRVITTCRASQSI----ANHLYNWKYQKPKAPKLLIYDGSFLKT 56  
QY 81 GVPFRFSGSGGTDTLTITISLQPEDFATYYCQSNEDPRTFGGKTVEIKRTVAAPSVF 140  
Db 57 GVPFRFSGSGGTDTLTITISLQPEDFATYYCQYHLLPFTFGGKTVDFTVAAPSVF 116

RESULT 13  
Q99M11 PRELIMINARY; PRT; 235 AA.  
AC Q99M11  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE HYPOTHETICAL 25.4 KDA PROTEIN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC002129; AAH02129.1; -.  
DR HSP; P01703; 7FAB.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR003597; Ig\_ci.  
DR InterPro; IPR003600; Ig\_like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; IGV; 2.  
DR SMART; SM00407; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR SMART; SM00410; IGV\_like; 2.  
DR PROSITE; PS00290; IGV\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 235 AA; 25403 MW; 39807BFE6782A3FB CRC64;

Query Match 34.9%; Score 431.5; DB 11; Length 235;

Best Local Similarity 42.6%; Pred. No. 5.4e-30;  
Matches 101; Conservative 37; Mismatches 86; Indels 13; Gaps 7;

QY 7 LLWVLLWVPGSGDVLVLTQSPSSLSASVGDRTVTICKASQSYVDYDGSYMNWYQKPK 66  
DB 6 LLLVFLHLHTGSCAQVLTQ-PSSVSTSLGSTAKLPKA--STGNIGDSYVWYQYMG 62  
QY 67 APKLLIYAASNLSEGVPSRFGSG--GSGTDFLTITSSLOPEDFATYVCOQSNEDPRTFG 124  
DB 63 STFNMYGGDLPSPGVSDRFGSSIDSSNSAFLTONVOADDEADYVCOYSGGIRVFG 122  
QY 125 GTKVEI-KRTVAAPSVFIPPPDEQLKSGTASVCLLNFFYPREAKVQWKVNDALQSGNS 183  
DB 123 GTKLVLSQPKTSPVTLFPPSSEELTNKATLVCTISDFYGVVTVDMKADG---TPVT 179  
QY 184 QESVTEQDSK--DSYSLSTLTLSKADYEKHKYVACEVTHOGLSPVTKSFNRGEC 238  
DB 180 QGVETQPSKQNNKYMASSTLTAKAWETHSSYSCQVTHEG--HTVEKSLSRADC 234

## RESULT 14

Q96E61  
ID Q96E61 PRELIMINARY; PRT; 236 AA.  
AC Q96E61;  
DT 01-DEC-2001 (TremBLrel. 19, Created)  
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)  
DE UNKNOWN (PROTEIN FOR MGC:17259).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN, AND GLIOBLASTOMA WITH EGFR AMPLIFICATION;  
RA Strausberg R.;  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC012876; AAH12876.1; -.  
SQ SEQUENCE 236 AA; 24712 MW; 7EC9FB3622FED957 CRC64;

Query Match 34.7%; Score 429; DB 4; Length 236;

Best Local Similarity 42.4%; Pred. No. 9e-30;  
Matches 100; Conservative 39; Mismatches 87; Indels 10; Gaps 7;

QY 7 LLWVLLWVPGSGDVLVLTQSPSSLSASVGDRTVTICKASQSYVDYDGSYMNWYQKPK 66  
DB 6 LLLTLLAHCTGSAQSVLAQ-PPSVSGAGQGVITISCTGS-STNIGAGYAVHWYQFPGA 63  
QY 67 APKLLIYAASNLSEGVPSRFGSGSGTDFLTITSSLOPEDFATYVCOQ--QSNEDPRTFG 124  
DB 64 APKVLIGYNNRPSGVDPDRFGSGKSGTSASLAITGLQAEADYVCOYSGLSGSVFGA 123  
QY 125 GTKVEI-KRTVAAPSVFIPPPDEQLKSGTASVCLLNFFYPREAKVQWKVNDNA-LQSGN 182  
DB 124 GTKVTVLGQPKANVTVTLFPPSSEELQANKATLVCLISDFYPCAVTVAMKADGSPYKAG- 182  
QY 183 SOESVTEQDSKSTSLSTLSKADYEKHKYVACEVTHOGLSPVTKSFNRGEC 238  
DB 183 -VETTKPSQSNKNYAASSYLSLTPEQWKSHRSYSCQVTHEG--STVEKTVAPTEC 235

## RESULT 15

Q920E9  
ID Q920E9 PRELIMINARY; PRT; 111 AA.  
AC Q920E9;  
DT 01-DEC-2001 (TremBLrel. 19, Created)  
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)  
DE PTERIN-MIMICKING ANTI-IDIOPOPE KAPPA CHAIN VARIABLE REGION (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;  
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307935; AAL09419.1; -.  
FT NON\_TER 1 111  
SQ SEQUENCE 111 AA; 12046 MW; 1E46988AA6858526 CRC64;

Query Match 33.5%; Score 415; DB 11; Length 111;

Best Local Similarity 72.1%; Pred. No. 5.6e-29;  
Matches 80; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVTICKASQSYVDYDGSYMNWYQKPKAPKLLIYAASNL 80  
DB 1 DIVLTQSPASLAVSLGQRATISCRASKSVSTSGSYMHYQKPGQPPKLLIYASNL 60  
QY 81 GVPSRFGSGSGTDFLTITSSLOPEDFATYVCOQSNEDPRTFGQTKVEIK 131  
DB 61 GVPARFSGSGTDFLTINHPVEEDATYVCOHSRELPTFTGGTKLEIK 111

Search completed: August 14, 2002, 15:22:14  
Job time: 682 sec



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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 15:15:34 ; Search time 230.21 Seconds  
(without alignments)  
114.832 Million cell updates/sec

Title: US-09-499-662-129  
Perfect score: 1237  
Sequence: 1 METDTILLWLLWVPGSTG.....EVTHQGLSSPVTKSFNRGEC 238

Scoring table:  
BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1237	100.0	238	21 AAW90931	Humanised anti-Fas
2	1233	99.7	238	21 AAW90930	Humanised anti-Fas
3	1232	99.6	238	21 AAW90932	Humanised anti-Fas
4	1177	95.1	238	19 AAW83034	Anti-Fas humanised
5	1177	95.1	238	21 AAB14777	Humanised anti-Fas
6	1177	95.1	238	21 AAW90927	Humanised HFE7A de
7	1172	94.7	238	19 AAW83031	Anti-Fas humanised
8	1172	94.7	238	21 AAB14772	Humanised anti-Fas
9	1172	94.7	238	21 AAW90922	Humanised anti-Fas
10	1159	93.7	238	19 AAW83032	Anti-Fas humanised
11	1159	93.7	238	21 AAB14773	Humanised anti-Fas

12	1159	93.7	238	21 AAW90923	Humanised anti-Fas
13	1158	93.6	238	19 AAW83035	Anti-Fas humanised
14	1158	93.6	238	21 AAB14778	Humanised anti-Fas
15	1158	93.6	238	21 AAW90928	Humanised HFE7A de
16	1157	93.5	238	19 AAW83033	Anti-Fas humanised
17	1157	93.5	238	21 AAB14774	Humanised anti-Fas
18	1157	93.5	238	21 AAW90924	Humanised anti-Fas
19	1108	89.6	218	18 AAW13563	Humanised anti-L-s
20	1096	88.6	218	21 AAW95658	Mus musculus anti-Light chain amino
21	1096	88.6	218	21 AAY85200	Mus musculus anti-Full variable ligh
22	1096	88.6	218	21 AAB76947	Humanised MaE11 Ve
23	1089	88.0	218	14 AAR33312	Human 227 anti-IgE
24	1073	86.7	218	20 AAY50030	Mus musculus anti-Mus musculus anti-
25	1073	86.7	218	20 AAW95662	Amino acid sequenc
26	1073	86.7	218	21 AAB07472	E27 anti-IgE antib
27	1073	86.7	218	21 AAB74211	Mus musculus anti-
28	1073	86.7	218	21 AAB76958	Anti-IgE antibody,
29	1070	86.5	218	20 AAW95669	Full length light
30	1070	86.5	218	20 AAW95664	Full length light
31	1070	86.5	218	22 AAB47087	Variable light cha
32	1070	86.5	218	22 AAB76949	Variable light cha
33	1070	86.5	218	22 AAB76951	Human IGFAM-10 imm
34	1070	86.5	218	22 AAB76953	Human IGFAM-10 imm
35	1070	86.5	218	22 AAB76958	Human IGFAM-13 imm
36	1049.5	84.8	237	21 AAY96298	Human anti-RSV mon
37	1048	84.7	240	20 AAY50161	Amino acid sequenc
38	1045.5	84.5	237	21 AAY96289	Human antilfc epsll
39	1043.5	84.4	241	22 AAB82912	Humanised 5G1.1 VL
40	1041.5	84.2	234	14 AAR38162	
41	1037.5	83.9	237	21 AAY96301	
42	1036	83.8	234	18 AAW11638	
43	1033	82.7	240	22 AAG63665	
44	1021	82.5	237	20 AAW73873	
45	1019	82.4	236	16 AAW77614	

#### ALIGNMENTS

RESULT 1

AAW90931

ID AAW90931 standard; Protein; 238 AA.

XX AC AAW90931;

XX DT 08-AUG-2000 (first entry)

XX DE Humanised anti-Fas designed light chain Leu 2 protein.

XX KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
XX KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;  
XX KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
XX KW nephrotropic; antinfertility; neuroprotective; antirheumatic;  
XX KW hepatotropic; humanized; rheumatoid arthritis; systemic lupus erythematosus;  
XX KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
XX KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;  
XX KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
XX KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
XX KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
XX KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

OS Synthetic.

XX EP990663-A2.

XX PD 05-APR-2000.

XX PF 29-SEP-1999; 99EP-0307711.

XX PR 30-SEP-1998; 98JP-0276881.

XX PR 30-SEP-1998; 98JP-0276882.

XX PA (SANY ) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 XX WPI: 2000-258930/23.  
 DR N-PSDB; AA11632.  
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems -  
 XX Claim 2; Page 159; 263pp; English.  
 XX This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thymimetic,  
 CC antiartherosclerotic, cardiant and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody light chain construct designated Leu 2  
 CC which is described in the method of the invention.  
 XX Sequence 238 AA;

Query Match 100.0%; Score 1237; DB 21; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-60;  
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METDTILLWVLLWPGSTGDIVLTQSPSSLSASVGDRTVTITCKASQSDYDGDSDYNNY 60  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 1 metdtillwvllwpgstgdivltqspsslsasvgdrtvtitckasqsdvdygdsymny 60  
 QY 61 QOKPGOAPKLLIYAASNLSESGVPSRFSGSGCTDFTLTSSLPQEDFATYXCQSQNEQPR 120  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 61 qokpggapklliyasnlsesgvpsrfsgsgctdftltsslpqedfatycqsgneqpr 120  
 QY 121 TFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQ 180  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 121 tfgggtkveikrtvaapsvfifppsdeqlksgtasvvcvllnnfybreakvqvkdnaqls 180  
 QY 181 GNSQSVTEQDSKDTYSLSSTLTLSKADYKHVYACEVTHQGLSSPVTKSFNRGEC 238  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 181 gnsqsvteqdskdtsyslstltlskadyekhvyacevthqglsspvtksfnrgec 238

RESULT 2  
 AAW90930  
 ID AAW90930 standard; Protein: 238 AA.  
 XX  
 AC AAW90930;  
 XX  
 DT 08-AUG-2000 (first entry)  
 XX

DE Humanised anti-Fas designed light chain Leu 1 protein.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;  
 KW dermatological; immunosuppressive; thymimetic; antirheumatic; anti-Fas;  
 KW nephrotropic; antiinfertility; neuroprotective; antiartherosclerotic;  
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
 XX Synthetic.  
 XX EP990663-A2.  
 PN 05-APR-2000.  
 PD 29-SEP-1999; 99EP-0307711.  
 PF 30-SEP-1998; 98JP-0276881.  
 PR 30-SEP-1998; 98JP-0276882.  
 XX (SANY ) SANKYO CO LTD.  
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 DR WPI: 2000-258930/23.  
 DR N-PSDB; AA11631.  
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems -  
 XX Claim 3; Page 156-157; 263pp; English.  
 XX This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thymimetic,  
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,  
 CC antiartherosclerotic, cardiant and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody light chain construct designated Leu 1  
 CC which is described in the method of the invention.  
 XX Sequence 238 AA;

Query Match 99.7%; Score 1233; DB 21; Length 238;  
 Best Local Similarity 99.6%; Pred. No. 6.7e-60;  
 Matches 237; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 METDTILLWVLLWPGSTGDIVLTQSPSSLSASVGDRTVTITCKASQSDYDGDSDYNNY 60



Db 1 metdtillwllwvpgstgdivltqspsslsasvgydrvtitckasqsvdydgsymwmy 60  
Qy 61 OQKPGQAPKLLIYAASNLSESGVPSRFSGSGTDFTLTISLQPDFAFYCCQSQSNEDEPR 120  
Db 61 qkpgkqkplliyaasnlsgvpsrfsqsgsgtdftltisslqpedfatyccqsgnedpr 120  
Qy 121 TFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQKVDNALQ 180  
Db 121 tfgggtkeikrtvaapsvfifppsdeqlksgtasvcllnnfypreakvqkvdnalqgs 180  
Qy 181 GNSQSVTEQDSKSTYSLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 238  
Db 181 gnsqsvteqdsksdstyslsstltlskadyekhkyacevthqglsspvtksfnrgec 238

RESULT 3  
ID AAW90932 standard; Protein: 238 AA.  
XX AAW90932;  
AC AAW90932;  
XX AAW90932;  
DT 08-AUG-2000 (first entry)  
XX Humanised anti-Fas designed light chain Leu 3 protein.  
DE  
XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
XX anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;  
XX dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
XX nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;  
XX hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
XX Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
XX Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;  
XX Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
XX multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
XX insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
XX cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
XX Synthetic.  
OS  
XX  
XX EP990663-A2.  
XX  
XX 05-APR-2000.  
XX  
XX 29-SEP-1999; 99EP-0307711.  
XX  
XX 30-SEP-1998; 98JP-0276881.  
XX  
XX 30-SEP-1998; 98JP-0276882.  
XX  
XX (SANY ) SANKYO CO LTD.  
XX  
XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
XX WPI: 2000-258930/23.  
XX  
XX N-PSDB: AAL11633.  
XX  
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
XX inflammatory or autoimmune disease, induces apoptosis selectively in  
XX cells with abnormal Fas-Fas ligand systems  
XX  
XX Claim 3; Page 161-162; 263pp; English.  
XX  
XX This invention describes a novel humanized anti-Fas antibody-like  
XX molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
XX ligand system, by binding to Fas on the cell surface, and prevents  
XX apoptosis in cells with a normal system, by inhibiting binding between  
XX Fas and its ligand. The products of the invention have anti-inflammatory,  
XX anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
XX immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
XX antirheumatic, nephrotropic, antinfertility, neuroprotective,  
XX antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce  
XX apoptosis by binding to cell surface Fas or inhibit it by competitive  
XX inhibition of ligand binding. (I) are used to treat and/or prevent

CC diseases associated with the Fas/Fas ligand system, especially systemic  
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic  
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
CC cells. They bind to both human and murine Fas, so can be evaluated in  
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
CC the native ligand, do not induce liver disease, and have reduced risk of  
CC inducing a human anti-murine antibody response. This sequence represents  
CC a humanised anti-Fas antibody light chain construct designated Leu 3  
CC which is described in the method of the invention.  
XX  
SQ Sequence 238 AA;  
Query Match 99.6%; Score 1232; DB 21; Length 238;  
Best Local Similarity 99.2%; Pred. No. 7.6e-60;  
Matches 236; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 METDTILLWLLWVPGSTGDIVLTQSPSSLSASVGYDRVTITCKASQSVDYDGSYMWY 60  
Db 1 metdtillwllwvpgstgdivltqspsslsasvgydrvtitckasqsvdydgsymwmy 60  
Qy 61 OQKPGQAPKLLIYAASNLSESGVPSRFSGSGTDFTLTISLQPDFAFYCCQSQSNEDEPR 120  
Db 61 qkpgkqkplliyaasnlsgvpsrfsqsgsgtdftltisslqpedfatyccqsgnedpr 120  
Qy 121 TFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQKVDNALQ 180  
Db 121 tfgggtkeikrtvaapsvfifppsdeqlksgtasvcllnnfypreakvqkvdnalqgs 180  
Qy 181 GNSQSVTEQDSKSTYSLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 238  
Db 181 gnsqsvteqdsksdstyslsstltlskadyekhkyacevthqglsspvtksfnrgec 238

RESULT 4  
AAW83034  
ID AAW83034 standard; Protein: 238 AA.  
XX AAW83034;  
AC AAW83034;  
XX AAW83034;  
DT 15-MAR-1999 (first entry)  
XX  
DE Anti-Fas humanised antibody HFE7A light chain PDHH type.  
XX  
XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;  
XX apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;  
XX systemic lupus erythematosus; graft versus host disease;  
XX Sjogren syndrome; pernicious anaemia; Addison's disease;  
XX scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
XX rheumatoid arthritis; autoimmune haemolytic anaemia;  
XX myasthenia gravis; multiple sclerosis; Basedow's disease;  
XX thrombopenia purpura; insulin-dependent diabetes; allergy;  
XX atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
XX glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
XX transplant rejection; therapy.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
XX Peptide 1..20 /label= Sig\_peptide  
XX Protein 21..238 /label= Mat\_protein  
XX Region 21..131 /label= variable  
FT



Best Local Similarity 93.3%; Pred. No. 7.2e-57; Matches 222; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 METDTILLWLLVPGSTGDIIVLTQSPSLASASVGRVITTCASQSDVDGDSYNNWY 60  
 Db 1 metdtillwllvpgstgeivltqspgtlispgeratlscasqsdvdgdsymnw 60

QY 61 QKPGQAPKLLIIYAASNLSESGVSRFSGSGGTDFTITISLQPEDFATYYCQOSNEDPR 120  
 Db 61 qkpgqaprllyaaasnlsgvdrfsgsgtdftitlsrlepedfavyycqgsnedpr 120

QY 121 TFGGKTVEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180  
 Db 121 tfggktleikrtvaapsvfifppdeqlksgtasvvcllnnfypreakvqwkvdnalqs 180

QY 181 GNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
 Db 181 gnsqesvteqdsksdystlsstltlskadyekkhvyacevthqglsspvtksfnrgec 238

RESULT 6  
 AAW90927  
 ID AAW90927 standard; Protein; 238 AA.  
 XX  
 AC AAW90927;  
 XX  
 DT 08-AUG-2000 (first entry)  
 XX  
 DE Humanised HFE7A designed light chain protein.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;  
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
 KW nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;  
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
 XX Synthetic.  
 XX  
 XX EP990663-A2.  
 XX  
 PD 05-APR-2000.  
 XX  
 XX 29-SEP-1999; 99EP-0307711.  
 XX  
 PR 30-SEP-1998; 98JP-0276881.  
 PR 30-SEP-1998; 98JP-0276882.  
 XX  
 XX (SANY ) SANKYO CO LTD.  
 XX  
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 PI WPI; 2000-258930/23.  
 DR N-PSDB; AAA11614.  
 XX  
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems  
 XX  
 XX Claim 3; Page 141-142; 263pp; English.  
 XX  
 XX This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,

CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,  
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody HFE7A designed light chain which is used in  
 CC the method described in the invention.  
 XX  
 XX Sequence 238 AA;  
 SQ

Query Match 95.1%; Score 1177; DB 21; Length 238;  
 Best Local Similarity 93.3%; Pred. No. 7.2e-57;  
 Matches 222; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 METDTILLWLLVPGSTGDIIVLTQSPSLASASVGRVITTCASQSDVDGDSYNNWY 60  
 Db 1 metdtillwllvpgstgeivltqspgtlispgeratlscasqsdvdgdsymnw 60

QY 61 QKPGQAPKLLIIYAASNLSESGVSRFSGSGGTDFTITISLQPEDFATYYCQOSNEDPR 120  
 Db 61 qkpgqaprllyaaasnlsgvdrfsgsgtdftitlsrlepedfavyycqgsnedpr 120

QY 121 TFGGKTVEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180  
 Db 121 tfggktleikrtvaapsvfifppdeqlksgtasvvcllnnfypreakvqwkvdnalqs 180

QY 181 GNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
 Db 181 gnsqesvteqdsksdystlsstltlskadyekkhvyacevthqglsspvtksfnrgec 238

RESULT 7  
 AAW83031  
 ID AAW83031 standard; Protein; 238 AA.  
 XX  
 AC AAW83031;  
 XX  
 DT 15-MAR-1999 (first entry)  
 XX  
 DE Anti-Fas humanised antibody HFE7A light chain HH type.  
 XX  
 KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;  
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;  
 KW systemic lupus erythematosus; graft versus host disease;  
 KW Sjorgen syndrome; pernicious anaemia; Addison's disease;  
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;  
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;  
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;  
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
 KW transplant rejection; therapy.  
 XX  
 XX Homo sapiens.  
 OS Synthetic.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Peptide 1..20  
 FT /label= Sig\_peptide  
 FT

FT Protein 21...238  
 FT /label= Mat\_protein  
 FT Region 21...131  
 FT /label= Variable  
 FT Region 132...238  
 FT /label= Constant  
 FT Region 44...58  
 FT /label= CDR\_L1  
 FT /note= "claim 9"  
 FT Region 74...80  
 FT /label= CDR\_L2  
 FT /note= "claim 9"  
 FT Region 113...121  
 FT /label= CDR\_L3  
 FT /note= "claim 9"  
 XX AU9859701-A.  
 XX  
 PD 08-OCT-1998.  
 XX  
 PF 30-MAR-1998; 98AU-0059701.  
 XX  
 PR 08-OCT-1997; 97JP-0276064.  
 PR 01-APR-1997; 97JP-0082953.  
 PR 25-JUN-1997; 97JP-0169088.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;  
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;  
 XX  
 DR WPI; 1998-543440/47.  
 DR N-PSDB; AAV70074.  
 XX  
 PT New antibodies and proteins bind conserved epitope of Fas antigen -  
 PT used to evaluate drugs in animal models and to treat Fas-associated  
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
 PT myocarditis, hepatitis and AIDS  
 XX  
 PS Claim 21: Page 199-199; 292pp; English.  
 XX  
 CC This is the amino acid sequence of the HH type humanised light  
 CC chain of murine anti-human Fas monoclonal antibody HFE7A.  
 CC Humanisation of the murine sequence (see AAW83042) entailed making  
 CC P47A, K49R, H80S, P81R, V82L, E84P, E85A, A87F and T89V amino acid  
 CC substitutions; these residues are conserved in the human light  
 CC chain (kappa chain). Host cell Escherichia coli PHSGH7 SANK 73497  
 CC harbors plasmid PHSGH7 carrying a fusion fragment of the humanised  
 CC HH type HFE7A light chain and DNA encoding the region of human  
 CC immunoglobulin kappa chain, and is deposited as FERM BP-6073  
 CC (claimed). The invention provides methods for producing humanised  
 CC antibodies by culturing host cells. Humanised versions of HFE7A  
 CC (see AAW83031-37), like native HFE7A, are capable of inducing  
 CC apoptosis in abnormal cells expressing Fas, and of inhibiting  
 CC Fas-induced apoptosis in normal cells. The humanised antibodies  
 CC are used to evaluate, in animal models, treatments of diseases that  
 CC involve Fas/Fas ligand interactions, and also to treat such  
 CC diseases, including autoimmune disease (e.g. systemic lupus  
 CC erythematosus, Hashimoto's disease, graft versus host disease,  
 CC Sjogren syndrome, pernicious anaemia, Addison's disease,  
 CC scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid  
 CC arthritis, autoimmune haemolytic anaemia, sterility, myasthenia  
 CC gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura  
 CC and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,  
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic  
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).  
 XX Sequence 238 AA;  
 SQ

QY 1 METDTILLWLLVPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSYDYDGDSYMNY 60  
 DB 1 metdtillwlllvpgstgdivltqspgtislsgeratlsckasqsvdygdsgymny 60  
 QY 61 QOKPGQAPKLLIYAASNLESVPSFSGSGGTDTLTITSSLOPEDFATYYCOQSNEDPR 120  
 DB 61 qokpgqaprllyaaanlesgipdrfsgsgsgtdltitrlsrlepafavyycqgsnedpr 120  
 QY 121 TFGQGTKEIKRTVAAPSFIPTPPSDEOLKSGTASVCLNNFYPREAKVOKVDNALOS 180  
 DB 121 tfgggtleikrtvaapsvfiptpsdeqlksgtasvcllnnfybreakvqkvdnals 180  
 QY 181 GNSQSVTEQSDKSTYSLSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 238  
 DB 181 gnsqsvteqsdkstyslsstltlskadyekhkyacevthqglsspytksfnrgec 238  
 RESULT 8  
 AAB14772  
 ID AAB14772 standard; Protein; 238 AA.  
 XX  
 AC AAB14772;  
 XX  
 DT 24-NOV-2000 (first entry)  
 XX  
 DE Humanised anti-Fas antibody light chain, SEQ ID NO:50.  
 XX  
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;  
 KW murine; humanised antibody; complementarity determining region; CDR;  
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;  
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;  
 KW hepatitis; AIDS; graft rejection; light chain.  
 XX  
 OS Chimeric - Mus musculus.  
 OS Chimeric - Homo sapiens.  
 XX  
 PN JP2000169393-A.  
 XX  
 PD 20-JUN-2000.  
 XX  
 PF 30-SEP-1999; 99JP-0278301.  
 XX  
 PR 30-SEP-1998; 98JP-0276883.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 DR WPI; 2000-485645/43.  
 DR N-PSDB; AAA72124.  
 XX  
 PT Preventive or treating agent for the diseases caused by an abnormality  
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains  
 PT anti-Fas antibody -  
 XX  
 PS Claim 20; Page 78-79; 139pp; Japanese.  
 CC The invention relates to compositions for the prevention or treatment  
 CC or diseases caused by an abnormality in the Fas/Fas ligand system  
 CC containing an anti-Fas antibody as the active component. The anti-Fas  
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,  
 CC or a humanised version of HFE7A containing identical CDRs  
 CC (complementarity determining regions) to antibody HFE7A. Via its  
 CC interaction with Fas, the antibody of the invention acts as a modulator  
 CC of apoptosis. The compositions of the invention may therefore be used in  
 CC the treatment or prevention of conditions such as autoimmune diseases,  
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,  
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS  
 CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778  
 CC represent the light chains of several humanised HFE7A-derived anti-Fas  
 CC antibodies.  
 XX Sequence 238 AA;  
 SQ

Query Match 94.7%; Score 1172; DB 19; Length 238;  
 Best Local Similarity 92.98; Pred. No. 1.3e-56;  
 Matches 221; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Query Match 94.7%; Score 1172; DB 21; Length 238;  
 Best Local Similarity 92.9%; Pred. No. 1.3e-56;  
 Matches 221; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 METDTILLWLLVPGSTGDIVLTQSPSSLSASVGRVITTCASQSDYDGDSPYNNWY 60  
 DB 1 metdtillwllvpgstgdivltqspgtlslspgeratlsckasqsdvdygdsgymnw 60

QY 61 QOKPGQAPKLLIYAASNLGSPRFSGSGTDTFTLTISLOPEDFATYVCQGSNEDPR 120  
 DB 61 qkpgqaprllyaaasnlsgipdrfsgsgtdftltisrlepadvfayvcqgsnedpr 120

QY 121 TFGGKTVEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPRKAVQWKVDNALQS 180  
 DB 121 tfggktrleikrtvaapsvfifpdsdeqlksgtasvvcllnnfyprkavqwkvdnalqs 180

QY 181 GNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
 DB 181 gnsqesvteqdsksdystlsstltlskadyekhkvyacevthqglsspvtksfnrgec 238

RESULT 9  
 AAW90922 standard; Protein: 238 AA.

XX AC AAW90922;  
 XX DT 08-AUG-2000 (first entry)  
 XX DE Humanised anti-Fas antibody HFE7A light chain HH type protein.

XX KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;  
 KW dermatological; immunosuppressive; thyromimetic; antiarthritis; anti-Fas;  
 KW nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;  
 KW hepatocytic; humanized; apoptosis; systemic lupus erythematosus;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjogren's syndrome; anemia; Addison's disease; sterility; myasthenia gravis;  
 KW Goodpasture syndrome; Crohn's disease; scleroderma; purpura; allergy;  
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
 XX OS Synthetic.  
 XX PN EP990663-A2.  
 XX PD 05-APR-2000.  
 XX PF 29-SEP-1999; 99EP-0307711.  
 XX PR 30-SEP-1998; 98JP-0276881.  
 XX PR 30-SEP-1998; 98JP-0276882.  
 XX PA (SANY ) SANKYO CO LTD.  
 XX PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 XX WP: 2000-258930/23.  
 XX DR N-PSDB; AAA11562.  
 XX PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems  
 XX PS Example reference 14; Page 114-115; 263pp; English.  
 XX CC This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between

CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antiarthritis, nephrotropic, cardiant and hepatropic activity. (I) induce  
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjogren's syndrome, pernicious anemia, Crohn's  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody HFE7A light chain HH type which is used in  
 XX the method described in the invention.

XX SQ Sequence 238 AA;

Query Match 94.7%; Score 1172; DB 21; Length 238;  
 Best Local Similarity 92.9%; Pred. No. 1.3e-56;  
 Matches 221; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 METDTILLWLLVPGSTGDIVLTQSPSSLSASVGRVITTCASQSDYDGDSPYNNWY 60  
 DB 1 metdtillwllvpgstgdivltqspgtlslspgeratlsckasqsdvdygdsgymnw 60

QY 61 QOKPGQAPKLLIYAASNLGSPRFSGSGTDTFTLTISLOPEDFATYVCQGSNEDPR 120  
 DB 61 qkpgqaprllyaaasnlsgipdrfsgsgtdftltisrlepadvfayvcqgsnedpr 120

QY 121 TFGGKTVEIKRTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPRKAVQWKVDNALQS 180  
 DB 121 tfggktrleikrtvaapsvfifpdsdeqlksgtasvvcllnnfyprkavqwkvdnalqs 180

QY 181 GNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
 DB 181 gnsqesvteqdsksdystlsstltlskadyekhkvyacevthqglsspvtksfnrgec 238

RESULT 10  
 AAW83032 standard; Protein: 238 AA.

XX AC AAW83032;  
 XX DT 15-MAR-1999 (first entry)  
 XX DE Anti-Fas humanised antibody HFE7A light chain HH type.

XX KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;  
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;  
 KW systemic lupus erythematosus; graft versus host disease;  
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;  
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;  
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;  
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;  
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
 KW transplant rejection; therapy.  
 XX OS Homo sapiens.  
 XX OS Synthetic.

FH Key Location/Qualifiers
FT Peptide 1..20
FT Protein /label= Sig\_peptide
FT 21..238
FT /label= Mat\_protein
FT Region 21..131
FT /label= Variable
FT Region 132..238
FT /label= Constant
FT Region 44..58
FT /label= CDR\_L1
FT /note= "claim 9"
FT Region 74..80
FT /label= CDR\_L2
FT /note= "claim 9"
FT Region 113..121
FT /label= CDR\_L3
FT /note= "claim 9"
XX AU9859701-A.
XX
XX 08-OCT-1998.
XX
XX 30-MAR-1998; 98AU-0059701.
XX
XX 08-OCT-1997; 97JP-0276064.
XX 01-APR-1997; 97JP-0082953.
XX 25-JUN-1997; 97JP-0169088.
XX
XX (SANY ) SANKYO CO LTD.
XX
XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
XX Masahiko O, Nobufusa S, Shin Y, Tohru T;
XX WPI: 1998-543440/47.
XX N-PSDB; AAV70075.
XX
XX New antibodies and proteins bind conserved epitope of Fas antigen -
XX used to evaluate drugs in animal models and to treat Fas-associated
XX diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
XX myocarditis, hepatitis and AIDS
XX
XX Claim 21; Page 200; 292pp; English.
XX
XX This is the amino acid sequence of the HM type humanised light
XX chain of murine anti-human Fas monoclonal antibody HFE7A.
XX Humanisation of the murine sequence (see AA83042) entailed making
XX P47A and K49R amino acid substitutions; these residues are
XX conserved in the human light (kappa) chain. Host cell E. coli
XX PHSGHM17 SANK 73597 harbors plasmid PHSGHM17 carrying a fusion
XX fragment of the humanised HM type HFE7A light chain and DNA
XX encoding the region of human immunoglobulin kappa chain, and is
XX deposited as FERM BP-6072 (claimed). The invention provides
XX methods for producing humanised antibodies by culturing host
XX cells. Humanised versions of HFE7A (see AA83031-37), like native
XX HFE7A, are capable of inducing apoptosis in abnormal cells
XX expressing Fas, and of inhibiting Fas-induced apoptosis in normal
XX cells. The humanised antibodies are used to evaluate, in animal
XX models, treatments of diseases that involve Fas/Fas ligand
XX interactions, and also to treat such diseases, including autoimmune
XX disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
XX graft versus host disease, Sjogren syndrome, pernicious anaemia,
XX Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
XX disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
XX sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
XX thrombopenia purpura and insulin-dependent diabetes), allergies,
XX atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
XX nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
XX rejection (all claimed).
XX
XX Sequence 238 AA;

Query Match 93.7%; Score 1159; DB 19; Length 238;
Best Local Similarity 92.0%; Pred. No. 6.8e-56;
Matches 219; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
QY 1 METDTILLWVLLWPGSTGDIVLTQSPSSLSASVGRVTITCKASQSDYDYGDSYNNWY 60
Db 1 metdtilllwvllwpgstgdivltqspgltlspgeratlsckasgsdydgdsgymwy 60
QY 61 QOKPGOAPKLLIYAASNLSESGVPSPFSGSGGTDFLTITSSLOPEDFATVYCOQSNEDPR 120
Db 61 qkpgqpaprlllyaaanlesgipdrfsqsgsgtdfltlthpveedaatyyccqgsnedpr 120
QY 121 TFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVYVCLNNFYPREAKVQWKVDNALQS 180
Db 121 tfgqgtrleikrtvaapsvfifppsdeqlksgtasvvcclnnfypreakvqwkvdnalqs 180
QY 181 GNSQESVTEODSKDSTYSLSSTLTLSKADYEHKHYACEVTHQGLSSPVTCKSFNRGEC 238
Db 181 gnsqesvteqgakdstyslssltltlskadyekhyacevthqglsspvtcksfnrgec 238
RESULT 11
AAB14773
ID AAB14773 standard; Protein; 238 AA.
XX
XX AC AAB14773;
XX
XX XX
XX DT 24-NOV-2000 (first entry)
XX
XX DE Humanised anti-Fas antibody light chain, SEQ ID NO:52.
XX
XX KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
XX murine; humanised antibody; complementarity determining region; CDR;
XX human Fas; Fas ligand; apoptosis modulator; programmed cell death;
XX autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
XX cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
XX hepatitis; AIDS; graft rejection; light chain.
XX
XX OS Chimeric - Mus musculus.
XX OS Chimeric - Homo sapiens.
XX
XX XX
XX PN JP2000169393-A.
XX
XX PD 20-JUN-2000.
XX
XX PF 30-SEP-1999; 99JP-0278301.
XX
XX PR 30-SEP-1998; 98JP-0276883.
XX
XX (SANY ) SANKYO CO LTD.
XX
XX WPI: 2000-485645/43.
XX N-PSDB; AAA72125.
XX
XX Preventive or treating agent for the diseases caused by an abnormality
XX in the Fas/Fas ligand system e.g. autoimmune diseases, contains
XX anti-Fas antibody -
XX
XX Claim 20; Page 80-81; 139pp; Japanese.
XX
XX The invention relates to compositions for the prevention or treatment
XX of diseases caused by an abnormality in the Fas/Fas ligand system
XX containing an anti-Fas antibody as the active component. The anti-Fas
XX antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
XX or a humanised version of HFE7A containing identical CDRs
XX (complementarity determining regions) to antibody HFE7A. Via its
XX interaction with Fas, the antibody of the invention acts as a modulator
XX of apoptosis. The compositions of the invention may therefore be used in
XX the treatment or prevention of conditions such as autoimmune diseases,
XX allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
XX glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
XX and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
XX represent the light chains of several humanised HFE7A-derived anti-Fas

CC antibodies.  
 XX Sequence 238 AA;  
 SQ

Query Match 93.78; Score 1159; DB 21; Length 238;  
 Best Local Similarity 92.0%; Pred. No. 6.8e-56;  
 Matches 219; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 METDTILLWLLWPGSTGDIVLTQSPSSLSASVGRVITTCASQSDVDGDSYNNWY 60  
 DB 1 metdtillwllwpgstgdivltqspgtlslpgeratlsckasqsvdydgsymnw 60

QY 61 QOKPGQAPKLLIYAASNLSEGVPRFSGSGTDTFTLTISLQPEDFATYYCQSQSNEPDR 120  
 DB 61 qkpgqaprllyaaasnlsegipdrfsgsgtdftltihpveeadaatyccqgsnedpr 120

QY 121 TFGOGTKVEIKRTVAASVFFPPSDQLKSGTASVVCLLNNFYPREAKVQKVDNALQS 180  
 DB 121 tfgogtgleikrtvaasvffppsdqlksgtasvvccllnfnfpreakvqkvdnalqs 180

QY 181 GNSQESVTEQDSKDYSLSTLTSLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
 DB 181 gnsqesvteqdsksdystlsstltslskadyekhkvyacevthqglsspvtksfngrec 238

RESULT 12  
 AAW90923  
 ID AAW90923 standard; Protein; 238 AA.  
 XX  
 AC AAW90923;  
 XX  
 DT 08-AUG-2000 (first entry)  
 XX  
 DE Humanised anti-Fas antibody HFE7A light chain HM type protein.  
 XX  
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;  
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;  
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
 XX  
 OS Synthetic.  
 XX  
 PN EP990663-A2.  
 XX  
 XX 05-APR-2000.  
 XX  
 XX 29-SEP-1999; 99EP-0307711.  
 XX  
 XX 30-SEP-1998; 98JP-0276881.  
 PR  
 PR 30-SEP-1998; 98JP-0276882.  
 XX  
 XX (SANY ) SANKYO CO LTD.  
 XX  
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 XX WPI; 2000-258930/23.  
 DR  
 DR N-PSDB; AAA11563.  
 DR  
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems  
 XX  
 XX Example reference 14; Page 117-118; 263pp; English.  
 PS  
 PS This invention describes a novel humanized anti-Fas antibody-like  
 XX

CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antirheumatic, nephrotropic, cardiant and hepatotropic activity. (I) induce  
 CC antiarteriosclerotic, cardiant and hepatotropic activity. (I) induce  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody HFE7A light chain HM type which is used in  
 CC the method described in the invention.  
 XX  
 SQ Sequence 238 AA;  
 XX

Query Match 93.78; Score 1159; DB 21; Length 238;  
 Best Local Similarity 92.0%; Pred. No. 6.8e-56;  
 Matches 219; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 METDTILLWLLWPGSTGDIVLTQSPSSLSASVGRVITTCASQSDVDGDSYNNWY 60  
 DB 1 metdtillwllwpgstgdivltqspgtlslpgeratlsckasqsvdydgsymnw 60

QY 61 QOKPGQAPKLLIYAASNLSEGVPRFSGSGTDTFTLTISLQPEDFATYYCQSQSNEPDR 120  
 DB 61 qkpgqaprllyaaasnlsegipdrfsgsgtdftltihpveeadaatyccqgsnedpr 120

QY 121 TFGOGTKVEIKRTVAASVFFPPSDQLKSGTASVVCLLNNFYPREAKVQKVDNALQS 180  
 DB 121 tfgogtgleikrtvaasvffppsdqlksgtasvvccllnfnfpreakvqkvdnalqs 180

QY 181 GNSQESVTEQDSKDYSLSTLTSLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
 DB 181 gnsqesvteqdsksdystlsstltslskadyekhkvyacevthqglsspvtksfngrec 238

RESULT 13  
 AAW83035  
 ID AAW83035 standard; Protein; 238 AA.  
 XX  
 AC AAW83035;  
 XX  
 DT 15-MAR-1999 (first entry)  
 XX  
 XX Anti-Fas humanised antibody HFE7A light chain PDHM type.  
 XX  
 KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;  
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;  
 KW systemic lupus erythematosus; graft versus host disease;  
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;  
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;  
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;  
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;  
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
 KW transplant rejection; therapy.  
 XX

OS Homo sapiens.  
OS Synthetic.  
XX Key Location/Qualifiers  
FH Peptide 1..20  
FT label= Sig\_peptide  
FT 21..238  
FT Protein  
FT label= Mat\_protein  
FT 21..131  
FT Region  
FT label= Variable  
FT 132..238  
FT Region  
FT label= Constant  
FT 44..58  
FT label= CDR\_L1  
FT /note= "claim 9"  
FT 74..80  
FT Region  
FT label= CDR\_L2  
FT /note= "claim 9"  
FT 113..121  
FT Region  
FT label= CDR\_L3  
FT /note= "claim 9"  
XX AU9859701-A.  
XX 08-OCT-1998.  
XX 30-MAR-1998; 98AU-0059701.  
XX 08-OCT-1997; 97JP-0276064.  
XX 01-APR-1997; 97JP-0082953.  
XX 25-JUN-1997; 97JP-0169088.  
XX (SANY ) SANKYO CO LTD.  
XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;  
XX Masahiko O, Nobufusa S, Shin Y, Tohru T;  
XX NPI; 1998-543440/47.  
XX N-PSDB; AAV70078.  
XX New antibodies and proteins bind conserved epitope of Fas antigen -  
XX used to evaluate drugs in animal models and to treat Fas-associated  
XX diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
XX myocarditis, hepatitis and AIDS  
XX Claim 21; Page 220-221; 292pp; English.  
XX This is the amino acid sequence of the PDHM type humanised light  
XX chain of murine anti-human Fas monoclonal antibody HFE7A.  
XX Humanisation of the murine sequence (see AAW83042) entailed making  
XX D1E, P47A, K49R and R107K amino acid substitutions; these  
XX residues are conserved in the human light (kappa) chain. Host  
XX cell Escherichia coli pSHW2 SANK 70198 harbors plasmid pSHW2  
XX carrying a fusion of the humanised PDHM type HFE7A light chain and  
XX DNA encoding the region of human immunoglobulin kappa chain, and is  
XX deposited as FERM BP-6272 (claimed). The invention provides  
XX methods for producing humanised antibodies by culturing host  
XX cells. Humanised versions of HFE7A (see AAW83031-37), like native  
XX HFE7A, are capable of inducing apoptosis in abnormal cells  
XX expressing Fas, and of inhibiting Fas-induced apoptosis in normal  
XX cells. The humanised antibodies are used to evaluate, in animal  
XX models, treatments of diseases that involve Fas/Fas ligand  
XX interactions, and also to treat such diseases, including autoimmune  
XX disease (e.g. systemic lupus erythematosus, Hashimoto's disease,  
XX Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
XX disease, rheumatoid arthritis, autoimmune haemolytic anaemia,  
XX sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,  
XX thrombopenia purpura and insulin-dependent diabetes), allergies,  
XX atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular  
XX nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant  
XX rejection (all claimed).

SQ Sequence 238 AA;  
Query Match 93.6%; Score 1158; DB 19; Length 238;  
Best Local Similarity 92.0%; Pred. No. 7.7e-56;  
Matches 219; Conservative 10; Mismatches 9; Indels 0; Gaps 0;  
QY 1 METDTILLWVLLIWPVGSTGDIVLTSQPSLSASVGDRTVITCKASQSDYDGDGSDYNNWY 60  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 metdtillwvlllwpvgstgeivltspgtlspsgeratlsckasqsdvdgdsymnw 60  
QY 61 QQKPGQAPKLLIYAASNLESGVPSRFGSGSGTDFLTITSSIQPEDFAIYYCQSQSNEDPR 120  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 qdkpgqaprllyaaenlesgipdrfsgsgsgtdftltihpveeedaatyccqgsnedpr 120  
QY 121 TFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFPPREAKVQWVDNALQS 180  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 121 tfgggtkleikrtvaapsvfifppsdeqlksgtasvvcilnnfybreakvqwkvdnalg 180  
QY 181 GNSQESVTEQDSKDSYSLSSSTLTLSKADYEHKVVACEVTHQGLSPVTKSFNRGEC 238  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 181 gnsqesvteqdsksystslstltlskadyekhkvyacevthqglssptvtskfnrgec 238  
RESULT 14  
AAB14778  
ID AAB14778 standard; Protein; 238 AA.  
XX AAB14778;  
XX AC AAB14778;  
XX DT 24-NOV-2000 (first entry)  
XX DE Humanised anti-Fas antibody light chain, SEQ ID NO:109.  
XX KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;  
KW murine; humanised antibody; complementarity determining region; CDR;  
KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;  
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;  
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;  
KW hepatitis; AIDS; graft rejection; light chain.  
XX OS Chimeric - Mus musculus.  
XX OS Chimeric - Homo sapiens.  
XX PN JP2000169393-A.  
XX PD 20-JUN-2000.  
XX PF 30-SEP-1999; 99JP-0278301.  
XX PR 30-SEP-1998; 98JP-0276883.  
XX PA (SANY ) SANKYO CO LTD.  
XX DR WPI; 2000-485645/43.  
XX DR N-PSDB; AAA72177.  
XX PT Preventive or treating agent for the diseases caused by an abnormality  
XX in the Fas/Fas ligand system e.g. autoimmune diseases, contains  
XX anti-Fas antibody -  
XX Claim 20; Page 103; 139pp; Japanese.  
XX The invention relates to compositions for the prevention or treatment  
XX of diseases caused by an abnormality in the Fas/Fas ligand system  
XX containing an anti-Fas antibody as the active component. The anti-Fas  
XX antibody is either the murine anti-human Fas monoclonal antibody HFE7A,  
XX or a humanised version of HFE7A containing identical CDRs  
XX (complementarity determining regions) to antibody HFE7A. Via its  
XX interaction with Fas, the antibody of the invention acts as a modulator  
XX of apoptosis. The compositions of the invention may therefore be used in  
XX the treatment or prevention of conditions such as autoimmune diseases,  
XX allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy.



CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS  
CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778  
CC represent the light chains of several humanised HFE7A-derived anti-Fas  
CC antibodies.  
XX  
SQ Sequence 238 AA;

Query Match 93.6%; Score 1158; DB 21; Length 238;  
Best Local Similarity 92.0%; Pred. No. 7.7e-56;  
Matches 219; Conservative 10; Mismatches 9; Indels 0; Gaps 0;  
QY 1 METDTILLVLLWLLVPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSTYMWY 60  
DB 1 metdtillvllwllwpgstgeivltqspgtslsppgeratlsckasqsdvdygdsgymwy 60  
QY 61 OOKPGQAPKLLIYAASNLESVPSRFGSGGTDFTLTISLQPEDFATYYCQSQSNEPR 120  
DB 61 qkpgqaprllyaaashlesgipdrfsgsgtdftlihpveedaatyccqgsnedpr 120  
QY 121 TFGQGTKEIKRTVAAPSVFIFFPPSDEQLKSGTASVCLLNFFYPREAKVQKVDNALQS 180  
DB 121 tfgggtkleikrtvaapsvfifppdsedqlksgtasvcllnnfybreakvqkvdnalqs 180  
QY 181 GNSQSVTEQDSKDSYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 238  
DB 181 gnsqsvteqdsksdtsylsstltlskadyekhkyacevthqglsppvtsksfnrgec 238

RESULT 15  
AAW90928  
ID AAW90928 standard; Protein; 238 AA.  
XX  
AC AAW90928;  
XX  
XX 08-AUG-2000 (first entry)  
XX  
DE Humanised HFE7A designed light chain protein #2.

KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;  
KW dermatologic; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
KW nephrotropic; antifertility; neuroprotective; antirheosclerotic;  
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

XX Synthetic.  
XX  
XX EP990663-A2.  
XX  
XX 05-APR-2000.  
XX  
XX 29-SEP-1999; 99EP-0307711.  
XX  
XX 30-SEP-1998; 98JP-0276881.  
XX  
XX 30-SEP-1998; 98JP-0276882.  
XX  
XX (SANY ) SANKYO CO LTD.  
XX

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
XX  
XX WPI; 2000-258930/23.  
XX  
XX N-PSDB; AAA11615.  
XX  
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
XX inflammatory or autoimmune disease, induces apoptosis selectively in  
XX cells with abnormal Fas-Fas ligand systems

PS  
XX  
CC This invention describes a novel humanized anti-Fas antibody-like  
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
CC ligand system, by binding to Fas on the cell surface, and prevents  
CC apoptosis in cells with a normal system, by inhibiting binding between  
CC Fas and its ligand. The products of the invention have anti-inflammatory,  
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
CC antiarthritis, nephrotropic, antifertility, neuroprotective,  
CC antiarteriosclerotic, cardiac and hepatropic activity. (I) induce  
CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
CC inhibition of ligand binding. (I) are used to treat and/or prevent  
CC diseases associated with the Fas/Fas ligand system, especially systemic  
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
CC cells. They bind to both human and murine Fas, so can be evaluated in  
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
CC the native ligand, do not induce liver disease, and have reduced risk of  
CC inducing a human anti-murine antibody response. This sequence represents  
CC a humanised anti-Fas antibody HFE7A designed light chain which is used in  
CC the method described in the invention.

XX Sequence 238 AA;  
SQ  
Query Match 93.6%; Score 1158; DB 21; Length 238;  
Best Local Similarity 92.0%; Pred. No. 7.7e-56;  
Matches 219; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 METDTILLVLLWLLVPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSTYMWY 60  
DB 1 metdtillvllwllwpgstgeivltqspgtslsppgeratlsckasqsdvdygdsgymwy 60  
QY 61 OOKPGQAPKLLIYAASNLESVPSRFGSGGTDFTLTISLQPEDFATYYCQSQSNEPR 120  
DB 61 qkpgqaprllyaaashlesgipdrfsgsgtdftlihpveedaatyccqgsnedpr 120  
QY 121 TFGQGTKEIKRTVAAPSVFIFFPPSDEQLKSGTASVCLLNFFYPREAKVQKVDNALQS 180  
DB 121 tfgggtkleikrtvaapsvfifppdsedqlksgtasvcllnnfybreakvqkvdnalqs 180  
QY 181 GNSQSVTEQDSKDSYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 238  
DB 181 gnsqsvteqdsksdtsylsstltlskadyekhkyacevthqglsppvtsksfnrgec 238

Search completed: August 14, 2002, 15:15:35  
Job time: 833 sec

5  
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.

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:17:03 ; Search time 82.88 Seconds  
(without alignments)  
70.141 Million cell updates/sec

Title: US-09-499-662-129

Perfect score: 1237

Sequence: 1 METDRILLWLLLVPGSTG.....EVT HQGLSPVTKSNRGC 238

Scoring table:

BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1108	89.6	218	5	PCT-US96-13152-2
2	1096	88.6	218	2	US-08-887-352B-13
3	1096	88.6	218	3	US-08-466-151-9
4	1096	88.6	218	4	US-09-109-207C-13
5	1096	88.6	218	4	US-09-296-005-13
6	1096	88.6	218	4	US-08-466-163B-9
7	1073	86.7	218	4	US-09-282-505-1
8	1073	86.7	218	4	US-09-084-255-1
9	1070	86.5	218	2	US-08-887-352B-15
10	1070	86.5	218	2	US-08-887-352B-17
11	1070	86.5	218	2	US-08-887-352B-19
12	1070	86.5	218	2	US-08-887-352B-24
13	1070	86.5	218	4	US-09-109-207C-15
14	1070	86.5	218	4	US-09-109-207C-17
15	1070	86.5	218	4	US-09-109-207C-19
16	1070	86.5	218	4	US-09-109-207C-24
17	1070	86.5	218	4	US-09-296-005-15
18	1070	86.5	218	4	US-09-296-005-17
19	1070	86.5	218	4	US-09-296-005-19
20	1070	86.5	218	4	US-09-296-005-24
21	1018.5	82.3	233	2	US-07-934-373C-25
22	1018.5	82.3	233	3	US-08-437-642B-25
23	1018.5	82.3	233	5	PCT-US93-07832-25
24	1015	82.1	214	2	US-07-934-373C-39
25	1015	82.1	214	3	US-08-437-642B-39
26	1015	82.1	214	5	PCT-US93-07832-39
27	1010	81.6	214	2	US-07-934-373C-40

Sequence 11, Appl  
Sequence 40, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 40, Appl  
Sequence 6, Appl  
Sequence 10, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 62, Appl  
Sequence 62, Appl  
Sequence 97, Appl  
Sequence 51, Appl  
Sequence 51, Appl  
Sequence 51, Appl  
Sequence 72, Appl  
Sequence 72, Appl  
Sequence 56, Appl

28 1010 81.6 214 2 US-08-788-800-11  
29 1010 81.6 214 3 US-08-437-642B-40  
30 1010 81.6 214 3 US-09-097-309-2  
31 1010 81.6 214 4 US-09-097-171A-2  
32 1010 81.6 214 5 PCT-US93-07832-40  
33 1010 81.6 237 3 US-09-097-309-6  
34 1010 81.6 237 4 US-09-097-171A-10  
35 1010 81.6 237 4 US-09-422-712B-2  
36 1010 81.6 237 4 US-09-607-756-2  
37 1006.5 81.4 242 3 US-09-027-449-62  
38 1006.5 81.4 242 4 US-09-026-985-62  
39 1005.5 81.3 235 4 US-09-171-945-97  
40 1005.5 81.3 242 3 US-09-027-449-51  
41 1005.5 81.3 242 3 US-08-804-444A-51  
42 1005.5 81.3 242 4 US-09-026-985-51  
43 1002.5 81.0 219 3 US-09-027-449-72  
44 1002.5 81.0 219 4 US-09-026-985-72  
45 1002.5 81.0 242 3 US-09-027-449-56

#### ALIGNMENTS

RESULT 1

PCT-US96-13152-2

; Sequence 2, Application PC/TUS9613152

; GENERAL INFORMATION:

; APPLICANT: Martin, Ulrich, et al.

; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ f

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felfe & Lynch

; ADDRESSEE: Attn: Norman D. Hanson

; STREET: 805 Third Avenue

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Computer Disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/13152

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/578,953

; FILING DATE: 27-Dec-95

; APPLICATION NUMBER: EP 95 112 895.8

; FILING DATE: 17-Aug-95

; APPLICATION NUMBER: EP 95 114 969.9

; FILING DATE: 19-Sep-95

; ATTORNEY/AGENT INFORMATION:

; NAME: Norman D. Hanson

; REGISTRATION NUMBER: 30,946

; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 688-9200

; TELEFAX: (212) 838-3884

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 218

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; PCT-US96-13152-2

Query Match 89.6%; Score 1108; DB 5; Length 218;  
Best Local Similarity 97.7%; Pred. NO. 1.6e-87;



QY 141 IFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYLS 200  
|||  
Db 121 IFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYLS 180  
|||  
QY 201 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
|||  
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218  
|||

RESULT 4

US-09-109-207C-13  
; Sequence 13, Application US/09109207C  
; Patent No. 6172213  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiueu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide  
; FILE REFERENCE: P1123R1  
; CURRENT APPLICATION NUMBER: US/09/109,207C  
; CURRENT FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/051,554  
; PRIOR FILING DATE: 1997-07-03  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 13  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; NAME/KEY: Artificial  
; LOCATION: 1-218  
; OTHER INFORMATION: Light chain sequence derived from MAE11  
US-09-109-207C-13

Query Match 88.6%; Score 1096; DB 4; Length 218;  
Best Local Similarity 97.2%; Pred. No. 1.7e-86;  
Matches 212; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGQAPKLLIYAASNLES 80  
|||  
Db 1 DIQLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGKAPKLLIYAASYLE 60  
|||  
QY 81 GVPFRFSGSGGTDFLTITSSLPQEDFATYYCQSNEDPRTFGQGTKEIKRTVAAPSVF 140  
|||  
Db 61 GVPFRFSGSGGTDFLTITSSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120  
|||  
QY 141 IFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYLS 200  
|||  
Db 121 IFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYLS 180  
|||  
QY 201 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
|||  
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218  
|||

RESULT 5

US-09-296-005-13  
; Sequence 13, Application US/09296005  
; Patent No. 6290957  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiueu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides  
; FILE REFERENCE: P1123C1R  
; CURRENT APPLICATION NUMBER: US/09/296,005  
; CURRENT FILING DATE: 1999-04-21  
; EARLIER APPLICATION NUMBER: US 08/887,352  
; EARLIER FILING DATE: 1997-07-02  
; NUMBER OF SEQ ID NOS: 26  
; SEQ ID NO 13  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; NAME/KEY: Artificial

; LOCATION: 1-218  
; OTHER INFORMATION: Light chain sequence derived from MAE11  
US-09-296-005-13

Query Match 88.6%; Score 1096; DB 4; Length 218;  
Best Local Similarity 97.2%; Pred. No. 1.7e-86;  
Matches 212; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGQAPKLLIYAASNLES 80  
|||  
Db 1 DIQLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGKAPKLLIYAASYLE 60  
|||  
QY 81 GVPFRFSGSGGTDFLTITSSLPQEDFATYYCQSNEDPRTFGQGTKEIKRTVAAPSVF 140  
|||  
Db 61 GVPFRFSGSGGTDFLTITSSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120  
|||  
QY 141 IFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYLS 200  
|||  
Db 121 IFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYLS 180  
|||  
QY 201 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
|||  
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218  
|||

RESULT 6

US-08-466-163B-9  
; Sequence 9, Application US/08466163B  
; Patent No. 6329509  
; GENERAL INFORMATION:  
; APPLICANT: Jardiueu, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Immunoglobulin Variants  
; FILE REFERENCE: P0718P2C1d1  
; CURRENT APPLICATION NUMBER: US/08/466,163B  
; CURRENT FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: US 08/405,617  
; PRIOR FILING DATE: 1995-03-15  
; PRIOR APPLICATION NUMBER: US 08/185,899  
; PRIOR FILING DATE: 1994-01-26  
; PRIOR APPLICATION NUMBER: US 07/879,495  
; PRIOR FILING DATE: 1992-05-07  
; PRIOR APPLICATION NUMBER: US 07/744,768  
; PRIOR FILING DATE: 1991-08-14  
; NUMBER OF SEQ ID NOS: 64  
; SEQ ID NO 9  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: humanized mae11, version 1, light chain  
US-08-466-163B-9

Query Match 88.6%; Score 1096; DB 4; Length 218;  
Best Local Similarity 97.2%; Pred. No. 1.7e-86;  
Matches 212; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGQAPKLLIYAASNLES 80  
|||  
Db 1 DIQLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGKAPKLLIYAASYLE 60  
|||  
QY 81 GVPFRFSGSGGTDFLTITSSLPQEDFATYYCQSNEDPRTFGQGTKEIKRTVAAPSVF 140  
|||  
Db 61 GVPFRFSGSGGTDFLTITSSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120  
|||  
QY 141 IFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYLS 200  
|||  
Db 121 IFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYLS 180  
|||  
QY 201 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
|||

Db 181 STLTLSKADYEHKVKYACEVTHOGLSPVTKSFNRGEC 218

RESULT 7  
US-09-282-505-1  
; Sequence 1, Application US/09282505A  
; Patent No. 6194551  
; GENERAL INFORMATION:  
; APPLICANT: Esche Ekinaduese Idusogie et al.  
; TITLE OF INVENTION: Polypeptide Variants  
; FILE REFERENCE: P1266R1  
; CURRENT APPLICATION NUMBER: US/09/282,505A  
; CURRENT FILING DATE: 1999-03-31  
; NUMBER OF SEQ ID NOS: 2  
; SEQ ID NO 1  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: Artificial Sequence  
; LOCATION: 1-218  
; OTHER INFORMATION: Sequence is completely synthesized  
; Patent No. 6194551  
US-09-282-505-1

Query Match 86.7%; Score 1073; DB 4; Length 218;  
Best Local Similarity 95.4%; Pred. No. 1.6e-84;  
Matches 208; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGRVITITCRASKPVDPGEGSYNNWYQKPGKAPKLLIIYAASVLES 80  
|||  
Db 1 DIQLTQSPSSLSASVGRVITITCRASKPVDPGEGSYNNWYQKPGKAPKLLIIYAASVLES 60  
QY 81 GVPFRFSGSGGDTFTLTISLQPEDFATYYCQSNEDPRTFGOGTKVEIKRTVAAPSVF 140  
|||  
Db 61 GVPFRFSGSGGDTFTLTISLQPEDFATYYCQSHEDPTFGOGTKVEIKRTVAAPSVF 120  
QY 141 IFPPSDQLKSGTASVYVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYSLS 200  
|||  
Db 121 IFPPSDQLKSGTASVYVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYSLS 180  
QY 201 STLTLSKADYEHKVKYACEVTHOGLSPVTKSFNRGEC 238  
|||  
Db 181 STLTLSKADYEHKVKYACEVTHOGLSPVTKSFNRGEC 218

RESULT 8  
US-09-054-255-1  
; Sequence 1, Application US/09054255  
; Patent No. 6242195  
; GENERAL INFORMATION:  
; APPLICANT: Esche Ekinaduese Idusogie et al.  
; TITLE OF INVENTION: Polypeptide Variants  
; FILE REFERENCE: P1266  
; CURRENT APPLICATION NUMBER: US/09/054,255  
; CURRENT FILING DATE: 1998-04-02  
; NUMBER OF SEQ ID NOS: 2  
; SEQ ID NO 1  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: E27 anti-IgE antibody light chain  
US-09-054-255-1

Query Match 86.7%; Score 1073; DB 4; Length 218;  
Best Local Similarity 95.4%; Pred. No. 1.6e-84;  
Matches 208; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGRVITITCRASKPVDPGEGSYNNWYQKPGKAPKLLIIYAASVLES 80  
|||

Db 1 DIQLTQSPSSLSASVGRVITITCRASKPVDPGEGSYNNWYQKPGKAPKLLIIYAASVLES 60  
QY 81 GVPFRFSGSGGDTFTLTISLQPEDFATYYCQSNEDPRTFGOGTKVEIKRTVAAPSVF 140  
|||  
Db 61 GVPFRFSGSGGDTFTLTISLQPEDFATYYCQSHEDPTFGOGTKVEIKRTVAAPSVF 120  
QY 141 IFPPSDQLKSGTASVYVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYSLS 200  
|||  
Db 121 IFPPSDQLKSGTASVYVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYSLS 180  
QY 201 STLTLSKADYEHKVKYACEVTHOGLSPVTKSFNRGEC 238  
|||  
Db 181 STLTLSKADYEHKVKYACEVTHOGLSPVTKSFNRGEC 218

RESULT 9  
US-08-887-352B-15  
; Sequence 15, Application US/08887352B  
; Patent No. 5994511  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
; TITLE OF INVENTION: Improving Polypeptides  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,352B  
; FILING DATE: 03-Jul-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P1123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 218 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-887-352B-15

Query Match 86.5%; Score 1070; DB 2; Length 218;  
Best Local Similarity 95.0%; Pred. No. 2.9e-84;  
Matches 207; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGRVITITCRASKPVDPGEGSYNNWYQKPGKAPKLLIIYAASVLES 80  
|||  
Db 1 DIQLTQSPSSLSASVGRVITITCRASKPVDPGEGSYNNWYQKPGKAPKLLIIYAASVLES 60  
QY 81 GVPFRFSGSGGDTFTLTISLQPEDFATYYCQSNEDPRTFGOGTKVEIKRTVAAPSVF 140  
|||  
Db 61 GVPFRFSGSGGDTFTLTISLQPEDFATYYCQSHEDPTFGOGTKVEIKRTVAAPSVF 120  
QY 141 IFPPSDQLKSGTASVYVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYSLS 200  
|||  
Db 121 IFPPSDQLKSGTASVYVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYSLS 180  
QY 201 STLTLSKADYEHKVKYACEVTHOGLSPVTKSFNRGEC 238  
|||

Db 181 STLTSLKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 218

## RESULT 10

US-08-887-352B-17  
; Sequence 17, Application US/08887352B

; Patent No. 5994511

; GENERAL INFORMATION:

; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe

; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of

; TITLE OF INVENTION: Improving Polypeptides

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/887,352B

; FILING DATE: 03-Jul-1997

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Svoboda, Craig G.

; REGISTRATION NUMBER: 39,044

; REFERENCE/DOCKET NUMBER: P1123

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-1489

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 17:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 218 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-887-352B-17

Query Match 86.5%; Score 1070; DB 2; Length 218;

Best Local Similarity 95.0%; Pred. No. 2.9e-84;

Matches 207; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGRVTITCKASQSDYDGDGYNNWYQKPGQAPKLLIYAASNLES 80

Db 1 DIQLTQSPSSLSASVGRVTITCKASQSDYDGDGYNNWYQKPGQAPKLLIYAASNLES 60

QY 81 GVPFRFSGSGSGTDFTLTISSLQPEDFATYVCOQSNEDPRFTFGGKVEIKRTVAAPSVF 140

Db 61 GVPFRFSGSGSGTDFTLTISSLQPEDFATYVCOQSNEDPRFTFGGKVEIKRTVAAPSVF 120

QY 141 IFPPSDQLKSGTASVVCVLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYLS 200

Db 121 IFPPSDQLKSGTASVVCVLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYLS 180

QY 201 STLTSLKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238

Db 181 STLTSLKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 218

## RESULT 11

US-08-887-352B-19

; Sequence 19, Application US/08887352B

; Patent No. 5994511

; GENERAL INFORMATION:

; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe

; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of

; TITLE OF INVENTION: Improving Polypeptides

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/887,352B

; FILING DATE: 03-Jul-1997

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Svoboda, Craig G.

; REGISTRATION NUMBER: 39,044

; REFERENCE/DOCKET NUMBER: P1123

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-1489

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 218 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-887-352B-19

Query Match 86.5%; Score 1070; DB 2; Length 218;

Best Local Similarity 95.0%; Pred. No. 2.9e-84;

Matches 207; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGRVTITCKASQSDYDGDGYNNWYQKPGQAPKLLIYAASNLES 80

Db 1 DIQLTQSPSSLSASVGRVTITCKASQSDYDGDGYNNWYQKPGQAPKLLIYAASNLES 60

QY 81 GVPFRFSGSGSGTDFTLTISSLQPEDFATYVCOQSNEDPRFTFGGKVEIKRTVAAPSVF 140

Db 61 GVPFRFSGSGSGTDFTLTISSLQPEDFATYVCOQSNEDPRFTFGGKVEIKRTVAAPSVF 120

QY 141 IFPPSDQLKSGTASVVCVLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYLS 200

Db 121 IFPPSDQLKSGTASVVCVLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYLS 180

QY 201 STLTSLKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238

Db 181 STLTSLKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 218

## RESULT 12

US-08-887-352B-24

; Sequence 24, Application US/08887352B

; Patent No. 5994511

; GENERAL INFORMATION:

; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe

; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of

; TITLE OF INVENTION: Improving Polypeptides

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887.352B  
; FILING DATE: 03-Jul-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P1123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 218 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-887-352B-24

Query Match 86.5%; Score 1070; DB 2; Length 218;  
Best Local Similarity 95.0%; Pred. No. 2.9e-84;  
Matches 207; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTITCRASKPVVDGDSYMNWYQKPGQAPKLLIYAASNVLES 80  
|||  
Db 1 DIQLTQSPSSLSASVGDRTITCRASKPVVDGDSYLNWYQKPGKAPKLLIYAASYLE 60  
|||  
QY 81 GVPSRFSGSGGTDTLTITSSLPEDFAFYTCQSDNEDPRTFGQGTKEIKRTVAAPSVF 140  
|||  
Db 61 GVPSRFSGSGGTDTLTITSSLPEDFAFYTCQSDNEDPRTFGQGTKEIKRTVAAPSVF 120  
|||  
QY 141 IFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 200  
|||  
Db 121 IFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180  
|||

QY 201 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
|||  
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218  
|||

RESULT 13  
US-09-109-207C-15  
; Sequence 15, Application US/09109207C  
; Patent No. 6172213  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide  
; FILE REFERENCE: P1123R1  
; CURRENT APPLICATION NUMBER: US/09/109,207C  
; CURRENT FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/051,554  
; PRIOR FILING DATE: 1997-07-03  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 15  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Artificial  
; NAME/KEY: Artificial  
; LOCATION: 1-218  
; OTHER INFORMATION: Light chain sequence derived from MAE11  
US-09-109-207C-15

Query Match 86.5%; Score 1070; DB 4; Length 218;  
Best Local Similarity 95.0%; Pred. No. 2.9e-84;  
Matches 207; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTITCRASKPVVDGDSYMNWYQKPGQAPKLLIYAASNVLES 80  
|||  
Db 1 DIQLTQSPSSLSASVGDRTITCRASKPVVDGDSYLNWYQKPGKAPKLLIYAASYLE 60  
|||  
QY 81 GVPSRFSGSGGTDTLTITSSLPEDFAFYTCQSDNEDPRTFGQGTKEIKRTVAAPSVF 140  
|||

Db 61 GVPSRFSGSGGTDTLTITSSLPEDFAFYTCQSDNEDPRTFGQGTKEIKRTVAAPSVF 120  
|||  
QY 141 IFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 200  
|||  
Db 121 IFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180  
|||  
QY 201 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
|||  
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218  
|||

RESULT 14  
US-09-109-207C-17  
; Sequence 17, Application US/09109207C  
; Patent No. 6172213  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide  
; FILE REFERENCE: P1123R1  
; CURRENT APPLICATION NUMBER: US/09/109,207C  
; CURRENT FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/051,554  
; PRIOR FILING DATE: 1997-07-03  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 17  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Artificial  
; NAME/KEY: Artificial  
; LOCATION: 1-218  
; OTHER INFORMATION: Light chain sequence derived from MAE11  
US-09-109-207C-17

Query Match 86.5%; Score 1070; DB 4; Length 218;  
Best Local Similarity 95.0%; Pred. No. 2.9e-84;  
Matches 207; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTITCRASKPVVDGDSYMNWYQKPGQAPKLLIYAASNVLES 80  
|||  
Db 1 DIQLTQSPSSLSASVGDRTITCRASKPVVDGDSYLNWYQKPGKAPKLLIYAASYLE 60  
|||  
QY 81 GVPSRFSGSGGTDTLTITSSLPEDFAFYTCQSDNEDPRTFGQGTKEIKRTVAAPSVF 140  
|||  
Db 61 GVPSRFSGSGGTDTLTITSSLPEDFAFYTCQSDNEDPRTFGQGTKEIKRTVAAPSVF 120  
|||  
QY 141 IFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 200  
|||  
Db 121 IFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180  
|||  
QY 201 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
|||  
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218  
|||

RESULT 15  
US-09-109-207C-19  
; Sequence 19, Application US/09109207C  
; Patent No. 6172213  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide  
; FILE REFERENCE: P1123R1  
; CURRENT APPLICATION NUMBER: US/09/109,207C  
; CURRENT FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/051,554  
; PRIOR FILING DATE: 1997-07-03  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 19  
; LENGTH: 218  
; TYPE: PRT



```

; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain F(ab) sequence derived from MAE11
US-09-109-207C-19

Query Match      86.5%; Score 1070; DB 4; Length 218;
Best Local Similarity 95.0%; Pred. No. 2.9e-84;
Matches 207; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy  21 DIVLTQSPSSLSASVGDRTTITCKASQSDYDGDSYMNYQOKPGQAPKLLIYAASNLES 80
Db  1 DIQLTQSPSSLSASVGDRTTITCRASKPVDGSDSYLNWYQOKPGKAPKLLIYAASYLES 60

Qy  81 GVPFRFSGSGGTDFTLTISSLQPEDFATYYCQSQSNEDPRTFGGQTKVEIKRTVAAPSVF 140
Db  61 GVPFRFSGSGGTDFTLTISSLQPEDFATYYCQSQSHEDPYTFGGQTKVEIKRTVAAPSVF 120

Qy  141 IFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 200
Db  121 IFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180

Qy  201 STLTLKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 238
Db  181 STLTLKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218
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Search completed: August 14, 2002, 15:17:03  
Job time: 686 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 15:18:58 ; Search time 108.64 Seconds  
(without alignments)  
210.505 Million cell updates/sec

Title: US-09-499-662-129  
Perfect score: 1237  
Sequence: 1 METDTILLWILLWVPGSTG.....EVTHQGLSSPVTKSFNRGEC 238

Scoring table:  
BLOSUM62dx  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues  
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	949.5	76.8	215	2 JE0242	Ig kappa chain NIG
2	930.5	75.2	215	2 JE0244	Ig kappa chain NIG
3	907.5	73.4	215	2 JE0243	Ig kappa chain NIG
4	889.5	71.9	215	2 A32746	Ig kappa chain V-I
5	881	71.2	216	2 JE0241	Ig kappa chain Am3
6	813	65.7	240	2 S06084	Ig kappa chain pre
7	753	60.9	218	2 S68241	Ig kappa chain v r
8	752.5	60.8	230	2 S33161	Ig kappa chain v r
9	752	60.8	234	2 S14237	Ig kappa chain - s
10	751	60.7	218	2 JC5810	Ig kappa chain pre
11	730	59.0	220	2 A31790	monoclonal antibod
12	725	58.6	234	2 S01320	Ig kappa chain v r
13	722	58.4	210	2 A56169	Ig kappa chain pre
14	720.5	58.2	225	2 S37484	Ig kappa chain v r
15	713.5	57.7	219	2 PC4203	Ig kappa chain - m
16	707.5	57.2	219	2 S52028	Ig kappa chain (mo
17	706.5	57.1	219	2 S38865	Ig kappa chain - m
18	706.5	57.1	235	2 S25058	Ig kappa chain - m
19	701	56.7	214	2 S68212	Ig kappa chain (Ma
20	697.5	56.4	217	2 S42772	Ig kappa chain - m
21	691.5	55.9	219	2 S16112	Ig kappa chain v r
22	680.5	55.0	225	2 JC0029	Ig kappa chain pre
23	617.5	49.9	229	2 A20969	Ig kappa chain pre
24	612	49.5	178	2 PF0219	Ig kappa chain pre
25	608.5	49.2	135	2 S52059	Ig kappa chain V-C
26	586.5	47.4	197	2 S29593	JC-kappa protein -
27	583	47.1	131	2 PH1226	Ig kappa chain (WM
28	572.5	46.3	238	2 A49633	Ig kappa chain pre
29	551	44.5	144	2 PU0106	Ig kappa chain pre

30	548	44.3	106	1 K3HU	Ig kappa chain C r
31	536	43.3	131	1 KNSM6	Ig kappa chain pre
32	521	42.1	132	1 KNS32	Ig kappa chain pre
33	520	42.0	233	2 S29577	Ig light chain - r
34	518	41.9	123	2 S40331	Ig kappa chain - h
35	517	41.8	127	2 S40367	Ig kappa chain v-j
36	514	41.6	141	2 A49134	Ig kappa chain v-i
37	513	41.5	99	2 A37927	Ig kappa chain C r
38	509.5	41.2	145	2 S20631	Ig kappa chain - h
39	508	41.1	140	2 PN0446	Ig kappa chain pre
40	507	41.0	99	2 S26653	Ig kappa chain C r
41	507	41.0	139	2 S40365	Ig kappa chain - h
42	503	40.7	131	2 S55027	Ig light chain pre
43	500	40.4	122	2 S40370	Ig kappa chain - h
44	499	40.3	132	2 S40334	Ig kappa chain - h
45	497	40.2	130	2 S40368	Ig kappa chain - h

ALIGNMENTS

RESULT 1  
JE0242  
Ig kappa chain NIG26 precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0242  
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoca  
submitted to JPIID, November 1998  
A:Description: Structure relationship of kappatype light chains with AL amyloidosis:  
A:Reference number: JE0241  
A:Accession: JE0242  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F16-91/Domain: immunoglobulin homology <IMM>

Query Match 76.8%; Score 949.5; DB 2; Length 215;  
Best Local Similarity 83.9%; Pred. No. 4.2e-55;  
Matches 183; Conservative 14; Mismatches 18; Indels 3; Gaps 1;  
QY 21 DIVLTQSPSSLSASVGDRVTITCKASQSYVDYDGDSTWNNYQKPGQAPKLLIYAASNLDS 80  
Db 1 EIVLTQSPGTLSPGERATLSCRAQSY---SNNLAWYQKPGQAPSLIIYDASSRAT 57  
QY 81 GYPSRFSGSGCTDFTLTISLQPEDFATYVCOQSNEDPRTFGQGTVEIKRTVAAPSVF 140  
Db 58 GIPDRFSGSGSTDFLTISGLEPEDFATYVCOQYDRPPFTFGQGTVEIKRTVAAPSVF 117  
QY 141 IFPPSDEQLKSGTASVYCLLNNFYPREAKVQMKVDNALQSGNSQESVTEQDSKDSSTYSLS 200  
Db 118 IFPPSDEQLKSGTASVYCLLNNFYPREAKVQMKVDNALQSGNSQESVTEQDSKDSSTYSLS 177  
QY 201 STLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 238  
Db 178 STLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 215

RESULT 2  
JE0244  
Ig kappa chain NIG2 precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0244  
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H  
submitted to JPIID, November 1998  
A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL  
A:Reference number: JE0243  
A:Accession: JE0244  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology



R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.  
Nucleic Acids Res. 17, 7992, 1989  
A:Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA  
A:Reference number: S06084; MUID:90016888  
A:Accession: S06084  
A:Molecule type: mRNA  
A:Residues: 1-240 <CRO>  
A:Cross-references: EMBL:X16129; NID:g56457; PIDN:CAA34256.1; PID:g56458  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-240/Product: Ig kappa chain #status predicted <MAT>  
F:153-222/Domain: immunoglobulin homology <IMM>

Query Match 65.7%; Score 813; DB 2; Length 240;  
Best Local Similarity 65.0%; Pred. No. 3.6e-46;  
Matches 156; Conservative 30; Mismatches 52; Indels 2; Gaps 1;

Qy 1 METDTILLVLLWVPGSTGDIIVLTQSPSSLSASVGDRTVITCKASQSVVDYDGD--SYMN 58  
Db 1 MESQTQVLLMSLLWISGTCGDFVMTQSPSSLSAVSAGETVITNCKSSQSLFYSGNKNYLA 60

Qy 59 WYQKPGQAPKLLIYAASNLSEGVPSRFSGSGSGTDFLTITSSLOPEDFATYYCQSNED 118  
Db 61 WYQKPGQAPKLLIYAASNLSEGVPSRFSGSGSGTDFLTITSSLOPEDFATYYCQSNED 120

Qy 119 PRTEGGQKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 178  
Db 121 PYTFGAGTKLEKRAADAAPTSVISFPPSTEQLATGASVVCMLNMFYPRDISVKKWIDGTE 180

Qy 179 QSGNSQESVTPDQSDKSTSYLSSTLTLSKADYEHKHYACEVTHOGLSSPVTKSPNRGEC 238  
Db 181 RDGVLDSVTPDQSDKSTSYLSSTLTLSKADYEHSHLYTCEVHKHTSSSPVVKSPNRNEC 240

RESULT 7  
S68241  
Ig kappa chain V region (Mab13-1) - mouse (fragment)  
N:Alternate names: immunoglobulin light chain  
C:Species: Mus musculus (house mouse)  
C:Date: 24-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 20-Jun-2000  
A:Accession: S68214  
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.  
submitted to the EMBL Data Library, March 1994  
A:Description: Specific peroxidase activity by formation of an antibody L-chain-porphyrin  
A:Reference number: S68241  
A:Accession: S68241  
A:Molecule type: mRNA  
A:Residues: 1-218 <TAK>  
A:Cross-references: EMBL:D29670; NID:g473962; PIDN:BAA06141.1; PID:g473963  
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.  
FEBS Lett. 375, 273-276, 1995  
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin  
A:Reference number: S68211; MUID:96085223  
A:Accession: S68214  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 'NI', 3-212 <TAW>  
A:Cross-references: EMBL:D29670  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin

Query Match 60.9%; Score 753; DB 2; Length 218;  
Best Local Similarity 64.7%; Pred. No. 2.6e-42;  
Matches 141; Conservative 30; Mismatches 47; Indels 0; Gaps 0;

Qy 21 DIVLTQSPSSLSASVGDRTVITCKASQSVVDYDGSYMNWYQKPGQAPKLLIYAASNL 80  
Db 1 ELVLTQSPASLAVSLGQRATISCRASKSVASGVYIMHWYQKPGQPKLLISLATNLES 60

Qy 81 GVPFRFSGSGSGTDFLTITSSLOPEDFATYYCQSNEDPRFTGGTKVEIKRTVAAPSVF 140

Db 61 GVPARFSGSGSGTDFLTINHPVEEDVATYYCOHSRELPLTFGAGTKLEKRAADAAPTVS 120  
Qy 141 IFPPDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 200  
Db 121 IFPPSSEQLTSGGASVVCFLNNFYPKDNVKKWIDGSRQNGVLSWTDQDSKDSYSL 180  
Qy 201 STLTLSKADYEHKHYACEVTHOGLSSPVTKSPNRGEC 238  
Db 181 STLTLSKADYEHKHYACEVTHOGLSSPVTKSPNRGEC 218  
RESULT 8  
S33161  
Ig kappa chain - sheep  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Jun-2000  
A:Accession: S33161  
R:Foley, R.C.; Beh, K.J.  
submitted to the EMBL Data Library, July 1990  
A:Description: Isolation and characterization of sheep kappa light chain cDNA.  
A:Reference number: S33161  
A:Accession: S33161  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-230 <FOL>  
A:Cross-references: EMBL:X54110; NID:g297103; PIDN:CAA38046.1; PID:g1364221  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:143-212/Domain: immunoglobulin homology <IMM>

Query Match 60.8%; Score 752.5; DB 2; Length 230;  
Best Local Similarity 62.7%; Pred. No. 3e-42;  
Matches 146; Conservative 35; Mismatches 47; Indels 5; Gaps 2;

Qy 7 LLWVLLM-VPGSTGDIIVLTQSPSSLSASVGDRTVITCKASQSVVDYDGSYMNWYQKPG 65  
Db 2 LLGLLLM-LPGARDIQVTSPLSLASLTERVITCTQSQV---SNYLNWYQKPG 57

Qy 66 QAPKLLIYAASNLSEGVPSRFSGSGSGTDFLTITSSLOPEDFATYYCQSNEDPRFTGG 125  
Db 58 QAPKLLIYAATFLTDVPSRFSGSGSGTDFLTITSSLEANDTATYYCLOESTPLAFGG 117

Qy 126 TKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNS 185  
Db 118 TNVEIKRSDAQSVPFLKPESEQLRTGVSVCLVNDVFPKDNVKKVGVGTQNSFQN 177

Qy 186 SVTEQDSKDSYSLSTLTLSKADYEHKHYACEVTHOGLSSPVTKSPNRGEC 238  
Db 178 SFTDQDSKSTSYLSSTLTLSSEYQSHNAYACEVSHKSLPTALVKSPFNKNEC 230

RESULT 9  
S14237  
Ig kappa chain precursor (15C5) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jan-2000  
A:Accession: S14237  
R:Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.  
Eur. J. Biochem. 192, 767-775, 1990  
A:Title: Construction and characterization of a recombinant murine monoclonal antibody  
A:Reference number: S14236; MUID:91006173  
A:Accession: S14237  
A:Molecule type: mRNA  
A:Residues: 1-234 <VAN>  
A:Cross-references: EMBL:X56394; NID:g51622; PIDN:CAA39805.1; PID:g51623  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 60.8%; Score 752; DB 2; Length 234;

Best Local Similarity 60.1%; Pred. No. 3.3e-42;  
Matches 143; Conservative 35; Mismatches 56; Indels 4; Gaps 1;

QY 1 METDTILLVLLWVPGSTGDIVLTSQSPSLASVGDRTVITCKASQSDVDYDGDGYNNWY 60  
Db 1 MRPAPFLGILLWVFGIKDKMTQSPSWYASLGERVTVITCKASQDI----NSLSWI 56  
QY 61 QKPGQAPKLLIYAASNLGSGVSRFSGSGGTDFTLTSSLOPEDFATYVCOQSNEDPR 120  
Db 57 QKPGKSPKTLIYRNLVAGVSRFSGSGGDSITSSLEVEDGVYCYLRYDEFFP 116  
QY 121 TFGQGTKEIKRTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180  
Db 117 TFGSGTKLEIKRAADAAPTIVSIFPPSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSE 176  
QY 181 GNSQSVTEQDQSKDSTYLSSTLTSLKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 238  
Db 177 NGVLNSWTDQDQSKDSTYLSSTLTSLKDEYERHNSYTCETHATKSTSPIVKSFNRNEC 234

RESULT 10  
JC5810  
monoclonal antibody 13-1 light chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 04-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jan-2000  
C:Accession: JC5810  
R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.  
Biochem. Biophys. Res. Commun. 240, 566-572, 1997  
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin  
A:Reference number: JC5810; MUID:98063277  
A:Accession: JC5810  
A:Molecule type: protein  
A:Residues: 1-218 <AKA>  
C:Comment: This catalytic antibody has peroxidase oxidase. It is directed against a porphyrin  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-34/Domain: immunoglobulin homology <IMM>

Query Match 60.7%; Score 751; DB 2; Length 218;  
Best Local Similarity 65.1%; Pred. No. 3.5e-42;  
Matches 142; Conservative 28; Mismatches 48; Indels 0; Gaps 0;

QY 21 DIVLTQSPSLASVGDRTVITCKASQSDVDYDGDGYNNWYQKPGQAPKLLIYAASNLQS 80  
Db 1 NIVLTQSPASLAVSLQGRATISCRASKSVASGYIYMHVYQKPGQAPKLLISLANLES 60  
QY 81 GVPRESGSGSGTDFTLTSSLOPEDFATYVCOQSNEDPRTFQGTKEIKRTVAAPSVF 140  
Db 61 GVPARESGSGGTDFTLTSLNHPVEEDVATYVCOHSRELPLTFGAGTKLELKRADAAPTYS 120  
QY 141 IFPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQSVTEQDQSKDSTYLS 200  
Db 121 IFPPSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSEKQNGVLNSWTDQDQSKDSTYMS 180  
QY 201 STLTSLKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 238  
Db 181 STLTSLKDEYERHNSYTCETHATKSTSPIVKSFNRNEC 218

RESULT 11  
A31790  
Ig kappa chain V region (17/9) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 21-Jan-2000  
R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.  
J. Biol. Chem. 263, 17100-17105, 1988  
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an antibody  
A:Reference number: A92686; MUID:89034213  
A:Accession: A31790  
A:Molecule type: mRNA  
A:Residues: 1-220 <SCH>  
A:Cross-references: GB:M23626; GB:J04061; NID:g533234; PIDN:AAA39162.1; PID:g533235

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 59.0%; Score 730; DB 2; Length 220;  
Best Local Similarity 62.3%; Pred. No. 8.3e-41;  
Matches 137; Conservative 32; Mismatches 49; Indels 2; Gaps 1;

QY 21 DIVLTQSPSLASVGDRTVITCKASQSDVDYDGD--DSYNNWYQKPGQAPKLLIYAASNL 78  
Db 1 DIVMTQSPSLVTAAGEKVTMTCTSSQSLFNSQKQNNLYTWYQKPGQAPKLLIYMASTR 60  
QY 79 ESGVPSRFSGSGSGTDFTLTSSLOPEDFATYVCOQSNEDPRTFQGTKEIKRTVAAPS 138  
Db 61 ESGVPSRFSGSGSGTDFTLTSSLOPEDFATYVCOQSNEDPRTFQGTKEIKRTVAAPS 120  
QY 139 VTFPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQSVTEQDQSKDSTYS 198  
Db 121 VSIFPPSPSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSEKQNGVLNSWTDQDQSKDSTYS 180  
QY 199 LSSTLTSLKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 238  
Db 181 MSSTLTSLKDEYERHNSYTCETHATKSTSPIVKSFNRNEC 220

RESULT 12  
S01320  
Ig kappa chain precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 21-Jan-2000  
C:Accession: S01320  
R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.  
Eur. J. Biochem. 176, 287-295, 1988  
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed  
A:Reference number: S01320; MUID:88329081  
A:Accession: S01320  
A:Molecule type: mRNA  
A:Residues: 1-234 <DE1>  
A:Cross-references: EMBL:X13187; NID:g51784; PIDN:CAA31579.1; PID:g51785  
A:Note: this sequence was determined from the differentiated gene  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-234/Product: Ig kappa chain #status predicted <MAT>  
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 58.6%; Score 725; DB 2; Length 234;  
Best Local Similarity 57.9%; Pred. No. 1.9e-40;  
Matches 139; Conservative 38; Mismatches 55; Indels 8; Gaps 2;

QY 1 METDTILLVLLWVPGSTGDIVLTSQSPSLASVGDRTVITCKASQSDVDYDGDGYNN-- 58  
Db 1 MSVPTQVLGLLLWLTDAKCDIQMTQSPASLSVSGESVITCRASENI-----YSNLA 54  
QY 59 WYQKPGQAPKLLIYAASNLGSGVSRFSGSGGTDFTLTSSLOPEDFATYVCOQSNED 118  
Db 55 WYQKPGKSPQLLYVATKLYDGVPSRFSGSGSGTQYSLKINSLSQSDFGSYCQHFWD 114  
QY 119 PRTFQGTKEIKRTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 178  
Db 115 PRTFQGTKEIKRTVAAPSVFIIPPSPDEQLKSGTASVVCFLNNFYPKDINVKWKIDGSE 174  
QY 179 QSGNSQSVTEQDQSKDSTYLSSTLTSLKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 238  
Db 175 RQNGVLNSWTDQDQSKDSTYMSSTLTSLKDEYERHNSYTCETHATKSTSPIVKSFNRNEC 234

RESULT 13  
A56169  
Ig kappa chain V region (clone 23.2) - mouse (fragment)  
C:Species: Mus musculus (house mouse)







GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:23:13 ; Search time 53.64 Seconds  
(without alignments)  
171.798 Million cell updates/sec

Title: US-09-499-662-129

Perfect score: 1237

Sequence: 1 METDTILLWVLLWVPGSTG.....EVTHOGLSSPVTKSFNRGEC 238

Scoring table:  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	548	44.3	106	1 KAC_HUMAN	P01834 homo sapien
2	536	43.3	131	1 KV3I_MOUSE	P01661 mus musculus
3	521	42.1	132	1 KV3F_MOUSE	P01658 mus musculus
4	487	39.4	111	1 KV3M_MOUSE	P01665 mus musculus
5	485	39.2	111	1 KV3N_MOUSE	P01666 mus musculus
6	483	39.0	111	1 KV3O_MOUSE	P01667 mus musculus
7	482.5	39.0	129	1 KV3L_HUMAN	P18135 homo sapien
8	480	38.8	111	1 KV3Q_MOUSE	P01669 mus musculus
9	476	38.5	129	1 KV1W_HUMAN	P04431 homo sapien
10	472	38.2	111	1 KV3L_MOUSE	P01664 mus musculus
11	462.5	37.4	110	1 KV3P_MOUSE	P01668 mus musculus
12	460.5	37.2	129	1 KV3M_HUMAN	P18136 homo sapien
13	457	36.9	108	1 KV1H_HUMAN	P01600 homo sapien
14	452	36.5	134	1 KV4C_HUMAN	P06314 homo sapien
15	449	36.3	108	1 KV1M_HUMAN	P01605 homo sapien
16	448	36.2	108	1 KV1G_HUMAN	P01599 homo sapien
17	444	35.9	108	1 KV1K_HUMAN	P01603 homo sapien
18	442	35.7	108	1 KV1B_HUMAN	P01594 homo sapien
19	441	35.7	108	1 KV1E_HUMAN	P01597 homo sapien
20	441	35.7	108	1 KV1F_HUMAN	P01598 homo sapien
21	441	35.7	108	1 KV1N_HUMAN	P01606 homo sapien
22	440	35.6	111	1 KV3H_MOUSE	P01660 mus musculus
23	438	35.4	108	1 KV1V_HUMAN	P04430 homo sapien
24	437	35.3	108	1 KV1A_HUMAN	P01593 homo sapien
25	437	35.3	117	1 KV1J_HUMAN	P01602 homo sapien
26	436.5	35.3	133	1 KV4B_HUMAN	P06313 homo sapien
27	435.5	35.2	129	1 KV3H_HUMAN	P04207 homo sapien
28	434	35.1	108	1 KV1Y_HUMAN	P80362 homo sapien
29	431	34.8	108	1 KV1Q_HUMAN	P01607 homo sapien
30	431	34.8	111	1 KV3J_MOUSE	P01662 mus musculus
31	430	34.8	108	1 KV1P_HUMAN	P01608 homo sapien
32	430	34.8	111	1 KV3K_MOUSE	P01663 mus musculus
33	429	34.7	108	1 KV1R_HUMAN	P01610 homo sapien

## RESULT 1

ID	KAC_HUMAN	STANDARD;	PRT;	106 AA.
AC	P01834;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Ig kappa chain C region.			
GN	IGKC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064023; PubMed=5489770;			
RA	Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain."			
RT	Biochemistry 9:3155-3161(1970).			
RN	[2]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds."			
RL	Biochemistry 9:3188-3196(1970).			
RN	[3]			
RP	SEQUENCE (BENCE-JONES PROTEIN TI).			
RX	MEDLINE=72188439; PubMed=5027703;			
RA	Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;			
RT	"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81042304; PubMed=6775818;			
RA	Hietter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;			
RT	"Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments."			
RL	Cell 22:197-207(1980).			
RN	[5]			
RP	SEQUENCE (BENCE-JONES PROTEIN ROY).			
RA	Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;			
RL	(In) Franek F., Shugar D. (eds.);			
RL	Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).			
RN	[6]			
RP	SEQUENCE (BENCE-JONES PROTEIN CUM).			
RX	MEDLINE=68242259; PubMed=5586923;			
RA	Hilschmann N.;			
RT	"The complete amino acid sequence of Bence Jones protein Cum (kappa-type)."			

## ALIGNMENTS

```
RL Hoppe-Seyley's z. Physiol. Chem. 348:1718-1722(1967).
RN [7]
RP SEQUENCE (BENCE-JONES PROTEIN AG).
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969).
RN [8]
RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains.";
RL Science 169:56-59(1970).
CC -!- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
CC MARKER, 45-ALA AND 83-LEU.
CC -----
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CC -----
DR EMBL: J00241; AAA58989.1; -
DR EMBL: V00557; CAA23823.1; -
DR PIR: A02116; K3HU.
DR HSP: P01842; 7FAB.
DR MIM: 147200; -.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_c1.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00407; Igcl; 1.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 26 86
FT DISULFID 106 106
FT VARIANT 83 83
FT INTERCHAIN (WITH A HEAVY CHAIN).
FT V -> L (IN INV(1,2) MARKER).
FT /FTIG=VAR_003897.
FT D -> N (IN REF. 7 AND 8).
FT E -> Q (IN REF. 5 AND 6).
FT CONFLICT 14 14
FT CONFLICT 57 57
FT CONFLICT 57 57
SQ SEQUENCE 106 AA; 11609 MW; 51984D1FDD372CE8 CRC64;

Query Match 44.3%; Score 548; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.5e-37;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 TVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 192
DB 1 TVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60
QY 193 KOSTYLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238
DB 61 KOSTYLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 106

RESULT 2
KV3J_MOUSE
ID KV3J_MOUSE STANDARD; PRT; 131 AA.
AC P01661;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region MOPC 63 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
```

```
RN [1]
RP SEQUENCE OF 1-35.
RX MEDLINE=78235887; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes.";
RL Biochemistry 17:2392-2400(1978).
RN [2]
RP SEQUENCE OF 21-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences.";
RL Biochemistry 12:760-771(1973).
RN [3]
RP REVISIONS.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
DR PIR: A01935; KYMSW6.
DR HSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 131
FT DOMAIN 21 43
FT DOMAIN 44 58
FT DOMAIN 59 73
FT DOMAIN 74 80
FT DOMAIN 81 112
FT DOMAIN 113 121
FT DOMAIN 122 131
FT DISULFID 43 112
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;

Query Match 43.3%; Score 536; DB 1; Length 131;
Best Local Similarity 76.3%; Pred. No. 3e-36;
Matches 100; Conservative 17; Mismatches 14; Indels 0; Gaps 0;

QY 1 METDTLLWVLLWVPGSGDIVLTQSPSSLSASVGRVITTCASQSDYDGDSDYNNWY 60
DB 1 METDTLLWVLLWVPGSGTGNIVLTQSPASVLAVSLGORATISCRASESDYSGNSFMHWY 60
QY 61 QOKPGQAPKLLIYAASNLGSGVPSRFGSGGTDFLTITSSLOPEDFATYTCQSNEDPR 120
DB 61 QOKPGQAPKLLIYLANLNSGCVPARFSGSGSRDTFLTIDPVEADDAATYTCQNNEDPW 120
QY 121 TFGQGTKEIK 131
DB 121 TFGGGTKLEIK 131

RESULT 3
KV3F_MOUSE
ID KV3F_MOUSE STANDARD; PRT; 132 AA.
AC P01658;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region MOPC 321 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
```

RA	Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin diversity."
RL	Nature 276:785-790(1978).
DR	PIR; A01937; KVM543.
DR	HSSP; P01789; IMCP.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00406; IGv; 1.
KW	Immunoglobulin V region.
FT	DOMAIN 1 23
FT	DOMAIN 24 38
FT	DOMAIN 39 53
FT	DOMAIN 54 60
FT	DOMAIN 61 92
FT	DOMAIN 93 101
FT	DOMAIN 102 111
FT	DISULFID 23 92
FT	NON_TER 111 111
SQ	SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;
Query Match 39.4%; Score 487; DB 1; Length 111; Best Local Similarity 82.0%; Pred. No. 2e-32; Matches 91; Conservative 9; Mismatches 11; Indels 0; Gaps 0	
Qy	21 DIVLTQSPLSASGDRVITTCRASQSDVDGDSYMNWYQQKPGCAPKLLIYAASNLES 80
Dd	1 DIVLTQSPASLAVSLGRATISCKASQSDVDGDSYMNWYQQKPGPKLLIYAASNLES 60
Qy	81 GVPSRFSGSGGTFTLTISRISLPEDFAITYCOQSNEPDRTFGQTKVIEK 131
Dd	61 GIPARFSGGSGGTFTLNHPVEEDAITYCOQSNEPDFTFGSGTKLEIK 111
RESULT 5	
KV3N_MOUSE	STANDARD; PRT; 111 AA.
ID AC	P01666;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DE	15-JUL-1999 (Rel. 38, Last annotation update)
DB	Ig kappa chain V-HII region PC 7183.
OS	Mus musculus (Mouse),
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RX	NCBI_TaxID=10090;
ON	[1]
RP	SEQUENCE.
RA	MEDLINE=79073152; PubMed=103003;
RA	Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin diversity."
RL	Nature 276:785-790(1978).
DR	PIR; B01937; KVM583.
DR	HSSP; P01789; IMCP.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00406; IGv; 1.
KW	Immunoglobulin V region.
FT	DOMAIN 1 23
FT	DOMAIN 24 38
FT	DOMAIN 39 53
FT	DOMAIN 54 60
FT	DOMAIN 61 92
FT	DOMAIN 93 101
FT	DOMAIN 102 111
FT	DISULFID 23 92
FT	NON_TER 111 111
SQ	SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

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Query Match      39.2%; Score 485; DB 1; Length 111;
Best Local Similarity 81.1%; Pred. No. 2,8e-32;
Matches 90; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLASVGDRTVITCKASQSDYDGDSTMMNYQKPGQAPKLLIYAASNLES 80
DB 1 DIVLTQSPASLAVSLGORATISCKASQSDYDGDSTMMNYQKPGQAPKLLIYAASNLES 60

QY 81 GVPFRSGSGGTDFLTITSSLPQEPFATYCCQSNEDPRTFGQGTVEIK 131
DB 61 GIPARFSGSGGTDFLTINHPVEEDATYCCQSNEDPRTFGAGTKLEIK 111

RESULT 6
KV30_MOUSE STANDARD; PRT; 111 AA.
AC P01667;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 6308.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR: C01937; KVM508.
DR HSSP: P01789; 1MCP.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match      39.0%; Score 483; DB 1; Length 111;
Best Local Similarity 81.1%; Pred. No. 4,1e-32;
Matches 90; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLASVGDRTVITCKASQSDYDGDSTMMNYQKPGQAPKLLIYAASNLES 80
DB 1 DIVLTQSPASLAVSLGORATISCKASQSDYDGDSTMMNYQKPGQAPKLLIYTASNLES 60

QY 81 GVPFRSGSGGTDFLTITSSLPQEPFATYCCQSNEDPRTFGQGTVEIK 131
DB 61 GIPARFSGSGGTDFLTINHPVEEDATYCCQSNEDPRTFGAGTKLEIK 111

RESULT 7
KV3L_HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
LEUKEMIA.
DR PIR: PL0022; K3HUHA.
DR HSSP: P01789; 1MCP.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C5529272774D0 CRC64;

Query Match      39.0%; Score 482.5; DB 1; Length 129;
Best Local Similarity 69.7%; Pred. No. 5,4e-32;
Matches 92; Conservative 16; Mismatches 21; Indels 3; Gaps 1;

QY 1 METDTILLWLLVLPSTGSDIVLTQSPSSLASVGDRTVITCKASQSDYDGDSTMMNY 60
DB 1 METPAQLLFLLLLWLPDPTTGEIVLTQSPGTLSPGERATLSCRASQSV---SSSYLAWY 57

QY 61 QKQPGQAPKLLIYAASNLESQVPSRFSGSGGTDFLTITSSLPQEPFATYCCQSNEDPR 120
DB 58 QKQPGQAPRLIYVASSRATGIPDRFSGSGGTDFLTITSRLEPEDFAVYVCOQYGTSPR 117

QY 121 TFGQGTVEIKR 132
DB 118 TFGQGTVEIKR 129

RESULT 8
KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7769.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR: E01937; KVM569.
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DR HSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig: 1.
DR SMART: SM00406; IgV: 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 29 53
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match 38.8%; Score 480; DB 1; Length 111;
Best Local Similarity 80.2%; Pred. No. 7.1e-32;
Matches 89; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGRVITTCASQSDYDGDSDYNNWYQOKPGQAPKLLIYAASNL 80
DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSDYNNWYQOKPGQPKVLIFAA 60

QY 81 GVPFRFSGSGGTDTFTLTISLPEDFATYCCQSNEDPRTFGQGTVEIK 131
DB 61 GIPARFSGSGGTDTFTLTNIHPVEEDAATYCCQSNEDPRTFGSGTKLEIK 111

RESULT 9
KV1W_HUMAN STANDARD; PRT; 129 AA.
AC P0431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combrato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related."
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X00965; CAA25477.1; ALT_TERM.
DR PIR: A01883; KIHUK.
DR HSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig: 1.
DR SMART: SM00406; IgV: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129
FT DOMAIN 23 45
FT DOMAIN 23 45
FT DOMAIN 46 56
FT DOMAIN 57 71
FT DOMAIN 72 78
IG KAPPA CHAIN V-I REGION WALKER.
FRAMEWORK-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-1.
COMPLEMENTARITY-DETERMINING-2.
COMPLEMENTARITY-DETERMINING-3.
COMPLEMENTARITY-DETERMINING-4.
BY SIMILARITY.
```

```
FT DOMAIN 79 110
FT DOMAIN 111 119
FT DOMAIN 120 129
FT DISULFID 45 110
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 38.5%; Score 476; DB 1; Length 129;
Best Local Similarity 73.3%; Pred. No. 1.8e-31;
Matches 96; Conservative 13; Mismatches 18; Indels 4; Gaps 1;

QY 1 METDTILLWVLLVPGSTGDIVLTQSPSSLSASVGRVITTCASQSDYDGDSDYNNWY 60
DB 3 MRVPAQLIGLLLLWLGARCDIQMTQSPSSLSASVGRVITTCRASQSI----SNLWNY 58

QY 61 QOKPGQAPKLLIYAASNLGVPFRFSGSGGTDTFTLTISLPEDFATYCCQSNEDPRT 120
DB 59 QOKPGKAPKLLIYAASLQSGVTSRFGSGSGGTDTFTLTISLPEDSATYCCQSYSTLI 118

QY 121 TFGQGTVEIK 131
DB 119 TFGQGTVEIK 129

RESULT 10
KV3L_MOUSE STANDARD; PRT; 111 AA.
AC P01664;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region CBPC 101.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions."
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR: A01936; KVMSCI.
DR HSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig: 1.
DR SMART: SM00406; IgV: 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11964 MW; E2BLAD98AD965962 CRC64;

Query Match 38.2%; Score 472; DB 1; Length 111;
Best Local Similarity 79.3%; Pred. No. 3.1e-31;
Matches 88; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGRVITTCASQSDYDGDSDYNNWYQOKPGQAPKLLIYAASNL 80
DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSDYNNWYQONPQSPKLLIYAASNL 60

QY 81 GVPFRFSGSGGTDTFTLTISLPEDFATYCCQSNEDPRTFGQGTVEIK 131
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Db 61 GIPARFSGSGTDFTLNHPVEEDAATYYCQSNEDPTFGGKLEIK 111
:::|||||
RESULT 11
KV3P_MOUSE STANDARD; PRT; 110 AA.
AC P01668;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7210.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; D01937; KMS10.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 100
FT DOMAIN 101 110
FT DISULFID 23 92
FT NON_TER 110 110
SQ SEQUENCE 110 AA; 11950 MW; 69F1A5CE86B1249 CRC64;
```

```
Query Match 37.4%; Score 462.5; DB 1; Length 110;
Best Local Similarity 79.3%; Pred. No. 1.7e-30;
Matches 88; Conservative 10; Mismatches 12; Indels 1; Gaps 1;

QY 21 DIVLTQSPSSLSASVGDRTITCKASQSYDYGDSYMNYYQKPGQAPKLLIYAASNLES 80
|||
Db 1 DIVLTQSPASLAVSLGQRATISCKASQSLDYGDSYMNYYQKPGQPPKLLIYAASNLES 60
|||
QY 81 GVPSPRFGSGSGTDFTLTISLQPEDFATYYCQSNEDPRTFGGKLEIK 131
|||
Db 61 GIPARFSGSGTDFTLNHPVEEDAATYYCHQS-EDPTFGGKLEIK 110
|||
```

```
RESULT 12
KV3M_HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
```

```
RT mutation. Implications for etiology and immunotherapy.*;
RL J. Exp. Med. 167:840-852(1988).
CC -I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
DR PIR; P00021; K3HUHI.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129
FT DOMAIN 21 43
FT DOMAIN 44 55
FT DOMAIN 56 70
FT DOMAIN 71 77
FT DOMAIN 78 109
FT DOMAIN 110 118
FT DOMAIN 119 129
FT DISULFID 43 109
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match 37.2%; Score 460.5; DB 1; Length 129;
Best Local Similarity 68.2%; Pred. No. 3.1e-30;
Matches 90; Conservative 16; Mismatches 23; Indels 3; Gaps 1;

QY 1 METDTLLWVLLWPGSTGDIVLTQSPSSLSASVGDRTITCKASQSYDYGDSYMNYY 60
|||
Db 1 METPAQLLELLWLPDTEIGVLTQSPGTLSPGSRATLSRASQSV---SSSYLAWY 57
|||
QY 61 QKPGQAPKLLIYAASNLESQVPSRSGSGTDFTLTISLQPEDFATYYCQSNEDPR 120
|||
Db 58 QKPGQAPRLIYGASRATGIPDRFSGSGTDFTLTISRLPEXDFATYYCQYSSPW 117
|||
QY 121 TFGQGTKEIKR 132
|||
Db 118 TFGQGTKEIKR 129
|||

RESULT 13
KV1H_HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Hau); subdivision within
RT subgroups.";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01868; K1HUHU.
DR HSP; P80362; IWTIL.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FRAMEWORK-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-1.
COMPLEMENTARITY-DETERMINING-2.
COMPLEMENTARITY-DETERMINING-3.
COMPLEMENTARITY-DETERMINING-3.
JK1 SEGMENT.
BY SIMILARITY.
NON_TER 129 129
SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;
```

FT	DISULFID	43	114	BY SIMILARITY.
FT	NON_TER	134		
SQ	SEQUENCE	134 AA;	14966 MW;	6413A22FD0738832 CRC64;
Query Match 36.5%; Score 452; DB 1; Length 134;				
Best Local Similarity 71.8%; Pred. No. 1.5e-29;				
Matches 89; Conservative 10; Mismatches 23; Indels 2; Gaps 1;				
Qy	11	LLMWPGSTGDIVLTQSPSSLSASVGRVTTTCASOSVDYDGP--SYMNWYQOKPGQAP	68	
Db	11	LLLWISGAYGDIVMTQSPDLSAVSLGERATINCKSSILYSSDNKNYLAWYQOKPGQP	70	
Qy	69	KLLIYAASNLSSGVPSRFSGSGSTDTLTLTSSLPQDFATYYCQSNEDPRFTFGQTKV	128	
Db	71	KLLIYWASTREGVDPDRFSGSGSTDTLTLTSSLQADVAVYYCQYVNLPTWTFGQTKV	130	
Qy	129	EIKR 132		
Db	131	EIKR 134		
RESULT 15				
ID	KVIM_HUMAN	STANDARD;	PRT;	108 AA.
AC	P01605;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig kappa chain V-I region Lay.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=77038198; PubMed=824717;			
RA	Capra J.D., Klapper D.G.;			
RT	"Complete amino acid sequence of the variable domains of two human			
RT	IGM anti-gamma globulins (Lay/Pom) with shared idiotypic			
RT	specificities.";			
RL	Scand. J. Immunol. 5:677-684 (1976).			
CC	-1- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS			
CC	CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,			
CC	WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.			
CC	-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA			
CC	GLOBULIN ACTIVITY.			
DR	PIR; A01871; KIHULY.			
DR	HSP; P01607; IREI.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF000047; Ig; 1.			
DR	SMART; SM00406; IGV; 1.			
KW	Immunoglobulin V region.			
FT	DOMAIN 1 23			
FT	DOMAIN 24 34			
FT	DOMAIN 35 49			
FT	DOMAIN 50 56			
FT	DOMAIN 57 88			
FT	DOMAIN 89 97			
FT	DOMAIN 98 107			
FT	DISULFID 23 88			
FT	NON_TER 108 108			
SQ	SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;			
Query Match 36.3%; Score 449; DB 1; Length 108;				
Best Local Similarity 78.6%; pred. No. 2e-29;				
Matches 88; Conservative 8; Mismatches 12; Indels 4; Gaps 1;				
Qy	21	DIVLTQSPSSLSASVGRVTTTCASOSVDYDGSYNNWYQOKPGQAPKLLIYAASNL	80	
Db	1	DIOMTQSPSSLSASVGRVTTTCASQNV-----NAYLNWYQOKPGIAPKLLIYGASTREA	56	

Qy 81 GVPFRFSGSGTDFTLTISSLPEDFATYYCQSNEDPRTFGQTKVEIKR 132  
|||||  
Db 57 GVPFRFSGSGTDFTLTISSLPEDATYYCQYNNWPTFGQTKVEIKR 108  
|||||

Search completed: August 14, 2002, 15:23:13  
Job time: 686 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:22:14 ; Search time 187.61 Seconds  
(without alignments)  
219.459 Million cell updates/sec

Title: US-09-499-662-129

Perfect score: 1237

Sequence: 1 METDTILLWLLLVPGSTG.....EVTHQGLSSPVTKSFNRGEC 238

Scoring table:

BLOSUM62DX Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvrius.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	750.5	60.7	238	11 Q99M37	Q99M37 mus musculus
2	739	59.7	234	11 Q91WF8	Q91WF8 mus musculus
3	738	59.7	233	11 Q91WS9	Q91WS9 mus musculus
4	721	58.3	214	11 Q9RIA5	Q9RIA5 mus musculus
5	705.5	57.0	235	11 Q91W12	Q91W12 mus musculus
6	700	56.6	211	11 Q91XL0	Q91XL0 mus musculus
7	467	37.8	108	4 Q9UL77	Q9UL77 homo sapien
8	459.5	37.1	107	4 Q96SA9	Q96SA9 homo sapien
9	446	36.1	108	4 Q9UL70	Q9UL70 homo sapien
10	434.5	35.1	107	4 Q9UL81	Q9UL81 homo sapien
11	434	35.1	116	4 Q96PF6	Q96PF6 homo sapien
12	433	35.0	108	4 Q9UL79	Q9UL79 homo sapien
13	430.5	34.8	235	11 Q99M11	Q99M11 mus musculus
14	429	34.7	236	4 Q96E61	Q96E61 homo sapien
15	419	33.9	111	11 Q920E9	Q920E9 mus musculus
16	398.5	32.2	109	4 Q9UL78	Q9UL78 homo sapien

17	386.5	31.2	233	4	Q96I69	Q96I69 homo sapien
18	384	31.0	108	4	Q9UL83	Q9UL83 homo sapien
19	378	30.6	233	11	Q91V32	Q91V32 m adult mal
20	375.5	30.4	109	4	Q9UL86	Q9UL86 homo sapien
21	375.5	30.4	109	4	Q9UL85	Q9UL85 homo sapien
22	375	30.3	238	11	Q9QYF0	Q9QYF0 mus musculus
23	370	29.9	103	11	Q9UL80	Q9UL80 mus musculus
24	361	29.2	109	11	Q920E6	Q920E6 mus musculus
25	354	28.6	114	4	Q9UL80	Q9UL80 homo sapien
26	351	28.4	127	11	Q925S9	Q925S9 mus musculus
27	350	28.3	107	11	Q9ER29	Q9ER29 mus musculus
28	349	28.2	99	11	Q9JL74	Q9JL74 mus musculus
29	346.5	28.0	106	5	Q9U410	Q9U410 schistosoma
30	335	27.1	101	11	Q9JL78	Q9JL78 mus musculus
31	328	26.5	97	11	Q9JL76	Q9JL76 mus musculus
32	325.5	26.3	104	11	Q9JL82	Q9JL82 mus musculus
33	324.5	26.2	241	11	Q921A6	Q921A6 mus musculus
34	302	24.4	109	6	Q9N0W5	Q9N0W5 oryctolagus
35	297	24.0	107	11	Q9JL84	Q9JL84 mus musculus
36	279.5	22.6	218	11	Q925S1	Q925S1 mus musculus
37	247	20.0	107	4	Q9UL82	Q9UL82 homo sapien
38	242.5	19.6	107	4	Q9NSD6	Q9NSD6 homo sapien
39	236.5	19.1	108	4	Q96SB0	Q96SB0 homo sapien
40	236	19.1	130	4	Q9NP29	Q9NP29 homo sapien
41	225	18.2	130	11	Q9B8W4	Q9B8W4 mus musculus
42	215	17.4	112	4	Q96JD1	Q96JD1 homo sapien
43	212	17.1	267	13	Q90529	Q90529 ginglymosto
44	208.5	16.9	112	4	Q96JD2	Q96JD2 homo sapien
45	207.5	16.8	116	4	Q96JD0	Q96JD0 homo sapien

#### ALIGNMENTS

RESULT 1

Q99M37 ID Q99M37 PRELIMINARY; PRT; 238 AA.  
AC Q99M37;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE HYPOTHETICAL 26.3 KDA PROTEIN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS  
RC TISSUE.;  
RA Strausberg R.;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC002035; AAH02035.1; -  
DR HSSP; P01679; 2FBJ  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR003597; Ig\_cl.  
DR InterPro; IPR003600; Ig\_like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGcl; 1.  
DR SMART; SM00406; IGV; 1.  
DR SMART; SM00410; IG\_like; 1.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 60.7%; Score 750.5; DB 11; Length 238;  
Best Local Similarity 59.0%; Pred. No. 1e-57;  
Matches 138; Conservative 39; Mismatches 56; Indels 1; Gaps 1;



Db 57 GVPNRFSGSGQDYSLTISLEVEDMGYYCLOYDEFPFFGSGTKLEIKRADAPTVS 116  
 QY 141 IFPPSDEOLKSGTASVVCLLNNFYPREAKVQKYNALQSGNSQESVTEQDQSKDSTYSLS 200  
 Db 117 IFPPSSEQLTSGGASVVCFLNNFYPKDINVKKWIDGSRQGVLSNWTQDQSKDSTYSMS 176  
 QY 201 STLTLKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 238  
 Db 177 STLTLTKDEYERHNSYTCETHKTKTSTPIVKCFNRNEC 214

RESULT 5  
 Q91W12 PRELIMINARY; PRT; 235 AA.  
 AC Q91W12;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DE UNKNOW (PROTEIN FOR MGC:6582).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BREAST TUMOR;  
 RA Strausberg R.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC006643; AAH06643.1; -;  
 SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;

Query Match 57.0%; Score 705.5; DB 11; Length 235;  
 Best Local Similarity 61.3%; Pred. No. 8.5e-54;  
 Matches 135; Conservative 31; Mismatches 50; Indels 5; Gaps 1;  
 QY 18 STGDIVLTQSPSSLSASVGRVTTTCASQSDVDGDSYNNWYQKPGQAPKLLIYAASN 77  
 Db 20 SRGQIVLTQSPALMSASPGERVTTTCASSSV-----SHMHYQKSGTSPKRIYDTFK 74  
 QY 78 LESGVPFRFSGSGSTDTFTLTISLQPEDFATYCCQSNEDPRTFGGTKVEIKRTVAAP 137  
 Db 75 LTSQVPRFSGSGSTGTSYSLISNMEADVATYCCQSNRPPTFGVTKLELRADAAP 134  
 QY 138 SVFIFFPSDEOLKSGTASVVCLLNNFYPREAKVQKYNALQSGNSQESVTEQDQSKDSTY 197  
 Db 135 TVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKKWIDGSRQGVLSNWTQDQSKDSTY 194  
 QY 198 SLSTLTLKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 238  
 Db 195 SMSSTLTLTKDEYERHNSYTCETHKTKTSTPIVKCFNRNEC 235

RESULT 6  
 Q91XL0 PRELIMINARY; PRT; 211 AA.  
 AC Q91XL0;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DE ADULT MALE KIDNEY CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,  
 DE CLONE:0610010P20, FULL INSERT SEQUENCE.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=KIDNEY;  
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,  
 RA Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

RA Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y.,  
 RA Konno H., Kouda K., Koya S., Kurihara C., Matsuyama T., Miyazaki A.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T.,  
 RA Owa C., Saito H., Saito R., Sakai K., Sakai K., Sano H., Sasaki D.,  
 RA Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y.,  
 RA Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y.,  
 RA Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
 RA Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=KIDNEY;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA RIKEN FANTOM Consortium.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=KIDNEY;  
 RX MEDLINE=99279253; PubMed=10349636;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=KIDNEY;  
 RX MEDLINE=20499374; PubMed=11042159;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=KIDNEY;  
 RX MEDLINE=20530913; PubMed=11076861;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 DR EMBL: AK002514; BAB22154.1; -;  
 SQ SEQUENCE 211 AA; 23182 MW; 1A5FFA0F8BA50163 CRC64;

Query Match 56.6%; Score 700; DB 11; Length 211;  
 Best Local Similarity 61.3%; Pred. No. 2.2e-53;  
 Matches 133; Conservative 33; Mismatches 43; Indels 8; Gaps 2;  
 QY 24 LTQSPSSLSASVGRVTTTCASQSDVDGDSYNN--WYQKPGQAPKLLIYAASNLSG 81  
 Db 1 MTQSPASLSVSVGETVTTTCRASENI-----YSNLAWYQKQKSPOLLVYATNLADG 54  
 QY 82 VPSRFSGSGSTDTFTLTISLQPEDFATYCCQSNEDPRTFGGTKVEIKRTVAAPSVEFI 141  
 Db 55 VPSRFSGSGSTQYSLKINSQSEDFSGYFCQHFQWGTPTFGGCTKLEIKRADAAPTYSI 114  
 QY 142 FPPSDEOLKSGTASVVCLLNNFYPREAKVQKYNALQSGNSQESVTEQDQSKDSTYSLS 201  
 Db 115 FPPSSEQLTSGGASVVCFLNNFYPKDINVKKWIDGSRQGVLSNWTQDQSKDSTYSMS 174  
 QY 202 TLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 238  
 Db 175 TLTTLTKDEYERHNSYTCETHKTKTSTPIVKCFNRNEC 211

RESULT 7  
 Q9UL77

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ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 37.8%; Score 467; DB 4; Length 108;
Best Local Similarity 82.1%; Pred. No. 2e-33;
Matches 92; Conservative 8; Mismatches 8; Indels 4; Gaps 1;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGQAPKLLIYAASNL 80
Db 1 DIQMTQSPSSLSASVGDRTVITCKASQSI-----SSVLNWKYQKPGKAPKLLIYAAS 56

QY 81 GVPFRFSGSGGTDFLTITSSLPEDFATYYCQSNEDPRTFGQGTKEIKR 132
Db 57 GVPFRFSGSGGTDFLTITSSLPEDFATYYCQSQS-YSTLTFGGTKEIKR 108

RESULT 8
Q96SA9 PRELIMINARY; PRT; 107 AA.
ID Q96SA9;
AC Q96SA9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody v region genes.";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
DR NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 37.1%; Score 459.5; DB 4; Length 107;
Best Local Similarity 83.0%; Pred. No. 8.8e-33;
Matches 93; Conservative 7; Mismatches 7; Indels 5; Gaps 2;

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QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGQAPKLLIYAASNL 80
Db 1 DIQMTQSPSSLSASVGDRTVITCKASQSI-----SSVLNWKYQKPGKAPKLLIYAAS 56

QY 81 GVPFRFSGSGGTDFLTITSSLPEDFATYYCQSNEDPRTFGQGTKEIKR 132
Db 57 GVPFRFSGSGGTDFLTITSSLPEDFATYYCQSQS-YSTLTFGGTKEIKR 108

RESULT 9
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70;
AC Q9UL70;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 36.1%; Score 446; DB 4; Length 108;
Best Local Similarity 77.7%; Pred. No. 1.3e-31;
Matches 87; Conservative 9; Mismatches 12; Indels 4; Gaps 1;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGQAPKLLIYAASNL 80
Db 1 DIQMTQSPSSLSASVGDRTVITCKASQGI-----SNFLWYQKPGKVPKSLIYAAS 56

QY 81 GVPFRFSGSGGTDFLTITSSLPEDFATYYCQSNEDPRTFGQGTKEIKR 132
Db 57 GVPFRFSGSGGTDFLTITSSLPEDVATYYCQKYNAPRTFGGTKEIKR 108

RESULT 10
Q9UL81 PRELIMINARY; PRT; 107 AA.
ID Q9UL81;
AC Q9UL81;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;

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RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
DE Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56269.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 107
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 35.18; Score 434.5; DB 4; Length 107;
Best Local Similarity 77.78; Pred. No. 1.3e-30;
Matches 87; Conservative 10; Mismatches 10; Indels 5; Gaps 2;

QY 21 DIVLTQSPSSLSASVGRVTTTCASQSDYDGSYNNWYQKPGQAPKLLIYAASNL 80
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 1 DIQMTQSPSSLSASVGRVTTTCRASQSI----SNLWYQKPGKAPNLLIYAAS 56
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

QY 81 GVPFRFGSGSGTDTLTITSLQPEDFATYYCQSNEDPRTFGGKVEIKR 132
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 57 GVPFRFGSGSGTDTLTITSLQPEDFATYYCQSS-YSALTFGGTKVDIIR 107
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

RESULT 11
Q96PF6 ID Q96PF6 PRELIMINARY; PRT; 116 AA.
AC Q96PF6
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE KAPPA 1 LIGHT CHAIN VARIABLE REGION (FRAGMENT).
GN SDNK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21361171; PubMed=11468171;
RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
RT "The tropism of organ involvement in primary systemic amyloidosis:
RT contributions of Ig V(L) germ line gene use and clonal plasma cell
RT burden.";
RL Blood 98:714-720(2001).
DR EMBL; AF361758; AAK51465.1; -.
FT NON_TER 1
FT NON_TER 116
FT NON_TER 116
SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFCE57 CRC64;

Query Match 35.18; Score 434; DB 4; Length 116;
Best Local Similarity 70.88; Pred. No. 1.6e-30;
Matches 85; Conservative 14; Mismatches 17; Indels 4; Gaps 1;

QY 21 DIVLTQSPSSLSASVGRVTTTCASQSDYDGSYNNWYQKPGQAPKLLIYAASNL 80
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 1 DIQMTQSPSSLSASVGRVTTTCASQDI----ANHLNWKPGKEAPKFLIYDGSFL 56
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

QY 81 GVPFRFGSGSGTDTLTITSLQPEDFATYYCQSNEDPRTFGGKVEIKRTVAAPSV 140
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 57 GVPFRFGSGGSATFTVTITSLQPEDFATYYCQYHLLPFTFGGKTKVDKRTVAAPSV 116
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

RESULT 12
Q9UL79 ID Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035035; AAD56271.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 35.08; Score 433; DB 4; Length 108;
Best Local Similarity 76.88; Pred. No. 1.8e-30;
Matches 86; Conservative 8; Mismatches 14; Indels 4; Gaps 1;

QY 21 DIVLTQSPSSLSASVGRVTTTCASQSDYDGSYNNWYQKPGQAPKLLIYAASNL 80
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 1 DIVMTQSPSSLSASTGDRVTTISCRMSQI----SYLAWYQKPGKAPLLIYAAS 56
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

QY 81 GVPFRFGSGSGTDTLTITSLQPEDFATYYCQSNEDPRTFGGKVEIKR 132
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
Db 57 GVPFRFGSGSGTDTLTITSLQSEDFAYYCQYSPFTFGGKVEIKR 108
   |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

RESULT 13
Q99M11 ID Q99M11 PRELIMINARY; PRT; 235 AA.
AC Q99M11
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 25.4 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002129; AAH02129.1; -.
DR HSP; P01703; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25403 MW; 39807BFE6782A3FB CRC64;

Query Match 34.88; Score 430.5; DB 11; Length 235;
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Best Local Similarity 42.6%; Pred. No. 8.3e-30;  
Matches 101; Conservative 37; Mismatches 86; Indels 13; Gaps 7;

QY 7 LLVLLWVPGSGDVLVTQSPSLASVGDRTVTITCKASQSYDYGDSYNNWYQKPGQ 66  
Db 6 LLVFLHLHTGSCAQLVLTQ-PPSVSTSLGSTAKLPCKA--STGNIGDSYNNWYQYMG 62  
QY 67 APKLLIYAASNLGSGVPSRFGSG--GSGTDFTLTISLQPEDFATYCCQSNEDPRTFGQ 124  
Db 63 SPTMIYGGDLRPSGVSDFRSGIDSSNSAFLTIGNVQADDEADYQCYSYSGIRVFGG 122  
QY 125 GTKVEI-KRTVAAPSVFIIPPPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALSGNS 193  
Db 123 GTKLTVLSPKTSPTVLPSPSSSEELTKATLVCTISDFYGVVTVDMKADG---TPVT 179  
QY 184 QESVTEQDSK--DSTVSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238  
Db 180 QGVETTPQSKONNNKYMASSYLTLTAKAMETHSSYSQCVTHEG--HTVEKLSRADC 234

RESULT 14  
Q96E61 PRELIMINARY; PRT; 236 AA.

AC Q96E61;  
DT 01-DEC-2001 (TremBLrel. 19, Created)  
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)  
DE UNKNOWN (PROTEIN FOR MGC:17259).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BRAIN, AND GLIOBLASTOMA WITH EGFR AMPLIFICATION;  
RA Strausberg R.;  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC012876; AAH12876.1; -  
SQ SEQUENCE 236 AA; 24712 MW; 7EC9FB3622FED957 CRC64;

Query Match 34.7%; Score 429; DB 4; Length 236;  
Best Local Similarity 42.4%; Pred. No. 1.1e-29;  
Matches 100; Conservative 39; Mismatches 87; Indels 10; Gaps 7;

QY 7 LLVLLWVPGSGDVLVTQSPSLASVGDRTVTITCKASQSYDYGDSYNNWYQKPGQ 66  
Db 6 LLTLHAHTGSAQSVLAQ-PPSVGAPGQVTITISCTGS-STNIGAGYAVHWYQYFPGA 63  
QY 67 APKLLIYAASNLGSGVPSRFGSGSGTDFTLTISLQPEDFATYCC--QSNEDPRTFGQ 124  
Db 64 APKVLIIYGNVNRPSGVDPFRSGSKTSASLTGLQADEADYQCYSYDGLSGSVFGA 123  
QY 125 GTKVEI-KRTVAAPSVFIIPPPDEQLKSGTASVVCLLNNFYPREAKVQKVDNA-LQSGN 182  
Db 124 GTKVTVLGQPKANPTVLPSPSSSEELQANKATLVCTISDFYGVAVTVAMKADGSPVKAG- 182  
QY 183 SQESVTEQDSKDYSTVSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238  
Db 183 -VETTPQSKONNNKYMASSYLTLPQWKSHRYSYQCVTHEG--STVEKTVAPTEC 235

RESULT 15  
Q920E9 PRELIMINARY; PRT; 111 AA.

AC Q920E9;  
DT 01-DEC-2001 (TremBLrel. 19, Created)  
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)  
DE PTERIN-MIMICKING ANTI-IDIOPOPE KAPPA CHAIN VARIABLE REGION (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;  
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307935; AAL09419.1; -  
FT NON\_TER 1  
FT NON\_TER 111  
SQ SEQUENCE 111 AA; 12046 MW; 1E46988AA658526 CRC64;

Query Match 33.9%; Score 419; DB 11; Length 111;  
Best Local Similarity 73.0%; Pred. No. 3.2e-29;  
Matches 81; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 21 DIVLTQSPSLASVGDRTVTITCKASQSYDYGDSYNNWYQKPGQAPKLLIYAASNL 80  
Db 1 DIVLTQSPASLAVSLGORATISCRASKSVSTSGSYNMHWYQKPGQPKLLIYASNL 60  
QY 81 GYPSRFGSGSGTDFTLTISLQPEDFATYCCQSNEDPRTFGQTKVEIK 131  
Db 61 GVPARFSGSGSGTDFTLNHPVEEDATYCCQSHRELPTFTGGGKLEIK 111

Search completed: August 14, 2002, 15:22:15  
Job time: 683 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 15:15:35 ; Search time 230.21 seconds  
(without alignments)  
114.832 Million cell updates/sec

Title: US-09-499-662-131  
Perfect score: 1237  
Sequence: 1 METDTILLWLLLVPGSTG.....EVTHOGLSPVTKSPNRGEC 238

Scoring table: BLOSUM62GX  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_032802:\*

1:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1980.DAT.*
2:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1981.DAT.*
3:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1982.DAT.*
4:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1983.DAT.*
5:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1984.DAT.*
6:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1985.DAT.*
7:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1986.DAT.*
8:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1987.DAT.*
9:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1988.DAT.*
10:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1989.DAT.*
11:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1990.DAT.*
12:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1991.DAT.*
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19:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1998.DAT.*
20:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1999.DAT.*
21:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA2000.DAT.*
22:	/SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1237	100.0	238	21	AAW90932 Humanised anti-Fas
2	1236	99.9	238	21	AAW90930 Humanised anti-Fas
3	1232	99.6	238	21	AAW90931 Humanised anti-Fas
4	1174	94.9	238	19	AAW83034 Anti-Fas humanised
5	1174	94.9	238	21	AAW83031 Humanised anti-Fas
6	1174	94.9	238	21	AAW83032 Humanised anti-Fas
7	1169	94.5	238	19	AAW83031 Anti-Fas humanised
8	1169	94.5	238	21	AAW83031 Humanised anti-Fas
9	1169	94.5	238	21	AAW83032 Anti-Fas humanised
10	1156	93.5	238	19	AAW83032 Humanised anti-Fas
11	1156	93.5	238	21	AAW83032 Humanised anti-Fas

ALIGNMENTS

RESULT 1

AAW90932

ID AAW90932 standard; Protein; 238 AA.

AC AAW90932;

XX

DT 08-AUG-2000 (first entry)

XX

DE Humanised anti-Fas designed light chain Leu 3 protein.

XX

DE Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac; dermatologic; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

XX

OS Synthetic.

XX

OS EP990563-A2.

XX

OS 05-APR-2000.

XX

XX 29-SEP-1999; 99EP-0307711.

XX

XX 30-SEP-1998; 98JP-0276881.

XX

XX 30-SEP-1998; 98JP-0276882.

XX

XX (SANY ) SANKYO CO LTD.



DB 1 metdtillwllwvpgstgdivltqspsslsasvsgdrvtltckasgsdvdgdsymnw 60  
 QY 61 QOKPKAPKLLIYAASNLSEIPSRFSGSGSGTDFTLTISSIQPEDFATYTCQSQSNEEDPR 120  
 DB 61 qkpgkpklllyaaasnlsgvprfsgsgsgtftltisslqpedfatyycqgsnedpr 120  
 QY 121 TFGGKTVEIKRTVAAPSVFIPTSPDEQLKSGTASVCLLNFFPREAKVQKVDNALQS 180  
 DB 121 tfggktveikrtvaapsvfipstpsdeqlksgtasvcllnffpreakvqkvdnalqs 180  
 QY 181 GNSQESVTEQDSKDYSTLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
 DB 181 gnsqesvteqdsksdystlsstltlskadyekhkvyacevthqglsspvtksfnrgec 238

RESULT 3  
 AAW90931  
 ID AAW90931 standard; Protein: 238 AA.  
 XX  
 AC AAW90931;  
 XX  
 DT 08-AUG-2000 (first entry)  
 XX  
 DE Humanised anti-Fas designed light chain Leu 2 protein.  
 XX  
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;  
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;  
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
 XX  
 OS Synthetic.  
 XX  
 PN EP990663-A2.  
 XX  
 PD 05-APR-2000.  
 XX  
 PF 29-SEP-1999; 99EP-0307711.  
 XX  
 PR 30-SEP-1998; 98JP-0276881.  
 XX  
 PR 30-SEP-1998; 98JP-0276882.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 XX  
 DR WPI: 2000-258930/23.  
 DR  
 DR N-PSDB: AAA11632.  
 XX  
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems  
 XX  
 XX Claim 2; Page 159; 263pp; English.  
 PS  
 CC This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,  
 CC antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent

CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody light chain construct designated Leu 2  
 CC which is described in the method of the invention.  
 XX  
 SQ Sequence 238 AA;

Query Match 99.6%; Score 1232; DB 21; Length 238;  
 Best Local Similarity 99.2%; Pred. No. 8.1e-62;  
 Matches 236; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 METDTILLWLLWVPGSTGDIVLTQSPSSLSASVSGDRVTITCKASQSDVDGDSYMMWY 60  
 DB 1 metdtillwllwvpgstgdivltqspsslsasvsgdrvtitckasgsdvdgdsymnw 60  
 QY 61 QOKPKAPKLLIYAASNLSEIPSRFSGSGSGTDFTLTISSIQPEDFATYTCQSQSNEEDPR 120  
 DB 61 qkpgkpklllyaaasnlsgvprfsgsgsgtftltisslqpedfatyycqgsnedpr 120  
 QY 121 TFGGKTVEIKRTVAAPSVFIPTSPDEQLKSGTASVCLLNFFPREAKVQKVDNALQS 180  
 DB 121 tfggktveikrtvaapsvfipstpsdeqlksgtasvcllnffpreakvqkvdnalqs 180  
 QY 181 GNSQESVTEQDSKDYSTLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
 DB 181 gnsqesvteqdsksdystlsstltlskadyekhkvyacevthqglsspvtksfnrgec 238

RESULT 4  
 AAW83034  
 ID AAW83034 standard; Protein: 238 AA.  
 XX  
 AC AAW83034;  
 XX  
 DT 15-MAR-1999 (first entry)  
 XX  
 DE Anti-Fas humanised antibody HFE7A light chain PDHH type.  
 XX  
 KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;  
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;  
 KW systemic lupus erythematosus; graft versus host disease;  
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;  
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;  
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;  
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;  
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
 KW transplant rejection; therapy.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FT Peptide 1..20 /label= Sig\_peptide  
 FT Protein 21..238 /label= Mat\_protein  
 FT Region 21..131 /label= Variable



Best Local Similarity 93.3%; Pred. No. 1.4e-58;  
Matches 222; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 METDTILLWLLVPGSTGDIVLTQSPSSLSASVGRVITTCASQSDYDGDSDYNNWY 60  
DB 1 metdtillwllwpgstgeivltqspgtlslspggratiscasqsdvdygdsymnw 60

QY 61 QOKPGKAPKLLIYAASNLGSGIPSRFSGSGSGTDTLTITISLQPEDFATYYCQSQSNEDEPR 120  
DB 61 qqkpgqaprllyaaasnlsgipdrfsgsgsgtdftltisrlepedfavyycqsgsnepr 120

QY 121 TFGOGTKVEIKRTVAASVFIFFPSDQLKSGTASVCLLNFFPRAKVQWKVDNALQS 180  
DB 121 tfgogtkleikrtvaasvfiFFPSDQLKSGTASVCLLNFFPRAKVQWKVDNALQS 180

QY 181 GNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
DB 181 gnsqesvteqdsksdystlslstltlskadyekhkvyacevthqglsspvtksfnrgec 238

RESULT 6  
AAW90927  
ID AAW90927 standard; Protein; 238 AA.  
XX  
AC AAW90927;  
XX  
DT 08-AUG-2000 (first entry)  
XX  
DE Humanised HFE7A designed light chain protein.  
XX  
KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;  
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;  
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
OS Synthetic.  
XX  
XX EP990663-A2.  
XX  
XX 05-APR-2000.  
XX  
XX 29-SEP-1999; 99EP-0307711.  
XX  
XX 30-SEP-1998; 98JP-0276881.  
XX  
XX 30-SEP-1998; 98JP-0276882.  
XX  
XX (SANY ) SANKYO CO LTD.  
XX  
XX  
XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
XX  
XX WPI; 2000-258930/23.  
XX  
XX N-PSDB; AAAL1614.  
XX  
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
XX inflammatory or autoimmune disease, induces apoptosis selectively in  
XX cells with abnormal Fas-Fas ligand systems -  
XX  
XX Claim 3; Page 141-142; 263pp; English.  
XX  
XX This invention describes a novel humanized anti-Fas antibody-like  
XX molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
XX ligand system, by binding to Fas on the cell surface, and prevents  
XX apoptosis in cells with a normal system, by inhibiting binding between  
XX Fas and its ligand. The products of the invention have anti-inflammatory,  
XX anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
XX immunomodulatory, dermatological, immunosuppressive, thyromimetic.

CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,  
CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce  
CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
CC inhibition of ligand binding. (I) are used to treat and/or prevent  
CC diseases associated with the Fas/Fas ligand system, especially systemic  
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
CC cells. They bind to both human and murine Fas, so can be evaluated in  
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
CC the native ligand, do not induce liver disease, and have reduced risk of  
CC inducing a human anti-murine antibody response. This sequence represents  
CC a humanised anti-Fas antibody HFE7A designed light chain which is used in  
CC the method described in the invention.  
XX  
SQ Sequence 238 AA;

Query Match 94.9%; Score 1174; DB 21; Length 238;  
Best Local Similarity 93.3%; Pred. No. 1.4e-58;  
Matches 222; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 METDTILLWLLVPGSTGDIVLTQSPSSLSASVGRVITTCASQSDYDGDSDYNNWY 60  
DB 1 metdtillwllwpgstgeivltqspgtlslspggratiscasqsdvdygdsymnw 60

QY 61 QOKPGKAPKLLIYAASNLGSGIPSRFSGSGSGTDTLTITISLQPEDFATYYCQSQSNEDEPR 120  
DB 61 qqkpgqaprllyaaasnlsgipdrfsgsgsgtdftltisrlepedfavyycqsgsnepr 120

QY 121 TFGOGTKVEIKRTVAASVFIFFPSDQLKSGTASVCLLNFFPRAKVQWKVDNALQS 180  
DB 121 tfgogtkleikrtvaasvfiFFPSDQLKSGTASVCLLNFFPRAKVQWKVDNALQS 180

QY 181 GNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
DB 181 gnsqesvteqdsksdystlslstltlskadyekhkvyacevthqglsspvtksfnrgec 238

RESULT 7  
AAW83031  
ID AAW83031 standard; Protein; 238 AA.  
XX  
AC AAW83031;  
XX  
DT 15-MAR-1999 (first entry)  
XX  
DE Anti-Fas humanised antibody HFE7A light chain HH type.  
XX  
KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;  
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;  
KW systemic lupus erythematosus; graft versus host disease;  
KW Sjorgen syndrome; pernicious anaemia; Addison's disease;  
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
KW rheumatoid arthritis; autoimmune haemolytic anaemia;  
KW myasthenia gravis; multiple sclerosis; Basedow's disease;  
KW thrombopenia purpura; insulin-dependent diabetes; allergy;  
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
KW transplant rejection; therapy.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX  
XX  
XX Key Location/Qualifiers  
XX Peptide 1..20  
XX /label= Sig\_peptide  
FT

FT Protein 21..238  
 FT /label= Mat\_protein  
 FT Region 21..131  
 FT /label= Variable  
 FT Region 132..238  
 FT /label= Constant  
 FT Region 44..58  
 FT /label= CDR\_L1  
 FT /note= "claim 9"  
 FT Region 74..80  
 FT /label= CDR\_L2  
 FT /note= "claim 9"  
 FT Region 113..121  
 FT /label= CDR\_L3  
 FT /note= "claim 9"  
 XX AU9859701-A.  
 XX 08-OCT-1998.  
 XX 30-MAR-1998; 98AU-0059701.  
 XX 08-OCT-1997; 97JP-0276064.  
 PR 01-APR-1997; 97JP-0082953.  
 PR 25-JUN-1997; 97JP-0169088.  
 XX (SANY ) SANKYO CO LTD.  
 XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;  
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;  
 XX WPI; 1998-543440/47.  
 DR N-PSDB; AAV70074.  
 XX New antibodies and proteins bind conserved epitope of Fas antigen -  
 PT used to evaluate drugs in animal models and to treat Fas-associated  
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
 PT myocarditis, hepatitis and AIDS  
 XX Claim 21; Page 199-199; 292pp; English.  
 XX This is the amino acid sequence of the HH type humanised light  
 CC chain of murine anti-human Fas monoclonal antibody HFE7A.  
 CC Humanisation of the murine sequence (see AA83042) entailed making  
 CC P47A, K49R, H80S, P81R, V82L, E84P, E85A, A87F and T89V amino acid  
 CC substitutions; these residues are conserved in the human light  
 CC chain (kappa chain). Host cell Escherichia coli PHSGH7 SANK 73497  
 CC harbors plasmid PHSGH7 carrying a fusion fragment of the humanised  
 CC HH type HFE7A light chain, and is deposited as FERM BP-6073  
 CC immunoglobulin kappa chain, and is deposited as FERM BP-6073  
 CC (claimed). The invention provides methods for producing humanised  
 CC antibodies by culturing host cells. Humanised versions of HFE7A  
 CC antibodies (see AA83031-37), like native HFE7A, are capable of inducing  
 CC apoptosis in abnormal cells expressing Fas, and of inhibiting  
 CC Fas-induced apoptosis in normal cells. The humanised antibodies  
 CC are used to evaluate, in animal models, treatments of diseases that  
 CC involve Fas/Fas ligand interactions, and also to treat such  
 CC diseases, including autoimmune disease (e.g. systemic lupus  
 CC erythematosus, Hashimoto's disease, graft versus host disease,  
 CC Sjogren syndrome, pernicious anaemia, Addison's disease,  
 CC scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid  
 CC arthritis, autoimmune haemolytic anaemia, sterility, myasthenia  
 CC gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura  
 CC and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,  
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic  
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).  
 XX Sequence 238 AA;  
 SQ

Query Match 94.5%; Score 1169; DB 19; Length 238;  
 Best Local Similarity 92.9%; Pred. No. 2.7e-58;  
 Matches 221; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 METDTILLWVLLWPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSTYNNWY 60  
 |||||  
 Db 1 metdtillwvllwpgstgdivltqspgtslsgperatlscasqsvdydgdsgymwy 60  
 QY 61 QOKPGKAPKLLIYAASNLESGIPSPRSGSGTDFTLTITSSIQPEDFATYYCOQSNEDPR 120  
 |||||  
 Db 61 gkpgqaprllyyaasnlesgipdrfsgsgsgtdftltisrlepafavyycqgsnedpr 120  
 QY 121 TFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180  
 |||||  
 Db 121 tfggtrleikrtvaapsvfifppsqdeqlksgtasvvcvllnnfypreakvqwkvdnals 180  
 QY 181 GNSQESVTEQDSKDSYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 238  
 |||||  
 Db 181 gnsqesvteqdsksdstyslsstltlskadyekhykhyacevthqglsspvtksfnrgec 238  
 RESULT 8  
 AAB14772  
 ID AAB14772 standard; Protein; 238 AA.  
 XX  
 AC AAB14772;  
 XX  
 DT 24-NOV-2000 (first entry)  
 XX  
 DE Humanised anti-Fas antibody light chain, SEQ ID NO:50.  
 XX  
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;  
 KW murine; humanised antibody; complementarity determining region; CDR;  
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;  
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;  
 KW hepatitis; AIDS; graft rejection; light chain.  
 XX  
 OS Chimeric - Mus musculus.  
 OS Chimeric - Homo sapiens.  
 XX  
 PN JP2000169393-A.  
 XX  
 PD 20-JUN-2000.  
 XX  
 PF 30-SEP-1999; 99JP-0278301.  
 XX  
 PR 30-SEP-1998; 98JP-0276883.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 DR WPI; 2000-485645/43.  
 DR N-PSDB; AAA72124.  
 XX  
 PT Preventive or treating agent for the diseases caused by an abnormality  
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains  
 PT anti-Fas antibody -  
 PS Claim 20; Page 78-79; 139pp; Japanese.  
 CC The invention relates to compositions for the prevention or treatment  
 CC or diseases caused by an abnormality in the Fas/Fas ligand system  
 CC containing an anti-Fas antibody as the active component. The anti-Fas  
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,  
 CC or a humanised version of HFE7A containing identical CDRs  
 CC (complementarity determining regions) to antibody HFE7A. Via its  
 CC interaction with Fas, the antibody of the invention acts as a modulator  
 CC of apoptosis. The compositions of the invention may therefore be used in  
 CC the treatment or prevention of conditions such as autoimmune diseases,  
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,  
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS  
 CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778  
 CC represent the light chains of several humanised HFE7A-derived anti-Fas  
 CC antibodies.  
 XX Sequence 238 AA;  
 SQ

Query Match 94.5%; Score 1169; DB 21; Length 238;  
 Best Local Similarity 92.9%; Pred. No. 2.7e-58;  
 Matches 221; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 1 METDTILLWVLLWVPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSVVDGDSYMNWY 60  
 Db 1 metdtillwvllwvpgstgdivltqspgtlslspperatlsckasqsvdydgdsmwmy 60

Qy 61 QOKPCKAPKLIYAASNLSEGIPTSPFSGSGSGTDFTLTISLQPDFAFYVCQOSNEPR 120  
 Db 61 qkpgqaprllyaaasnlsegiptspfgsgsgtfdtlisrlpadfafvyyccqsgnepr 120

Qy 121 TFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPRKAVQWKVDNALQ 180  
 Db 121 tfggqtrleikrtvaapsvfifppsqdeqlksgtasvvcclnnfyprkavqwkvdnalq 180

Qy 181 GNSQESVTEQDSKSTYSLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 238  
 Db 181 gnsqesvteqdsksstyslsstltlskadyekhkyacevthqglsspvtksfnrgec 238

RESULT 9  
 AA90922  
 ID AAW90922 standard; Protein; 238 AA.  
 XX  
 AC AAW90922;  
 XX  
 DT 08-AUG-2000 (first entry)  
 XX

Humanised anti-Fas antibody HFE7A light chain HH type protein.

Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
 anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;  
 dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
 nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;  
 hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
 Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
 Synthetic.  
 OS  
 XX  
 PN EP990663-A2.  
 XX  
 PD 05-APR-2000.  
 XX  
 PF 29-SEP-1999; 99EP-0307711.  
 XX  
 PR 30-SEP-1998; 98JP-0276881.  
 XX  
 PR 30-SEP-1998; 98JP-0276882.  
 XX  
 FA (SANY ) SANKYO CO LTD.  
 XX  
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 PI  
 XX WPI: 2000-258930/23.  
 XX  
 DR N-PSDB; AAA11562.  
 XX

New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 inflammatory or autoimmune disease, induces apoptosis selectively in  
 cells with abnormal Fas-Fas ligand systems

Example reference 14; Page 114-115; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like  
 molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 ligand system, by binding to Fas on the cell surface, and prevents  
 apoptosis in cells with a normal system, by inhibiting binding between

CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,  
 CC antiarteriosclerotic, cardiac and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody HFE7A light chain HH type which is used in  
 CC the method described in the invention.  
 XX  
 SQ Sequence 238 AA;

Query Match 94.5%; Score 1169; DB 21; Length 238;  
 Best Local Similarity 92.9%; Pred. No. 2.7e-58;  
 Matches 221; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 1 METDTILLWVLLWVPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSVVDGDSYMNWY 60  
 Db 1 metdtillwvllwvpgstgdivltqspgtlslspperatlsckasqsvdydgdsmwmy 60

Qy 61 QOKPCKAPKLIYAASNLSEGIPTSPFSGSGSGTDFTLTISLQPDFAFYVCQOSNEPR 120  
 Db 61 qkpgqaprllyaaasnlsegiptspfgsgsgtfdtlisrlpadfafvyyccqsgnepr 120

Qy 121 TFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPRKAVQWKVDNALQ 180  
 Db 121 tfggqtrleikrtvaapsvfifppsqdeqlksgtasvvcclnnfyprkavqwkvdnalq 180

Qy 181 GNSQESVTEQDSKSTYSLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 238  
 Db 181 gnsqesvteqdsksstyslsstltlskadyekhkyacevthqglsspvtksfnrgec 238

RESULT 10  
 AAW83032  
 ID AAW83032 standard; Protein; 238 AA.  
 XX  
 AC AAW83032;  
 XX  
 DT 15-MAR-1999 (first entry)  
 XX

Anti-Fas humanised antibody HFE7A light chain HM type.

HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;  
 apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;  
 systemic lupus erythematosus; graft versus host disease;  
 Sjorgen syndrome; pernicious anaemia; Addison's disease;  
 scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
 rheumatoid arthritis; autoimmune haemolytic anaemia;  
 myasthenia gravis; multiple sclerosis; Basedow's disease;  
 thrombopenia purpura; insulin-dependent diabetes; allergy;  
 atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
 glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
 transplant rejection; therapy.  
 XX  
 XX Homo sapiens.  
 OS  
 OS Synthetic.  
 XX

FH Key Location/Qualifiers  
 FT Peptide 1..20  
 FT Protein /label= Sig\_peptide  
 FT 21..238  
 FT /label= Mat\_protein  
 FT 21..131  
 FT /label= Variable  
 FT 132..238  
 FT Region /label= Constant  
 FT 44..58  
 FT /label= CDR\_L1  
 FT /note= "claim 9"  
 FT 74..80  
 FT /label= CDR\_L2  
 FT /note= "claim 9"  
 FT 113..121  
 FT /label= CDR\_L3  
 FT /note= "claim 9"  
 PN AU9859701-A.  
 XX  
 XX 08-OCT-1998.  
 XX  
 PF 30-MAR-1998; 98AU-0059701.  
 XX  
 XX 08-OCT-1997; 97JP-0276064.  
 PR 01-APR-1997; 97JP-0082953.  
 PR 25-JUN-1997; 97JP-0169088.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 PI Akio S, Hideyuki H, Hiroko Y, Jun O, Kimhisa I;  
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;  
 DR WPI: 1998-543440/47.  
 DR N-PSDB; AA70075.  
 XX  
 PT New antibodies and proteins bind conserved epitope of Fas antigen -  
 PT used to evaluate drugs in animal models and to treat Fas-associated  
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
 PT myocarditis, hepatitis and AIDS  
 XX  
 PS Claim 21; Page 200; 292pp; English.  
 XX  
 CC This is the amino acid sequence of the HM type humanised light  
 CC chain of murine anti-human Fas monoclonal antibody HFE7A.  
 CC Humanisation of the murine sequence (see AA83042) entailed making  
 CC P47A and K49R amino acid substitutions; these residues are  
 CC conserved in the human light (kappa) chain. Host cell E. coli  
 CC PHSGHM17 SANK 73597 harbors plasmid PHSGHM17 carrying a fusion  
 CC fragment of the humanised HM type HFE7A light chain and DNA  
 CC encoding the region of human immunoglobulin kappa chain, and is  
 CC deposited as FERM BP-6072 (claimed). The invention provides  
 CC methods for producing humanised antibodies by culturing host  
 CC cells. Humanised versions of HFE7A (see AA83031-37), like native  
 CC HFE7A, are capable of inducing apoptosis in abnormal cells  
 CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal  
 CC cells. The humanised antibodies are used to evaluate, in animal  
 CC models, treatments of diseases that involve Fas/Fas ligand  
 CC interactions, and also to treat such diseases, including autoimmune  
 CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,  
 CC graft versus host disease, Sjogren syndrome, pernicious anaemia,  
 CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,  
 CC sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,  
 CC thrombopenia purpura and insulin-dependent diabetes), allergies,  
 CC atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular  
 CC nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant  
 CC rejection (all claimed).  
 XX  
 SQ Sequence 238 AA;

Query Match 93.5%; Score 1156; DB 19; Length 238;  
 Best Local Similarity 92.0%; Pred. No. 1.4e-57;  
 Matches 219; Conservative 10; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 METDITLLWVLLWPGSGDVIIVTQSPSSLSASVGDRTVITCKASQSDYDGDSYNNWY 60  
 DB 1 metdtillwvllwpgsgtdviltqspgtlsipgeratlsckasqsvdygdsgymwy 60  
 QY 61 QOKPGKAPKLLIYAASNLESIGIPRSFGSGGTDFTLTSSLOPEDFATVYCOQSNEDPR 120  
 DB 61 qqkpgqaprllyaaanlesigipdrfsgsgsgtdftltshpveedaatyycqgsnedpr 120  
 QY 121 TFGQGTKEIKRTVAAPSVFIFFPSDEQLKSGTASVYVCLNNFYPREAKYQWVDNALQS 180  
 DB 121 tfggtrleikrtvaapsvfi fppsdeqlksgtasvvc llnnfypreakvqwvdnalqs 180  
 QY 181 GNSQSVTEQDSKDSYSLSSSTLTLSKADYEKHVKYACEVTHQGLSSPVTYKSNRREC 238  
 DB 181 gnsqsvteqdkdstyslsstltlskadyekkhvyacevthqglspvtksnrgec 238  
 RESULT 11  
 AAB14773  
 ID AAB14773 standard; Protein; 238 AA.  
 XX  
 AC AAB14773;  
 XX  
 DT 24-NOV-2000 (first entry)  
 XX  
 DE Humanised anti-Fas antibody light chain, SEQ ID NO:52.  
 XX  
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;  
 KW murine; humanised antibody; complementarity determining region; CDR;  
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;  
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;  
 KW hepatitis; AIDS; graft rejection; light chain.  
 XX  
 OS Chimeric - Mus musculus.  
 OS Chimeric - Homo sapiens.  
 XX  
 PN JP2000169393-A.  
 XX  
 PD 20-JUN-2000.  
 XX  
 PF 30-SEP-1999; 99JP-0278301.  
 XX  
 PR 30-SEP-1999; 99JP-0276883.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 DR WPI: 2000-485645/43.  
 DR N-PSDB; AA72125.  
 XX  
 PT Preventive or treating agent for the diseases caused by an abnormality  
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains  
 PT anti-Fas antibody -  
 PS  
 PS Claim 20; Page 80-81; 139pp; Japanese.  
 CC  
 CC The invention relates to compositions for the prevention or treatment  
 CC or diseases caused by an abnormality in the Fas/Fas ligand system  
 CC containing an anti-Fas antibody as the active component. The anti-Fas  
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,  
 CC or a humanised version of HFE7A containing identical CDRs  
 CC (complementarity determining regions) to antibody HFE7A. Via its  
 CC interaction with Fas, the antibody of the invention acts as a modulator  
 CC of apoptosis. The compositions of the invention may therefore be used in  
 CC the treatment or prevention of conditions such as autoimmune diseases,  
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,  
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS  
 CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778  
 CC represent the light chains of several humanised HFE7A-derived anti-Fas



```

CC antibodies.
XX
SQ Sequence 238 AA;

Query Match 93.5%; Score 1156; DB 21; Length 238;
Best Local Similarity 92.0%; Pred. No. 1.4e-57;
Matches 219; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy 1 METDTILLWVLLWPGSTGDIVLTQSPSSLSASVGRVTITCKASQSDVDGDSYNNWY 60
Db 1 metdtillwvllwpgstgdivltqspgtlslpgeratiscasqsdvdgdsynnwy 60

Qy 61 QOKPGKAPKLLIYAASNLGSGIPRFGSGSGTDTFTITISLQPEDFATYYCQSQSNEPDR 120
Db 61 qkpgqaprllyaaasnlsgipdrfsgsgsgtdftltihpveedaatyyccqgsneqdr 120

Qy 121 TFGGOTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPRKAKVQWKVDNALQS 180
Db 121 tfgggtleikrtvaapsvfifppsdqksgtasvvcclnnfyprakvqwkvdnalqs 180

Qy 181 GNSQESVTEQDSKDYSLSTLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 gnsqesvteqskdstylsstltlslkadyekhkvyacevthqglsspvtksfnrgec 238

RESULT 12
AAW90923
ID AAW90923 standard; Protein; 238 AA.
AC AAW90923;
XX
XX 08-AUG-2000 (first entry)
XX
XX Humanised anti-Fas antibody HFE7A light chain HM type protein.
DE
DE Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX
OS Synthetic.
XX
XX EP990663-A2.
XX
XX 05-APR-2000.
XX
XX 29-SEP-1999; 99EP-0307711.
XX
XX 30-SEP-1998; 98JP-0276881.
XX
XX 30-SEP-1998; 98JP-0276882.
XX
XX (SANY ) SANKYO CO LTD.
XX
XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX WPI; 2000-258930/23.
XX
XX N-PSDB; AAA11563.
XX
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
XX inflammatory or autoimmune disease, induces apoptosis selectively in
XX cells with abnormal Fas-Fas ligand systems
XX
XX Example reference 14; Page 117-118; 263pp; English.
XX
XX This invention describes a novel humanized anti-Fas antibody-like
XX

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```

CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin,
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a humanised anti-Fas antibody HFE7A light chain HM type which is used in
CC the method described in the invention.
XX
SQ Sequence 238 AA;

Query Match 93.5%; Score 1156; DB 21; Length 238;
Best Local Similarity 92.0%; Pred. No. 1.4e-57;
Matches 219; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy 1 METDTILLWVLLWPGSTGDIVLTQSPSSLSASVGRVTITCKASQSDVDGDSYNNWY 60
Db 1 metdtillwvllwpgstgdivltqspgtlslpgeratiscasqsdvdgdsynnwy 60

Qy 61 QOKPGKAPKLLIYAASNLGSGIPRFGSGSGTDTFTITISLQPEDFATYYCQSQSNEPDR 120
Db 61 qkpgqaprllyaaasnlsgipdrfsgsgsgtdftltihpveedaatyyccqgsneqdr 120

Qy 121 TFGGOTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPRKAKVQWKVDNALQS 180
Db 121 tfgggtleikrtvaapsvfifppsdqksgtasvvcclnnfyprakvqwkvdnalqs 180

Qy 181 GNSQESVTEQDSKDYSLSTLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 gnsqesvteqskdstylsstltlslkadyekhkvyacevthqglsspvtksfnrgec 238

RESULT 13
AAW83035
ID AAW83035 standard; Protein; 238 AA.
XX
XX AAW83035;
XX
XX 15-MAR-1999 (first entry)
XX
XX Anti-Fas humanised antibody HFE7A light chain PDHM type.
XX
XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
KW systemic lupus erythematosus; graft versus host disease;
KW Sjorgen syndrome; pernicious anaemia; Addison's disease;
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KW rheumatoid arthritis; autoimmune haemolytic anaemia;
KW myasthenia gravis; multiple sclerosis; Basedow's disease;
KW thrombopenia purpura; insulin-dependent diabetes; allergy;
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KW transplant rejection; therapy.
XX

```

OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key  
 FH Peptide  
 FT /label= Sig\_peptide  
 FT 21..238  
 FT Protein  
 FT /label= Mat\_protein  
 FT 21..131  
 FT Region  
 FT /label= Variable  
 FT 132..238  
 FT Region  
 FT /label= Constant  
 FT 44..58  
 FT /label= CDR\_L1  
 FT /note= "claim 9"  
 FT 74..80  
 FT Region  
 FT /label= CDR\_L2  
 FT /note= "claim 9"  
 FT 113..121  
 FT Region  
 FT /label= CDR\_L3  
 FT /note= "claim 9"  
 XX  
 XX AU9859701-A.  
 XX  
 XX 08-OCT-1998.  
 XX  
 XX 30-MAR-1998; 98AU-0059701.  
 XX  
 XX 08-OCT-1997; 97JP-0276064.  
 XX 01-APR-1997; 97JP-0082953.  
 XX 25-JUN-1997; 97JP-0169088.  
 XX  
 XX (SANY ) SANKYO CO LTD.  
 XX  
 XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;  
 XX Masahiko O, Nobufusa S, Shin Y, Tohru T;  
 XX  
 XX WPI; 1998-543440/47.  
 XX N-PSDB; AAV70078.  
 XX  
 XX New antibodies and proteins bind conserved epitope of Fas antigen -  
 XX used to evaluate drugs in animal models and to treat Fas-associated  
 XX diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
 XX myocarditis, hepatitis and AIDS  
 XX  
 XX Claim 21; Page 220-221; 292pp; English.  
 XX  
 XX This is the amino acid sequence of the PDHM type humanised light  
 XX chain of murine anti-human Fas monoclonal antibody HFE7A.  
 XX Humanisation of the murine sequence (see AAW83042) entailed making  
 XX D1E, P47A, K49R and R107K amino acid substitutions; these  
 XX residues are conserved in the human light (kappa) chain. Host  
 XX cell Escherichia coli pSHM2 SANK 70198 harbors plasmid pSHM2  
 XX carrying a fusion of the humanised PDHM type HFE7A light chain and  
 XX DNA encoding the region of human immunoglobulin kappa chain, and is  
 XX deposited as FERM BP-6272 (claimed). The invention provides  
 XX methods for producing humanised antibodies by culturing host  
 XX cells. Humanised versions of HFE7A (see AAW83031-37), like native  
 XX HFE7A, are capable of inducing apoptosis in abnormal cells  
 XX expressing Fas, and of inhibiting Fas-induced apoptosis in normal  
 XX cells. The humanised antibodies are used to evaluate, in animal  
 XX models, treatments of diseases that involve Fas/Fas ligand  
 XX interactions, and also to treat such diseases, including autoimmune  
 XX disease (e.g. systemic lupus erythematosus, Hashimoto's disease,  
 XX graft versus host disease, Sjogren syndrome, pernicious anaemia,  
 XX Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 XX disease, rheumatoid arthritis, autoimmune haemolytic anaemia,  
 XX sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,  
 XX thrombopenia purpura and insulin-dependent diabetes), allergies,  
 XX atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular  
 XX nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant  
 XX rejection (all claimed).

SQ Sequence 238 AA;  
 Query Match 93.4%; Score 1155; DB 19; Length 238;  
 Best Local Similarity 92.0%; Pred. NO. 1.6e-57;  
 Matches 219; Conservative 10; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 METDTILLVLLWPGSTGDIVLTQSPSLSASVGDRTVTITCKASQSDVDYDGSYNNWY 60  
 Db 1 metdtillvllwpgstgeivltqspgtlsipgeratlsckasqsdvdgdsymnw 60  
 QY 61 QQKPGKAPKAPLLIYAASNLESGIPSRFSGSGGTDFLTITSSLPEDFATYYCOOSNEDPR 120  
 Db 61 qqkpggqprlllyaaasnlesgipdrfsgsggtfdltithpveedaatyccqgsnedpr 120  
 QY 121 TFCQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNYPRREAKVQWKVDNALQS 180  
 Db 121 tfcggtkleikrtvaapsvfifppsdeqiksgtasvvcllnnfybreakvqwkvdnalqs 180  
 QY 181 GNSQESVTEQDSKDSYSLSSSTLTLSKADYERKHVYACEVTHQGLSPVTKSFNRGEC 238  
 Db 181 gnsqesvteqdsksdyslsstltlskadyekkhvyacevthqglspvtksfnrgec 238  
 RESULT 14  
 AAB14778  
 ID AAB14778 standard; Protein; 238 AA.  
 AC AAB14778;  
 XX  
 DT 24-NOV-2000 (first entry)  
 XX  
 DE Humanised anti-Fas antibody light chain, SEQ ID NO:109.  
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;  
 KW murine; humanised antibody; complementarity determining region; CDR;  
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;  
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;  
 KW hepatitis; AIDS; graft rejection; light chain.  
 OS Chimeric - Mus musculus.  
 OS Chimeric - Homo sapiens.  
 PN JP2000169393-A.  
 XX  
 PD 20-JUN-2000.  
 XX  
 PF 30-SEP-1999; 99JP-0278301.  
 XX  
 PR 30-SEP-1998; 98JP-0276883.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 DR WPI; 2000-485645/43.  
 DR N-PSDB; AAA72177.  
 XX  
 PT Preventive or treating agent for the diseases caused by an abnormality  
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains  
 PT anti-Fas antibody -  
 XX  
 PS Claim 20; Page 103; 139pp; Japanese.  
 XX  
 XX The invention relates to compositions for the prevention or treatment  
 XX of diseases caused by an abnormality in the Fas/Fas ligand system  
 XX containing an anti-Fas antibody as the active component. The anti-Fas  
 XX antibody is either the murine anti-human Fas monoclonal antibody HFE7A,  
 XX or a humanised version of HFE7A containing identical CDRs  
 XX (complementarity determining regions) to antibody HFE7A. Via its  
 XX interaction with Fas, the antibody of the invention acts as a modulator  
 XX of apoptosis. The compositions of the invention may therefore be used in  
 XX the treatment or prevention of conditions such as autoimmune diseases,  
 XX allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,

CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS  
CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778  
CC represent the light chains of several humanised HFE7A-derived anti-Fas  
XX antibodies.  
SQ Sequence 238 AA;

Query Match 93.4%; Score 1155; DB 21; Length 238;  
Best Local Similarity 92.0%; Pred. No. 1.6e-57;  
Matches 219; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 METDPIILLWVLLWVPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSVVDYDGDSYMNNY 60  
DB 1 metdtillwllwvpgstgeivltqspgtislsperatlsckasqsvdydgdSYMNNY 60

QY 61 QOKPKAKPLLIYAASNLSESGIPSRFSGSGTDFTLTISSLOPEDFATYYCQGSNEQDP 120  
DB 61 qkpgqaprllyaaasnlsgipdrfsgsgtdftltihpveedaatyyccgsneqdp 120

QY 121 TFGQGTKEIKRTVAAPSVFIPPPDEQLKSGTASVCLNNFYPREAKVQKVDNALQS 180  
DB 121 tfgggtkieikrtvaapsvfifppsdqlksgtasvclnnfyprcakvqkvdnalqs 180

QY 181 GNSQESVTEQDSKSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238  
DB 181 gnsqesvteqdsksdtsylsstltlskadyekhkyvacevthqglsppvtskfsnrgec 238

RESULT 15  
AAW90928  
ID AAW90928 standard; Protein: 238 AA.  
XX  
XX AAW90928;  
XX  
XX 08-AUG-2000 (first entry)  
XX  
XX Humanised HFE7A designed light chain protein #2.  
XX  
XX Fas; antibody: human; anti-inflammatory; anti-anemic; antidiabetic;  
XX anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;  
XX dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
XX nephrotropic; antinfertility; neuroprotective; antirheosclerotic;  
XX hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
XX Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
XX Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
XX Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
XX multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
XX insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
XX cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
XX  
XX Synthetic.  
XX  
XX EP990563-A2.  
XX  
XX 05-APR-2000.  
XX  
XX 29-SEP-1999; 99EP-0307711.  
XX  
XX 30-SEP-1998; 98JP-0276881.  
XX  
XX 30-SEP-1998; 98JP-0276882.  
XX  
XX (SANY ) SANKYO CO LTD.  
XX  
XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
XX  
XX WPI; 2000-258930/23.  
XX  
XX N-PSDB; AAA11615.  
XX  
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
XX inflammatory or autoimmune disease, induces apoptosis selectively in  
XX cells with abnormal Fas-Fas ligand systems

PS  
XX Example reference 21; Page 144-145; 263pp; English.  
XX This invention describes a novel humanized anti-Fas antibody-like  
XX molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
XX ligand system, by binding to Fas on the cell surface, and prevents  
XX apoptosis in cells with a normal system, by inhibiting binding between  
XX Fas and its ligand. The products of the invention have anti-inflammatory,  
XX anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
XX immunomodulatory, dermatologic, immunosuppressive, thyromimetic,  
XX antirheumatic, nephrotropic, antinfertility, neuroprotective,  
XX antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce  
XX apoptosis by binding to cell surface Fas or inhibit it by competitive  
XX inhibition of ligand binding. (I) are used to treat and/or prevent  
XX diseases associated with the Fas/Fas ligand system, especially systemic  
XX lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
XX versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
XX anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
XX disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
XX multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
XX dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
XX cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
XX (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
XX inhibit apoptosis in normal cells but selectively induce it in abnormal  
XX cells. They bind to both human and murine Fas, so can be evaluated in  
XX murine disease models. (I) act on the active site of Fas, i.e. they mimic  
XX the native ligand, do not induce liver disease, and have reduced risk of  
XX inducing a human anti-murine antibody response. This sequence represents  
XX a humanised anti-Fas antibody HFE7A designed light chain which is used in  
XX the method described in the invention.  
XX  
XX Sequence 238 AA;

Query Match 93.4%; Score 1155; DB 21; Length 238;  
Best Local Similarity 92.0%; Pred. No. 1.6e-57;  
Matches 219; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 METDPIILLWVLLWVPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSVVDYDGDSYMNNY 60  
DB 1 metdtillwllwvpgstgeivltqspgtislsperatlsckasqsvdydgdSYMNNY 60

QY 61 QOKPKAKPLLIYAASNLSESGIPSRFSGSGTDFTLTISSLOPEDFATYYCQGSNEQDP 120  
DB 61 qkpgqaprllyaaasnlsgipdrfsgsgtdftltihpveedaatyyccgsneqdp 120

QY 121 TFGQGTKEIKRTVAAPSVFIPPPDEQLKSGTASVCLNNFYPREAKVQKVDNALQS 180  
DB 121 tfgggtkieikrtvaapsvfifppsdqlksgtasvclnnfyprcakvqkvdnalqs 180

QY 181 GNSQESVTEQDSKSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238  
DB 181 gnsqesvteqdsksdtsylsstltlskadyekhkyvacevthqglsppvtskfsnrgec 238

Search completed: August 14, 2002, 15:15:35  
Job time: 833 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 15:17:03 ; Search time 82.88 Seconds  
(without alignments)  
70.141 Million cell updates/sec

Title: US-09-499-662-131

Perfect score: 1237

Sequence: 1 METDTILLWVLLLVPGSTG.....EVTHQGLSPVTKSFNRGEC 238

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

- 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1113	90.0	218	5	PCT-US96-13152-2
2	1099	88.8	218	2	US-08-887-352B-13
3	1099	88.8	218	3	US-08-466-151-9
4	1099	88.8	218	4	US-09-109-207C-13
5	1099	88.8	218	4	US-09-296-005-13
6	1099	88.8	218	4	US-08-466-163B-9
7	1076	87.0	218	4	US-09-282-505-1
8	1076	87.0	218	4	US-09-054-255-1
9	1073	86.7	218	2	US-08-887-352B-15
10	1073	86.7	218	2	US-08-887-352B-17
11	1073	86.7	218	2	US-08-887-352B-19
12	1073	86.7	218	2	US-08-887-352B-24
13	1073	86.7	218	4	US-09-109-207C-15
14	1073	86.7	218	4	US-09-109-207C-17
15	1073	86.7	218	4	US-09-109-207C-19
16	1073	86.7	218	4	US-09-109-207C-24
17	1073	86.7	218	4	US-09-296-005-15
18	1073	86.7	218	4	US-09-296-005-17
19	1073	86.7	218	4	US-09-296-005-19
20	1073	86.7	218	4	US-09-296-005-24
21	1021.5	82.6	233	2	US-07-934-373C-25
22	1021.5	82.6	233	3	US-08-437-642B-25
23	1021.5	82.6	233	5	PCT-US93-07832-25
24	1018	82.3	214	2	US-07-934-373C-39
25	1018	82.3	214	3	US-08-437-642B-39
26	1018	82.3	214	5	PCT-US93-07832-39
27	1013	81.9	214	2	US-07-934-373C-40

28	1013	81.9	214	2	US-08-788-800-11	Sequence 11, Appl
29	1013	81.9	214	3	US-08-437-642B-40	Sequence 40, Appl
30	1013	81.9	214	3	US-09-097-309-2	Sequence 2, Appl
31	1013	81.9	214	4	US-09-097-171A-2	Sequence 2, Appl
32	1013	81.9	214	5	PCT-US93-07832-40	Sequence 40, Appl
33	1013	81.9	237	3	US-09-097-309-6	Sequence 6, Appl
34	1013	81.9	237	4	US-09-097-171A-10	Sequence 10, Appl
35	1013	81.9	237	4	US-09-422-712B-2	Sequence 2, Appl
36	1013	81.9	237	4	US-09-607-756-2	Sequence 2, Appl
37	1009.5	81.6	242	3	US-09-027-449-62	Sequence 62, Appl
38	1009.5	81.6	242	4	US-09-026-985-62	Sequence 62, Appl
39	1008.5	81.5	235	4	US-09-171-945-97	Sequence 97, Appl
40	1008.5	81.5	242	3	US-09-027-449-51	Sequence 51, Appl
41	1008.5	81.5	242	3	US-08-804-444A-51	Sequence 51, Appl
42	1008.5	81.5	242	4	US-09-026-985-51	Sequence 51, Appl
43	1005.5	81.3	219	3	US-09-027-449-72	Sequence 72, Appl
44	1005.5	81.3	219	4	US-09-026-985-72	Sequence 72, Appl
45	1005.5	81.3	242	3	US-09-027-449-56	Sequence 56, Appl

ALIGNMENTS

RESULT 1

PCT-US96-13152-2

; Sequence 2, Application PC/TUS9613152

; GENERAL INFORMATION:

; APPLICANT: Martin, Ulrich, et al.

; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ f

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felfe & Lynch

; ADDRESSEE: Attn: Norman D. Hanson

; STREET: 805 Third Avenue

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Computer Disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/13152

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/578,953

; FILING DATE: 27-Dec-95

; APPLICATION NUMBER: EP 95 112 895.8

; FILING DATE: 17-Aug-95

; APPLICATION NUMBER: EP 95 114 969.9

; FILING DATE: 19-Sep-95

; ATTORNEY/AGENT INFORMATION:

; NAME: Norman D. Hanson

; REGISTRATION NUMBER: 30,946

; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 688-9200

; TELEFAX: (212) 838-3884

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 218

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US96-13152-2

Query Match 90.0%; Score 1113; DB 5; Length 218;  
Best Local Similarity 98.6%; Pred. No. 5.3e-88;

Matches 215; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQOKPGKAPKLLIYAASNLES 80  
|| :|||||  
Db 1 DIQMTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQOKPGKAPKLLIYAASNLES 60

QY 81 GIPSRFSGSGSGTDFTLTITSSLOPEDFATYYCQSQNEDPRTFGQGTKEIKRTVAAPSVE 140  
:|||||  
Db 61 GIPSRFSGSGSGTDFTLTITSSLOPEDFATYYCQSQNEDPRTFGQGTKEIKRTVAAPSVE 120

QY 141 IPPPSDEQLKSGTASVVCVLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYSLS 200  
:|||||  
Db 121 IPPPSDEQLKSGTASVVCVLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYSLS 180

QY 201 STLTLSKADYEHKHYACVETHQGLSSPVTKSFNRGEC 238  
:|||||  
Db 181 STLTLSKADYEHKHYACVETHQGLSSPVTKSFNRGEC 218

RESULT 2  
US-08-887-352B-13  
; Sequence 13, Application US/08887352B  
; Patent No. 5994511  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IGE Antibodies and Method of  
; TITLE OF INVENTION: Improving Polypeptides  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,352B  
; FILING DATE: 03-Jul-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P1123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 218 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-887-352B-13

Query Match 88.8%; Score 1099; DB 2; Length 218;  
Best Local Similarity 97.2%; Pred. No. 8.3e-87;  
Matches 212; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQOKPGKAPKLLIYAASNLES 80  
|| :|||||  
Db 1 DIQLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQOKPGKAPKLLIYAASNLES 60

QY 81 GIPSRFSGSGSGTDFTLTITSSLOPEDFATYYCQSQNEDPRTFGQGTKEIKRTVAAPSVE 140  
:|||||  
Db 61 GIPSRFSGSGSGTDFTLTITSSLOPEDFATYYCQSQNEDPRTFGQGTKEIKRTVAAPSVE 120

QY 141 IPPPSDEQLKSGTASVVCVLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYSLS 200  
:|||||

Db 121 IPPPSDEQLKSGTASVVCVLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYSLS 180

QY 201 STLTLSKADYEHKHYACVETHQGLSSPVTKSFNRGEC 238  
:|||||  
Db 181 STLTLSKADYEHKHYACVETHQGLSSPVTKSFNRGEC 218

RESULT 3  
US-08-466-151-9  
; Sequence 9, Application US/08466151  
; Patent No. 6037453  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,151  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/466163  
; FILING DATE: 06-Jun-1995  
; APPLICATION NUMBER: 08/405617  
; FILING DATE: 15-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/185899  
; FILING DATE: 26-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/879495  
; FILING DATE: 07-MAY-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/744768  
; FILING DATE: 14-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P0718P2C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 218 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-466-151-9

Query Match 88.8%; Score 1099; DB 3; Length 218;  
Best Local Similarity 97.2%; Pred. No. 8.3e-87;  
Matches 212; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQOKPGKAPKLLIYAASNLES 80  
|| :|||||  
Db 1 DIQLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQOKPGKAPKLLIYAASNLES 60

QY 81 GIPSRFSGSGSGTDFTLTITSSLOPEDFATYYCQSQNEDPRTFGQGTKEIKRTVAAPSVE 140  
:|||||  
Db 61 GIPSRFSGSGSGTDFTLTITSSLOPEDFATYYCQSQNEDPRTFGQGTKEIKRTVAAPSVE 120

QY 141 IFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 200  
Db 121 IFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180

QY 201 STLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238  
Db 181 STLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 218

RESULT 4  
US-09-109-207C-13  
; Sequence 13, Application US/09109207C  
; Patent No. 6172213  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide  
; FILE REFERENCE: P1123R1  
; CURRENT APPLICATION NUMBER: US/09/109,207C  
; CURRENT FILING DATE: 1998-08-30  
; PRIOR APPLICATION NUMBER: US 60/051,554  
; PRIOR FILING DATE: 1997-07-03  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 13  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Artificial  
; NAME/KEY: Artificial  
; LOCATION: 1-218  
; OTHER INFORMATION: Light chain sequence derived from MAE11  
US-09-109-207C-13

Query Match 88.8%; Score 1099; DB 4; Length 218;  
Best Local Similarity 97.2%; Pred. No. 8.3e-87;  
Matches 212; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYVDYDGDSDYNNYQOKPGKAPKLLIYAASNLES 80  
Db 1 DIQLTQSPSSLSASVGDRTVITCKASQSYVDYDGDSDYNNYQOKPGKAPKLLIYAASYLE 60  
QY 81 GIPSRFSGSGSTDFLTITSSLPQEDFATYYCQSHEDPRTFGQGTKEIKRTVAAPSVF 140  
Db 61 GVPFRSGSGSTDFLTITSSLPQEDFATYYCQSHEDPRTFGQGTKEIKRTVAAPSVF 120  
QY 141 IFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 200  
Db 121 IFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180  
QY 201 STLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238  
Db 181 STLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 218

RESULT 5  
US-09-296-005-13  
; Sequence 13, Application US/09296005  
; Patent No. 6290957  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides  
; FILE REFERENCE: P1123C1r  
; CURRENT APPLICATION NUMBER: US/09/296,005  
; CURRENT FILING DATE: 1999-04-21  
; EARLIER APPLICATION NUMBER: US 08/887,352  
; EARLIER FILING DATE: 1997-07-02  
; NUMBER OF SEQ ID NOS: 26  
; SEQ ID NO 13  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Artificial  
; NAME/KEY: Artificial

; LOCATION: 1-218  
; OTHER INFORMATION: Light chain sequence derived from MAE11  
US-09-296-005-13

Query Match 88.8%; Score 1099; DB 4; Length 218;  
Best Local Similarity 97.2%; Pred. No. 8.3e-87;  
Matches 212; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYVDYDGDSDYNNYQOKPGKAPKLLIYAASNLES 80  
Db 1 DIQLTQSPSSLSASVGDRTVITCKASQSYVDYDGDSDYNNYQOKPGKAPKLLIYAASYLE 60  
QY 81 GIPSRFSGSGSTDFLTITSSLPQEDFATYYCQSHEDPRTFGQGTKEIKRTVAAPSVF 140  
Db 61 GVPFRSGSGSTDFLTITSSLPQEDFATYYCQSHEDPRTFGQGTKEIKRTVAAPSVF 120  
QY 141 IFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 200  
Db 121 IFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180  
QY 201 STLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238  
Db 181 STLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 218

RESULT 6  
US-08-466-163B-9  
; Sequence 9, Application US/08466163B  
; Patent No. 6329509  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Immunoglobulin Variants  
; FILE REFERENCE: P0718P2C1D1  
; CURRENT APPLICATION NUMBER: US/08/466,163B  
; CURRENT FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: US 08/405,617  
; PRIOR FILING DATE: 1995-03-15  
; PRIOR APPLICATION NUMBER: US 08/185,899  
; PRIOR FILING DATE: 1994-01-26  
; PRIOR APPLICATION NUMBER: US 07/879,495  
; PRIOR FILING DATE: 1992-05-07  
; PRIOR APPLICATION NUMBER: US 07/744,768  
; PRIOR FILING DATE: 1991-08-14  
; NUMBER OF SEQ ID NOS: 64  
; SEQ ID NO 9  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: humanized mae11, version 1, light chain  
US-08-466-163B-9

Query Match 88.8%; Score 1099; DB 4; Length 218;  
Best Local Similarity 97.2%; Pred. No. 8.3e-87;  
Matches 212; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYVDYDGDSDYNNYQOKPGKAPKLLIYAASNLES 80  
Db 1 DIQLTQSPSSLSASVGDRTVITCKASQSYVDYDGDSDYNNYQOKPGKAPKLLIYAASYLE 60  
QY 81 GIPSRFSGSGSTDFLTITSSLPQEDFATYYCQSHEDPRTFGQGTKEIKRTVAAPSVF 140  
Db 61 GVPFRSGSGSTDFLTITSSLPQEDFATYYCQSHEDPRTFGQGTKEIKRTVAAPSVF 120  
QY 141 IFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 200  
Db 121 IFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180  
QY 201 STLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238  
Db 181 STLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 218





Db 181 STLTSLKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 10

```

US-08-887-352B-17
; Sequence 17, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA: US/08/887,352B
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-887-352B-17

```

Query Match 86.7%; Score 1073; DB 2; Length 218;

Best Local Similarity 95.0%; Pred. No. 1.4e-84;

Matches 207; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

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QY 21 DIVLTQSPSSLSASVGRVTITCKASQSDYDGSYMNWYQKPKAPKLLIYAASNLES 80
   |||
Db 1 DIQLTQSPSSLSASVGRVTITCKASQSDYDGSYMNWYQKPKAPKLLIYAASYLE 60
   |||
QY 81 GIPSRFSGSGSGTDTLTITSLQPEDFATYYCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
   |||
Db 61 GVPFRFSGSGSGTDTLTITSLQPEDFATYYCQSHEDPYTFGGQTKVEIKRTVAAPSVF 120
   |||
QY 141 IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 200
   |||
Db 121 IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
   |||
QY 201 STLTSLKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 238
   |||
Db 181 STLTSLKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 218

```

RESULT 11

```

US-08-887-352B-19
; Sequence 19, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26

```

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA: US/08/887,352B

; APPLICATION NUMBER: US/08/887,352B

; FILING DATE: 03-Jul-1997

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Svoboda, Craig G.

; REGISTRATION NUMBER: 39,044

; REFERENCE/DOCKET NUMBER: P1123

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-1489

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 218 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

; US-08-887-352B-19

Query Match

Best Local Similarity 95.0%; Pred. No. 1.4e-84;

Matches 207; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

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QY 21 DIVLTQSPSSLSASVGRVTITCKASQSDYDGSYMNWYQKPKAPKLLIYAASNLES 80
   |||
Db 1 DIQLTQSPSSLSASVGRVTITCKASQSDYDGSYMNWYQKPKAPKLLIYAASYLE 60
   |||
QY 81 GIPSRFSGSGSGTDTLTITSLQPEDFATYYCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
   |||
Db 61 GVPFRFSGSGSGTDTLTITSLQPEDFATYYCQSHEDPYTFGGQTKVEIKRTVAAPSVF 120
   |||
QY 141 IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 200
   |||
Db 121 IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
   |||
QY 201 STLTSLKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 238
   |||
Db 181 STLTSLKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 218

```

RESULT 12

```

US-08-887-352B-24
; Sequence 24, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)

```

;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/887,352B  
;; FILING DATE: 03-Jul-1997  
;; CLASSIFICATION: 530  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Svoboda, Craig G.  
;; REGISTRATION NUMBER: 39,044  
;; REFERENCE/DOCKET NUMBER: P1123  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 650/225-1489  
;; TELEFAX: 650/952-9881  
;; INFORMATION FOR SEQ ID NO: 24:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 218 amino acids  
;; TYPE: Amino Acid  
;; TOPOLOGY: Linear  
US-08-887-352B-24

Query Match 86.7%; Score 1073; DB 2; Length 218;  
Best Local Similarity 95.0%; Pred. No. 1.4e-84;  
Matches 207; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSDYNNYQKPGKAPKLLIYAASNLES 80  
DB 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGEGDYLNNYQKPGKAPKLLIYAASYLE 60  
QY 81 GIPRSFGSGSGTDFLTITSSLPQEDFATYYCQSNEDPRTFGQGTKEIKRTVAAPSVF 140  
DB 61 GVPFRSGSGSGTDFLTITSSLPQEDFATYYCQSHEDPYTFQGTKEIKRTVAAPSVF 120  
QY 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLS 200  
DB 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLS 180  
QY 201 STLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 238  
DB 181 STLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 13  
US-09-109-207C-15  
; Sequence 15, Application US/09109207C  
; Patent No. 6172213

;; GENERAL INFORMATION:  
;; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
;; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide  
;; FILE REFERENCE: P1123R1  
;; CURRENT APPLICATION NUMBER: US/09/109,207C  
;; CURRENT FILING DATE: 1998-06-30  
;; PRIOR APPLICATION NUMBER: US 60/051,554  
;; PRIOR FILING DATE: 1997-07-03  
;; NUMBER OF SEQ ID NOS: 44  
;; SEQ ID NO 15  
;; LENGTH: 218  
;; TYPE: PRT  
;; ORGANISM: Artificial  
;; FEATURE:  
;; NAME/KEY: Artificial  
;; LOCATION: 1-218  
;; OTHER INFORMATION: Light chain sequence derived from MAE11  
US-09-109-207C-15

Query Match 86.7%; Score 1073; DB 4; Length 218;  
Best Local Similarity 95.0%; Pred. No. 1.4e-84;  
Matches 207; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSDYNNYQKPGKAPKLLIYAASNLES 80  
DB 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGEGDYLNNYQKPGKAPKLLIYAASYLE 60  
QY 81 GIPRSFGSGSGTDFLTITSSLPQEDFATYYCQSNEDPRTFGQGTKEIKRTVAAPSVF 140

DB 61 GVPFRSGSGSGTDFLTITSSLPQEDFATYYCQSHEDPYTFQGTKEIKRTVAAPSVF 120  
QY 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLS 200  
DB 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLS 180  
QY 201 STLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 238  
DB 181 STLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 14  
US-09-109-207C-17  
; Sequence 17, Application US/09109207C  
; Patent No. 6172213

;; GENERAL INFORMATION:  
;; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
;; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide  
;; FILE REFERENCE: P1123R1  
;; CURRENT APPLICATION NUMBER: US/09/109,207C  
;; CURRENT FILING DATE: 1998-06-30  
;; PRIOR APPLICATION NUMBER: US 60/051,554  
;; PRIOR FILING DATE: 1997-07-03  
;; NUMBER OF SEQ ID NOS: 44  
;; SEQ ID NO 17  
;; LENGTH: 218  
;; TYPE: PRT  
;; ORGANISM: Artificial  
;; FEATURE:  
;; NAME/KEY: Artificial  
;; LOCATION: 1-218  
;; OTHER INFORMATION: Light chain sequence derived from MAE11  
US-09-109-207C-17

Query Match 86.7%; Score 1073; DB 4; Length 218;  
Best Local Similarity 95.0%; Pred. No. 1.4e-84;  
Matches 207; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSDYNNYQKPGKAPKLLIYAASNLES 80  
DB 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGEGDYLNNYQKPGKAPKLLIYAASYLE 60  
QY 81 GIPRSFGSGSGTDFLTITSSLPQEDFATYYCQSNEDPRTFGQGTKEIKRTVAAPSVF 140  
DB 61 GVPFRSGSGSGTDFLTITSSLPQEDFATYYCQSHEDPYTFQGTKEIKRTVAAPSVF 120  
QY 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLS 200  
DB 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLS 180  
QY 201 STLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 238  
DB 181 STLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 15  
US-09-109-207C-19  
; Sequence 19, Application US/09109207C  
; Patent No. 6172213

;; GENERAL INFORMATION:  
;; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
;; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide  
;; FILE REFERENCE: P1123R1  
;; CURRENT APPLICATION NUMBER: US/09/109,207C  
;; CURRENT FILING DATE: 1998-06-30  
;; PRIOR APPLICATION NUMBER: US 60/051,554  
;; PRIOR FILING DATE: 1997-07-03  
;; NUMBER OF SEQ ID NOS: 44  
;; SEQ ID NO 19  
;; LENGTH: 218  
;; TYPE: PRT

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; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain F(ab) sequence derived from MAE11
US-09-109-207C-19

Query Match      86.7%; Score 1073; DB 4; Length 218;
Best Local Similarity 95.0%; Pred. No. 1.4e-84;
Matches 207; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 21 DIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSDYNNWYQOKPGKAPKLLIYAASNLES 80
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQOKPGKAPKLLIYAASYLES 60
Qy 81 GIPSRFSGSGSDTFTLTISLQPEDFATYYCQOSNEDPRTFGQGTKVEIKRTVAAPSVF 140
Db 61 GVPFRFSGSGSDTFTLTISLQPEDFATYYCQOSHEDPYTFGQGTKVEIKRTVAAPSVF 120
Qy 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 200
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
Qy 201 STLTLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
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Search completed: August 14, 2002, 15:17:04  
Job time: 687 sec

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F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 927.5; DB 2; Length 215;  
Best Local Similarity 83.6%; Pred. No. 1.5e-53;  
Matches 183; Conservative 13; Mismatches 18; Indels 5; Gaps 2;

QY 21 DIVLTQSPSSLSASVGRVITITCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNLES 80  
Db 1 EVVLTQSPATLSVSPGERATLSCRASQSV---HSNLAWYQKPGQAPRLLIYRASTRAT 56  
QY 81 GIPRSFGSGSGTDFLTITSSLOPEDFATYYCOQSNEDPRTFGQGTKEIKRTVAAPSV 139  
Db 57 GIPAREFGSGSGTDFLTITSSLOPEDFATYYCOQSNEDPRTFGQGTKEIKRTVAAPSV 116  
QY 140 FIPPPDEQLKSGTASVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKSTYSL 199  
Db 117 FIPPPDEQLKSGTASVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKSTYSL 176  
QY 200 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
Db 177 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215

RESULT 3  
JE0243  
Ig kappa chain NIG93 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0243  
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, H.; T  
submitted to JIPID, November 1998  
A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amy  
A:Reference number: JE0243  
A:Accession: JE0243  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 73.0%; Score 902.5; DB 2; Length 215;  
Best Local Similarity 81.3%; Pred. No. 6.3e-52;  
Matches 178; Conservative 17; Mismatches 19; Indels 5; Gaps 2;

QY 21 DIVLTQSPSSLSASVGRVITITCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNLES 80  
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSV---ATNVWYMKLGQAPRLLIYDASTRAT 56  
QY 81 GIPRSFGSGSGTDFLTITSSLOPEDFATYYCOQSNEDPRTFGQGTKEIK-RTVAAPSV 139  
Db 57 GVPAREFGSGSGTDFLTITSSLOPEDFATYYCOHNNAPPTFGQGTKEIKRTVAAPSV 116  
QY 140 FIPPPDEQLKSGTASVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKSTYSL 199  
Db 117 FIPPPDEQLKSGTASVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKSTYSL 176  
QY 200 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
Db 177 SSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215

RESULT 4  
A23746  
Ig kappa chain V-II (KAU cold agglutinin) - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 21-Jan-2000  
C:Accession: A23746  
R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.  
J. Biol. Chem. 266, 2836-2842, 1991  
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl  
A:Reference number: A23746; MUID:91131575  
A:Accession: A23746

A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-215 <LEO>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 71.7%; Score 886.5; DB 2; Length 215;  
Best Local Similarity 82.0%; Pred. No. 6.9e-51;  
Matches 178; Conservative 13; Mismatches 23; Indels 3; Gaps 1;

QY 21 DIVLTQSPSSLSASVGRVITITCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNLES 80  
Db 1 EIVLTQSPATLSVSPGERATLSGASQSV---SSNLAWYQKPGQAPRLLIYDASSRAT 57  
QY 81 GIPRSFGSGSGTDFLTITSSLOPEDFATYYCOQSNEDPRTFGQGTKEIKRTVAAPSV 140  
Db 58 GIPDRFSGSGSGTDFLTITSRLEPEDFATYYGOQYSSPLTFGGGTKEIKRTVAAPSV 117  
QY 141 FIPPPDEQLKSGTASVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKSTYSL 200  
Db 118 FIPPPDEQLKSGTASVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKSTYSL 177  
QY 201 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGE 237  
Db 178 STLTLSKADYKHKVYAGEVTHQGLSSPVTKSFNRGE 214

RESULT 5  
JE0241  
Ig kappa chain Am37 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0241  
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda  
submitted to JIPID, November 1998  
A:Description: Structure relationship of kappa type light chains with AL amyloidosis:  
A:Reference number: JE0241  
A:Accession: JE0241  
A:Molecule type: protein  
A:Residues: 1-216 <ALI>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-92/Domain: immunoglobulin homology <IMM>

Query Match 70.8%; Score 876; DB 2; Length 216;  
Best Local Similarity 79.4%; Pred. No. 3.3e-50;  
Matches 173; Conservative 16; Mismatches 27; Indels 2; Gaps 2;

QY 21 DIVLTQSPSSLSASVGRVITITCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNLES 80  
Db 1 DIVLTQSPDFLAVSLGERATINCKSSQSVLYNSKFLAWYQKPGQ-PKLLIW-ANVRS 58  
QY 81 GIPRSFGSGSGTDFLTITSSLOPEDFATYYCOQSNEDPRTFGQGTKEIKRTVAAPSV 140  
Db 59 GVPDRFSGSGTDFLTITSLQAEVLAVYVYQYQYTYSTYPSFGQGRLEIKRTVAAPSV 118  
QY 141 FIPPPDEQLKSGTASVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKSTYSL 200  
Db 119 FIPPPDEQLKSGTASVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKSTYSL 178  
QY 201 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
Db 179 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 216

RESULT 6  
S06084  
Ig kappa chain precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 21-Jan-2000  
C:Accession: S06084



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Best Local Similarity   61.8%; Pred. No. 7.9e-42;
Matches 144; Conservative    37; Mismatches 47; Indels      5; Gaps      0;

Qy       7 LLWLLLM-VPGSGTDIVLTQPSSLASVGDRVTITCKASGVSDYDGDGYNNMYQQKPG 65
          ||| :||| | :| :||||| :||| :||| :||| :||| :||| :||| :||| :|||
Db       2 LGLLWLWPAGRCDIQTQSPSSLASILTERVSIICRTSQSV---SNYLNYAQKP 57

Qy      66 KAPKLIIYAASNLESIGPSRFGSGGDTFTLTISIQPEDFANYYYCOQSNEDEPRTFQG 125
          :||||| |:| :| :||||| :||| :||| :||| :||| :||| :||| :||| :|||
Db     58 QAKPLIYYATRLTDPVSFRFGSGGGTYTLTSNLEANDTAYVCCLQEYSFLAFEGG 117

Qy     126 TKVEIKRTVAAPSFIIPPDSQLKSGTASVVLCNLNFYPREAKVMKVDNALGSNQE 185
          ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db    118 TNVEIKSRDAQPVSLFKPSEQRGTGTVSVVCLVNDFPYKDINVKVDGVTQNSEQN 177

Qy     186 SVTEQDKSSTYSLSSTLTISKADYEKKHVACEVTHOGLSSPVTKSFNRGEC 238
          | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db    178 SFTPDQSKYSTYSLSSTLTLSSEYQHNAFACEVSHKSLPTALKVFENKNKC 230


RESULT 10
JC5810
monoclonal antibody l3-1 light chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 04-Feb-1989 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: JC5810
R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; 
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A>Title: Structural characterization of mouse monoclonal antibody l3-1 against
A:Reference number: JC5810; PMID:98063277
A:Accession: JC5810
A:Molecule type: protein
A:Residues: 1-218 <AKA>
C:Comment: This catalytic antibody has peroxidase oxidase. It is directed again
C:Superfamily: immunoglobulin V region; Immunoglobulin homology
F:l6-94/Domain: immunoglobulin homology <IMM>

Query Match              60.3% ; Score 746; DB 2; Length 218;
Best Local Similarity   64.2% ; Pred. No. 9.3e-42;
Matches 140; Conservative    30; Mismatches 48; Indels      0; Gaps      0;

Qy      21 DIVLTQSPSSLASVGDRVTITCKASGVSDYDGDGYNNMYQQKPKAPKLIIYAASNLES 80
          ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db       1 NVILTQSPASLAFLAGRIQCASCRAKSVSASGIYMHYQQKPGQPPKLIIASLNLES 60

Qy     81 GPIRFSGSGTGDTFLTISILOPEPATYCQOSNEDEPRTFGGTKVEIKRTVAAPSVF 140
          | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db     61 GVPA RFSGSGTGDTFLNIHPVEDVATYCQRSRELPLTFGGAGTKLELRADAAPTFS 120

Qy     141 IFPPDSDLKGSTAVSYVCLLNFFPREAKVMKYDNALQNSGESVTEQDKSSTYSLS 200
          ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db    121 IFPPSSQLTAGGASVYCVLFNFPDYKIDGGERQGNVLNSWTQDKQDKSSTYSMS 180

Qy     201 STLTLSRADYEKKHXYACEVTHOGLSSPVTKSFNRGEC 238
          ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db    181 STLTLTKDEXERHNHSYTCEATHKTSTSPIVKSFNREC 218


RESULT 11
SO1320
Ig kappa chain precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 21-Jan-2000
C:Accession: SO1320
Eur. J. Biochem. 176, 287-295, 1988
A>Title: Expression in non-Lymphoid cells of mouse recombinant immunoglobulin A;
A:Reference number: SO1320; PMID:88329081
A:Accession: SO1320
A:Molecule type: mRNA
A:Residues: 1-234 <DEL>
A:Cross-references: EMBL:X13187; NID:g51784; PID:CAA31579.1; PFD:g51785
```

A>Note: this sequence was determined from the differentiated gene  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-23/Product: Ig kappa chain #status predicted <MAT>  
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 58.9%; Score 728; DB 2; Length 234;  
Best Local Similarity 57.9%; Pred. No. 1.5e-40;  
Matches 139; Conservative 38; Mismatches 55; Indels 8; Gaps 2;

QY 1 METDTILLWLLVWPSTGDIVLTQTSPSSLSASVGDRVTITCKASQSDVDGDSYWN-- 58  
| :|||:: | :|||::||| |||:||||:||||: |  
Db 1 MSPTQLVLGLLLLMLTDARCDIQMTQPASLUSVGSVITCRASENI-----YSNLA 54

QY 59 WYQQKPKAPKLIIYAASNLESIGPSRFGSGGTDFTLTISSLQPEDFAITYYCQNED 118  
||||:|:||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Db 55 WYQQKQGKSPQLLYVATKLVDGVPRSFSGSGGTQYSLKINSLOSEDFGSYCOHEFWDT 114

QY 119 PRFPGQGTKVEIKRTVAAPSVFIFPPDEQLKGSTASVCVLLNNFYBREAKVKVDNAL 178  
| |||:|:||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Db 115 PFTFGSGETKLEMRADAAPTVSIFPPSEQLTGGASVCFLNFPKDINVKWKIDGSE 174

QY 179 QSGNSQSRSVEDSKDSTYSLSSTLTLSKADYEKKHYACEVTHQGLSSPVTKSRNGEC 238  
| :|||:|:||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Db 175 RQCVLNWSWDQDSDKSTYSMSSTLTILTKDEYERHNSYTCEATHKTSTPIVKSFNREC 234

RESULT 12  
A31790  
Ig kappa chain V region (17/9) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 21-Jan-2000  
C;Accession: A31790  
R;Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.  
J. Biol. Chem. 263, 17100-17105, 1988  
A;Title: Preliminary crystallographic data, primary sequence, and binding data for an  
A;Reference number: A92686; MUID:89034213  
A;Accession: A31790  
A:Molecule type: mRNA  
A;Residues: 1-220 <SCH>  
A;Cross-references: GB:M23626; GB:J04061; NID:9533234; PIDN:AAA39162.1; PID:9533235  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 58.6%; Score 725; DB 2; Length 220;  
Best Local Similarity 61.4%; Pred. No. 2.2e-40;  
Matches 135; Conservative 34; Mismatches 49; Indels 2; Gaps 1;

QY 21 DIVLTQTSPSSLSASVGDRVTITCKASQSDVDG--DSYMNYQQKGPAPKLIIYAASNL 78  
|||:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Db 1 DIVMTQSPSSLIYTAGKEVMTSCSTSSGLENSGKNYLTYQQKPQPKVIYWASTR 60

QY 79 ESGIPSRFGSGGTDFTLTISSLQPEDFAITYYCQNEDPRTFPGQGTKVEIKRTVAAPS 138  
|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~::~|||:|:|:|:|:|:|:|:|:  
Db 61 ESGVPDRFTGGSGTDFTLTISSYAQDLAVIYCONDYSNPFTFGGCTKLELKRAADAAPT 120

QY 139 VFIFPPSDEOLKGSTASVCVLLNNFYBREAKVKVDNALQSGNSQSRSVEDSKDSTYS 198  
| ||||| ||| ||| ||| ||| ||| ||| |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Db 121 VSIFPPSSEQLTGGASVCFLNFPKDINVKWKIDGSRQCNGLSNWDDQDSDKSTYS 180

QY 199 LSSTLTLSKADYEKKHYACEVTHQGLSSPVTKSRNGEC 238  
:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
Db 181 MSSLTILTDEYERHNSYTCEATHKTSTPIVKSFNREC 220

RESULT 13  
A56169  
Ig kappa chain V region (clone 23.2) - mouse (fragment)  
C;Species: Mus musculus (house mouse)



C;Date: 19-Oct-1995 #sequence\_revision 19-Oct-1995 #text\_change 11-Jan-2000  
C;Accession: A56169  
R;Monfardini, C.; Kieber-Emmons, T.; VonFeldt, J.M.; O'Malley, B.; Rosenbaum, H.; Godill  
J. Biol. Chem. 270, 6628-6638, 1995  
A;Title: Recombinant antibodies in bioactive peptide design.  
A;Reference number: A56169; MUID:95204454  
A;Accession: A56169  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-210 <NON>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 58.0%; Score 717; DB 2; Length 210;  
Best Local Similarity 64.0%; Pred. No. 6.9e-40;  
Matches 135; Conservative 29; Mismatches 45; Indels 0; Gaps 0;  
Qy 21 DIVLTQSPSSLSASVGRVITTCASQSDYDGDSDYNNWYQOKPGKAPKLLIYAASNLES 80  
Db 1 DIVLTQSPASLTSLGQRATISCRASKSVSSGYSYHWHYQOKPGQPKVLIYLASNLES 60  
Qy 81 GIPSRFSGSGGDTFTLTISLQPEDFATYCCQSNEDPRTFGGTVKEIKRTVAAPSVF 140  
Db 61 GVPRFSGSGGDTFTLTNIHPVEEDATYCCQHSRELPTWTFGGTTRLEIKRADAAPTVS 120  
Qy 141 IFPPSDQLKSGTASVYVCLLNFFYPRAKQVQKVDNALQSGNSQESVTEQDSKDSYLS 200  
Db 121 IFPPSEQLTSGGASVYVCFLLNFFPKDINVKWKIDGSRQNGVLNSWTDQDSKDSYMS 180  
Qy 201 STLTLSKADYEKKHYACEVTHOGLSSPV 229  
Db 181 STLTLTKDEYERHNSYTCETHKTSTSPI 209

RESULT 14  
S37484  
Ig kappa chain - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 11-Jan-2000  
C;Accession: S37484  
R;Ducancel, F.F.D.  
submitted to the EMBL Data Library, February 1993  
A;Reference number: S37483  
A;Accession: S37484  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-225 <DUC>  
A;Cross-references: EMBL:X70424; NID:g406254; PIDN:CAA49869.1; PID:g406255  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 57.8%; Score 715.5; DB 2; Length 225;  
Best Local Similarity 61.4%; Pred. No. 9.2e-40;  
Matches 140; Conservative 30; Mismatches 53; Indels 5; Gaps 2;  
Qy 11 LLLVWPGSTGDIVLTQSPSSLSASVGRVITTCASQSDYDGDSDYNNWYQOKPGKAPKL 70  
Db 3 LLLCVSGAHSGIVMTQPKFLLSAGDRVITTCASQSVND----VAVYQOKPGQSPKL 58  
Qy 71 LIYAASNLESGIPSRFSGSGGDTFTLTISLQPEDFATYCCQSNEDPRTFGGTVKEI 130  
Db 59 LIYYASSRYTGVPDRFTGGSGYGTDTFTISTVQAEADLAVYFCQQ-DYSSVTFGGGKTLEI 117  
Qy 131 KRTVAAPSVFIFPPSDQLKSGTASVYVCLLNFFYPRAKQVQKVDNALQSGNSQESVTEQ 190  
Db 118 KRDAAPATVSIFPPSSQLTSGGASVYVCFLLNFFPKDINVKWKIDGSRQNGVLNSWTDQ 177  
Qy 191 DSKDSTYLSLSTLTLSKADYEKKHYACEVTHOGLSSPVTKSFNRGEC 238  
Db 178 DSKDSTYMSSTLTLTKDEYERHNSYTCETHKTSTSPIVKSFNREC 225

RESULT 15  
PC4203  
Ig kappa chain (monoclonal antibody MAbA34) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Dec-1996 #sequence\_revision 31-Dec-1996 #text\_change 11-Jan-2000  
C;Accession: PC4203  
R;Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.  
Gene 173, 257-259, 1996  
A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a  
A;Reference number: PC4202; MUID:97082978  
A;Accession: PC4203  
A;Molecule type: mRNA  
A;Residues: 1-219 <KWA>  
A;Cross-references: GB:U29147; NID:gi1594225; PIDN:AAC52821.1; PID:gi1594226  
C;Comment: This protein is specific for human plasma apolipoprotein A-I of high-density  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;1-112/Domain: V region #status predicted <VRG>  
F;113-219/Domain: C region #status predicted <CRG>

Query Match 57.3%; Score 708.5; DB 2; Length 219;  
Best Local Similarity 59.4%; Pred. No. 2.6e-39;  
Matches 130; Conservative 38; Mismatches 50; Indels 1; Gaps 1;  
Qy 21 DIVLTQSPSSLSASVGRVITTCASQSDY-DGDSYNNWYQOKPGKAPKLLIYAASNLE 79  
Db 1 DVLMTQTPLSLPSVLGDAQSISCRSSQSIHTNGNTYLEWYLQKPGQSPKLLIYKVSNR 60  
Qy 80 SGIPSRFSGSGGDTFTLTISLQPEDFATYCCQSNEDPRTFGGTVKEIKRTVAAPSV 139  
Db 61 SGVPRFSGSGGDTFTLTISRVEADLGVIYCFQGSVHPRTFGGTGKLEIKRADAAPTV 120  
Qy 140 FIFPPSDQLKSGTASVYVCLLNFFYPRAKQVQKVDNALQSGNSQESVTEQDSKDSYSL 199  
Db 121 SIFPPSEQLTSGGASVYVCFLLNFFPKDINVKWKIDGSRQNGVLNSWTDQDSKDSYMS 180  
Qy 200 SSTLTLSKADYEKKHYACEVTHOGLSSPVTKSFNRGEC 238  
Db 181 SSTLTLTKDEYERHNSYTCETHKTSTSPIVKSFNREC 219

Search completed: August 14, 2002, 15:18:59  
Job time: 687 sec

us-09-499-662-131.rpr

Thu Aug 15 07:56:01 2002

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:23:13 ; Search time 53.64 Seconds  
(without alignments)  
171.798 Million cell updates/sec

Title: US-09-499-662-131

Perfect score: 1237

Sequence: 1 METDTILLWLLWVGSTG.....EVTHQGLSSPVTKSFNRGEC 238

Scoring table:  
BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	548	44.3	106	1	KAC_HUMAN	P01834 homo sapien
2	531	42.9	131	1	KV3J_MOUSE	P01661 mus musculus
3	520	42.0	132	1	KV3K_MOUSE	P01658 mus musculus
4	484	39.1	111	1	KV3M_MOUSE	P01665 mus musculus
5	482	39.0	111	1	KV3N_MOUSE	P01666 mus musculus
6	480	38.8	111	1	KV3O_MOUSE	P01667 mus musculus
7	479.5	38.8	129	1	KV3L_HUMAN	P18135 homo sapien
8	479	38.7	129	1	KV1W_HUMAN	P04431 homo sapien
9	477	38.6	111	1	KV3Q_MOUSE	P01669 mus musculus
10	469	37.9	111	1	KV3L_MOUSE	P01664 mus musculus
11	460	37.2	108	1	KV1H_HUMAN	P01600 homo sapien
12	459.5	37.1	110	1	KV3P_MOUSE	P01668 mus musculus
13	457.5	37.0	129	1	KV3M_HUMAN	P18136 homo sapien
14	451	36.5	108	1	KV1G_HUMAN	P01599 homo sapien
15	448	36.2	108	1	KV1M_HUMAN	P01605 homo sapien
16	447	36.1	108	1	KV1K_HUMAN	P01603 homo sapien
17	447	36.1	134	1	KV4C_HUMAN	P06314 homo sapien
18	445	36.0	108	1	KV1B_HUMAN	P01594 homo sapien
19	444	35.9	108	1	KV1E_HUMAN	P01597 homo sapien
20	444	35.9	108	1	KV1F_HUMAN	P01598 homo sapien
21	444	35.9	108	1	KV1N_HUMAN	P01606 homo sapien
22	441	35.7	108	1	KV1V_HUMAN	P04430 homo sapien
23	440	35.6	108	1	KV1A_HUMAN	P01593 homo sapien
24	440	35.6	117	1	KV1J_HUMAN	P01602 homo sapien
25	437	35.3	111	1	KV3H_MOUSE	P01660 mus musculus
26	434	35.1	108	1	KV1O_HUMAN	P01607 homo sapien
27	433	35.0	108	1	KV1P_HUMAN	P01608 homo sapien
28	432.5	35.0	129	1	KV3H_HUMAN	P04207 homo sapien
29	431.5	34.9	133	1	KV4B_HUMAN	P06313 homo sapien
30	429	34.7	108	1	KV1Y_HUMAN	P80362 homo sapien
31	428	34.6	108	1	KV1R_HUMAN	P01610 homo sapien
32	428	34.6	108	1	KV1S_HUMAN	P01611 homo sapien
33	428	34.6	129	1	KV1X_HUMAN	P04432 homo sapien

RESULT 1

ID	KAC_HUMAN	STANDARD;	PRT;	106 AA.
AC	P01834;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Ig kappa chain C region.			
GN	IGKC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064023; PubMed=5489770;			
RA	Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";			
RL	Biochemistry 9:3155-3161(1970).			
RN	[2]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";			
RL	Biochemistry 9:3188-3196(1970).			
RN	[3]			
RP	SEQUENCE (BENCE-JONES PROTEIN TI).			
RX	MEDLINE=72188439; PubMed=5027703;			
RA	Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;			
RT	"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81042304; PubMed=6775818;			
RA	Hietter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;			
RT	"Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments.";			
RL	Cell 22:197-207(1980).			
RN	[5]			
RP	SEQUENCE (BENCE-JONES PROTEIN ROY).			
RA	Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;			
RL	(In) Franek F., Shugar D. (eds.);			
RL	Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).			
RN	[6]			
RP	SEQUENCE (BENCE-JONES PROTEIN CUM).			
RX	MEDLINE=68242259; PubMed=5586923;			
RA	Hilschmann N.;			
RT	"The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";			

```
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [17]
RP SEQUENCE (BENCE-JONES PROTEIN AG).
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges."
RL J. Biol. Chem. 244:3550-3560(1969).
RN [18]
RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains."
RL Science 169:56-59(1970).
CC -1- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
CC MARKER, 45-ALA AND 83-LEU.
CC -----
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DR EMBL; J00241; AAA58989.1; -.
DR EMBL; V00557; CAA23823.1; -.
DR PIR; A02116; K3HU.
DR HSP; P01842; 7FAB.
DR MIM; 147240; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00407; Igcl; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 106 106
FT VARIANT 83 83
FT INTERCHAIN (WITH A HEAVY CHAIN).
FT V -> L (IN INV(1,2) MARKER).
FT /FTIG-VAR_003897.
FT CONFLICT 14 14
FT CONFLICT D -> N (IN REF. 7 AND 8).
FT CONFLICT 57 57
FT CONFLICT E -> Q (IN REF. 5 AND 6).
FT SEQUENCE 106 AA; 11609 MW; 51984D1FD372CE8 CRC64;
SQ
Query Match 44.3%; Score 548; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.9e-37;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 TVAAPSVFPPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 192
Db 1 TVAAPSVFPPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60
QY 193 KSTYSLSTLTKSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 61 KSTYSLSTLTKSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 106

RESULT 2
KV3L_MOUSE
ID KV3L_MOUSE STANDARD; PRT; 131 AA.
AC P01661;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region MOPC 63 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
```

```
RN [1]
RP SEQUENCE OF 1-35.
RX MEDLINE=78235887; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes."
RL Biochemistry 17:2392-2400(1978).
RN [2]
RP SEQUENCE OF 21-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences."
RL Biochemistry 12:760-771(1973).
RN [3]
RP REVISIONS.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions."
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
DR PIR; A01935; KVM5M6.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 131
FT DOMAIN 21 43
FT DOMAIN 44 58
FT DOMAIN 59 73
FT DOMAIN 74 80
FT DOMAIN 81 112
FT DOMAIN 113 121
FT DOMAIN 122 131
FT DISULFID 43 112
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;
Query Match 42.9%; Score 531; DB 1; Length 131;
Best Local Similarity 74.8%; Pred. No. 5.7e-36;
Matches 98; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

QY 1 METDTLLWVLLWVPGTGDIIVLTQSPSLSASVGDRTVITCKASQSDYDGDSTANWY 60
Db 1 METDTLLWVLLWVPGTGDIIVLTQSPSLSASVGDRTVITCKASQSDYDGDSTANWY 60
QY 61 QKQPGKAPKLLIYAASNLESGIPSRFSGSGGTDFLTITISLSLOPEDFATYCCQSNEDPR 120
Db 61 QKQPGKAPKLLIYAASNLESGIPSRFSGSGGTDFLTITISLSLOPEDFATYCCQSNEDPR 120
QY 121 TFGQGTQKVEIK 131
Db 121 TFGQGTQKVEIK 131

RESULT 3
KV3F_MOUSE
ID KV3F_MOUSE STANDARD; PRT; 132 AA.
AC P01658;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region MOPC 321 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
```

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RA  SEQUENCE OF 1-37.
RP  MEDLINE=78235887; PubMed=981179;
RX  Burstein Y., Schechter I.;
RA  "Primary structures of N-terminal extra peptide segments linked to
RT  the variable and constant regions of immunoglobulin light chain
FT  precursors: implications on the organization and controlled
RT  expression of immunoglobulin genes.";
RL  Biochemistry 17:2392-2400(1978).
[2]
RP  SEQUENCE OF 21-132.
RX  MEDLINE=73140224; PubMed=4120629;
RA  McKean D.J., Potter M., Hood L.E.;
RT  "Mouse immunoglobulin chains. Partial amino acid sequence of a kappa
FT  chain.";
RL  Biochemistry 12:749-759(1973).
CC  -!- MISCELLANEOUS: THE PARTIAL SEQUENCE OF THE C REGION OF THIS
CC  BENCE-JONES PROTEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT
CC  REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY
CC  RESIDUES.
DR  PIR; A01933; KVM532.
DR  HSSP; P01607; IRE1.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_V.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; IGV; 1.
KW  Immunoglobulin V region; Bence-Jones protein; Signal.
FT  SIGNAL 1 20
FT  CHAIN 21 132 IG KAPPA CHAIN V-III REGION MOPC 321.
FT  DOMAIN 21 43 FRAMEWORK-1.
FT  DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.
FT  DOMAIN 59 73 FRAMEWORK-2.
FT  DOMAIN 74 80 COMPLEMENTARITY-DETERMINING-2.
FT  DOMAIN 81 112 FRAMEWORK-3.
FT  DOMAIN 113 121 COMPLEMENTARITY-DETERMINING-3.
FT  DOMAIN 122 131 FRAMEWORK-4.
FT  DISULFID 43 112 BY SIMILARITY.
FT  NON_TER 132 132
SQ  SEQUENCE 132 AA; 14523 MW; 9F3B809BB773FBE9 CRC64;

Query Match 42.08; Score 520; DB 1; Length 132;
Best Local Similarity 68.98; Pred. No. 4.4e-35;
Matches 91; Conservative 26; Mismatches 15; Indels 0; Gaps 0;

QY 1 METDTLLWVLLWVPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDVDGDSYMNWY 60
    ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 1 METDTLLWVLLWVPGSTGDIVLTQSPASLAVSLGQRATISCRASKSVNTYGSFMZWY 60
    ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 61 QOKPKGAPKLLIYAASNLSEGIPIRFGSGSGTDTFTLTSSLPQEDFATYYCQSNEDPR 120
    ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 61 ZZKPGZPPKLLIYRASNLZSGIPARFSGSGSRBTFTLTBPVABDVATYFCZSBBZBPW 120
    ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 121 TFGQGTKEIKR 132
    ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 121 TFGSGTKLEIKR 132
    ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 4
KV3M_MOUSE STANDARD; PRT; 111 AA.
AC P01665;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7043.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
FT diversity.";
RL Nature 276:785-790(1978).
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
FT diversity.";
RL Nature 276:785-790(1978).
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 39.18; Score 484; DB 1; Length 111;
Best Local Similarity 82.08; Pred. No. 2.7e-32;
Matches 91; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSDVDGDSYMNWYQOKPKGAPKLLIYAASNLSE 80
    ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 1 DIVLTQSPASLAVSLGQRATISCRASKSVDVDGDSYMNWYQOKPKGAPKLLIYAASNLSE 60
    ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 81 GIPRFGSGSGTDTFTLTSSLPQEDFATYYCQSNEDPRTFGQGTKEIK 131
    ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 61 GIPARFSGSGSGTDTFTLTNHPVEEDAATYYCQSNEDPRTFGSGTKLEIK 111
    ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 5
KV3N_MOUSE STANDARD; PRT; 111 AA.
AC P01666;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7183.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
FT diversity.";
RL Nature 276:785-790(1978).
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;
```

Query Match 39.0%; Score 482; DB 1; Length 111;  
Best Local Similarity 81.1%; Pred. No. 3.8e-32;  
Matches 90; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 21 DIVLTQSPSLASVGDRTVITCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNL 80  
DB 1 DIVLTQSPSLASVGLQRTATISCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNL 60

QY 81 GIPRSFGSGSGTDFLTITSSLOPEDFATYYCQSQSDNEDPRTFGQTKVEIK 131  
DB 61 GIPARESGSGTDFLTINHPVEEDAAATYYCQSQSDNEDPRTFGQTKLEIK 111

RESULT 6  
KV30\_MOUSE STANDARD; PRT; 111 AA.  
AC P01667;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-III region PC 6308.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=79073152; PubMed=103003;  
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
RT "Rearrangement of genetic information may produce immunoglobulin  
diversity.";  
RL Nature 276:785-790(1978).  
DR PIR: C01937; KVM08.  
DR HSSP: P01789; 1MCP.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IGV; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 29 53 FRAMEWORK-2.  
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 61 92 FRAMEWORK-3.  
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 102 111 FRAMEWORK-4.  
FT DISULFID 23 92 BY SIMILARITY.  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 38.8%; Score 480; DB 1; Length 111;  
Best Local Similarity 81.1%; Pred. No. 5.5e-32;  
Matches 90; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 21 DIVLTQSPSLASVGDRTVITCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNL 80  
DB 1 DIVLTQSPSLASVGLQRTATISCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNL 60

QY 81 GIPRSFGSGSGTDFLTITSSLOPEDFATYYCQSQSDNEDPRTFGQTKVEIK 131  
DB 61 GIPARESGSGTDFLTINHPVEEDAAATYYCQSQSDNEDPRTFGQTKLEIK 111

RESULT 7  
KV3L\_HUMAN STANDARD; PRT; 129 AA.  
AC P18135;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-III region HAH precursor.

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88171307; PubMed=3127527;  
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;  
RT "Autoantibody-associated kappa light chain variable region gene  
expressed in chronic lymphocytic leukemia with little or no somatic  
mutation. Implications for etiology and immunotherapy.";  
RL J. Exp. Med. 167:840-852(1988).  
CC -I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M  
AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC  
LEUKEMIA.  
DR PIR: P0022; K3HUHA.  
DR HSSP: P01789; 1MCP.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; IGV; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 20  
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.  
FT DOMAIN 21 43 FRAMEWORK-1.  
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 56 70 FRAMEWORK-2.  
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 78 109 FRAMEWORK-3.  
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 119 129 JK1 SEGMENT.  
FT DISULFID 43 109 BY SIMILARITY.  
FT NON\_TER 129 129  
SQ SEQUENCE 129 AA; 14073 MW; D3C5529272774D0 CRC64;

Query Match 38.8%; Score 479.5; DB 1; Length 129;  
Best Local Similarity 69.7%; Pred. No. 7.3e-32;  
Matches 92; Conservative 16; Mismatches 21; Indels 3; Gaps 1;

QY 1 METDTLLWVLLWVPGSTGDI VLTQSPSLASVGDRTVITCKASQSDYDGDSDYNNWY 60  
DB 1 METPAQLLFLLWLPDITGEIVLTQSPGTLSPGERATLSCRASQSV---SSSYLAWY 57  
QY 61 QKPGKAPKLLIYAASNLGSGIPRSFGSGSGTDFLTITSSLOPEDFATYYCQSQSDNEDP 120  
DB 58 QKPGQAPRLIYGAASSRATGIDRFSGSGSGTDFLTITISRLPEDFATYYCQYGTSPR 117  
QY 121 TFGQGTKEIKR 132  
DB 118 TFGQGTKEIKR 129

RESULT 8  
KV1W\_HUMAN STANDARD; PRT; 129 AA.  
AC P04431;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region Walker precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85014148; PubMed=6091049;  
RA Klobeck H.G., Combrato G., Zachau H.G.;  
RT "Immunoglobulin genes of the kappa light chain type from two human  
lymphoid cell lines are closely related.";  
RL Nucleic Acids Res. 12:6995-7005(1984).  
CC -----



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FT	DOMAIN	/8	109	E

RX MEDLINE=79073152; PubMed=103003;



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FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match 37.0%; Score 457.5; DB 1; Length 129;
Best Local Similarity 68.2%; Pred. No. 4.2e-30;
Matches 90; Conservative 16; Mismatches 23; Indels 3; Gaps 1;

Qy 1 METDFTLLVLLWVPGSTGDIVLTQSPSSLSASVGDRTITCKASQSVVDYDGDSDYMMWY 60
Db 1 METPAQLFLLLWLPDITGEIVLTQSPGTLISLGERATUSCRASQSV---SSYLAWY 57

Qy 61 QOKPGKAPKLLIYAASNLSPSSSGSGTDTFTLTSSLPQEDFAFYCCQSNEDPRTFGQTKVEIKR 120
Db 58 QOKPGQAPRLIYGASSRATGIPDRFSGSGSGTDTFTLTSLRLEPDXDFAVIYCCQYGSSEPW 117

Qy 121 TFGQGTKEIKR 132
Db 118 TFGQGTKEIKR 129

RESULT 14
KVIM_HUMAN
ID KVIG_HUMAN STANDARD; PRT; 108 AA.
AC P01599;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region GAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059122; PubMed=4215718;
RA Laure C.J., Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
FT (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
RT kappa-type, subgroup 1.;
RL Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504 (1973).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
CC PIR: A01867; KIHUGL.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34 FRAMEWORK-1.
FT DOMAIN 35 49 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 50 56 FRAMEWORK-2.
FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 89 97 FRAMEWORK-3.
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 FRAMEWORK-4.
FT NON_TER 108 108 BY SIMILARITY.
SQ SEQUENCE 108 AA; 11814 MW; C1AD3CB0F600FF73 CRC64;

Query Match 36.5%; Score 451; DB 1; Length 108;
Best Local Similarity 78.6%; Pred. No. 1.1e-29;
Matches 88; Conservative 9; Mismatches 11; Indels 4; Gaps 1;

Qy 21 DIVLTQSPSSLSASVGDRTITCKASQSVVDYDGDSDYMMWYQOKPGKAPKLLIYAASNLQS 80
Db 1 DIQMTQSPSSLSASVGDRTITCKASQSVVDYDGDSDYMMWYQOKPGKAPKLLIYAASNLQS 56

Qy 21 DIVLTQSPSSLSASVGDRTITCKASQSVVDYDGDSDYMMWYQOKPGKAPKLLIYAASNLQS 80
Db 1 DIQMTQSPSSLSASVGDRTITCKASQSVVDYDGDSDYMMWYQOKPGKAPKLLIYAASNLQS 56
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Qy 81 GIPSRFSGSGSGTDTFTLTSSLPQEDFAFYCCQSNEDPRTFGQTKVEIKR 132
Db 57 GVPFRFSGSGAGCTFTLTSSLPQEDFAFYCYLQNSYPRSGQGTKEIKR 108

RESULT 15
KVIM_HUMAN
ID KVIM_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human
FT IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
FT specificities.";
RL Scand. J. Immunol. 5:677-684 (1976).
CC -!- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
CC PIR: A01871; KIHULY.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34 FRAMEWORK-1.
FT DOMAIN 35 49 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 50 56 FRAMEWORK-2.
FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 89 97 FRAMEWORK-3.
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 FRAMEWORK-4.
FT NON_TER 108 108 BY SIMILARITY.
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 36.2%; Score 448; DB 1; Length 108;
Best Local Similarity 77.7%; Pred. No. 1.9e-29;
Matches 87; Conservative 9; Mismatches 12; Indels 4; Gaps 1;

Qy 21 DIVLTQSPSSLSASVGDRTITCKASQSVVDYDGDSDYMMWYQOKPGKAPKLLIYAASNLQS 80
Db 1 DIQMTQSPSSLSASVGDRTITCKASQSVVDYDGDSDYMMWYQOKPGKAPKLLIYGASTREA 56

Qy 81 GIPSRFSGSGSGTDTFTLTSSLPQEDFAFYCCQSNEDPRTFGQTKVEIKR 132
Db 57 GVPFRFSGSGSGTDTFTLTSSLPQEDFAFYCCQSNEDPRTFGQTKVEIKR 108
```

Search completed: August 14, 2002, 15:23:13  
Job time: 686 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:22:15 ; Search time 187.61 Seconds  
(without alignments)  
219.459 Million cell updates/sec

Title: US-09-499-662-131  
Perfect score: 1237  
Sequence: 1 METDTILLWVLLWVPGSTG.....EVTHQGLSPVTKSPNRGEC 238

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_19:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	745.5	60.3	238	11 Q99M37	Q99M37 mus musculus
2	738	59.7	234	11 Q91WF8	Q91WF8 mus musculus
3	737	59.6	233	11 Q91WS9	Q91WS9 mus musculus
4	724	58.5	214	11 Q91IA5	Q91IA5 mus musculus
5	704.5	57.0	235	11 Q91W12	Q91W12 mus musculus
6	703	56.8	211	11 Q91XL0	Q91XL0 mus musculus
7	470	38.0	108	4 Q9UL77	Q9UL77 homo sapien
8	462.5	37.4	107	4 Q96SA9	Q96SA9 homo sapien
9	449	36.3	108	4 Q9UL70	Q9UL70 homo sapien
10	437.5	35.4	107	4 Q9UL81	Q9UL81 homo sapien
11	436	35.2	108	4 Q9UL79	Q9UL79 homo sapien
12	432	34.9	116	4 Q96PF6	Q96PF6 homo sapien
13	430.5	34.8	235	11 Q99M11	Q99M11 mus musculus
14	428	34.6	236	4 Q96E61	Q96E61 homo sapien
15	414	33.5	111	11 Q920E9	Q920E9 mus musculus
16	395.5	32.0	109	4 Q9UL78	Q9UL78 homo sapien

17	383.5	31.0	233	4	Q96169	Q96169 homo sapien
18	381	30.8	108	4	Q9UL83	Q9UL83 homo sapien
19	378	30.6	298	11	Q9QYF0	Q9QYF0 mus musculus
20	376	30.4	233	11	Q91V32	Q91V32 m adult mal
21	372.5	30.1	109	4	Q9UL86	Q9UL86 homo sapien
22	372.5	30.1	109	4	Q9UL85	Q9UL85 homo sapien
23	365	29.5	103	11	Q9JL80	Q9JL80 mus musculus
24	364	29.4	109	11	Q920E6	Q920E6 mus musculus
25	350	28.3	127	11	Q925S9	Q925S9 mus musculus
26	349	28.2	114	4	Q9UL80	Q9UL80 homo sapien
27	345.5	27.9	106	5	Q9U410	Q9U410 schistosoma
28	345	27.9	107	11	Q9ERZ9	Q9ERZ9 mus musculus
29	344	27.8	99	11	Q9JL74	Q9JL74 mus musculus
30	334	27.0	101	11	Q9JL78	Q9JL78 mus musculus
31	329.5	26.6	241	11	Q921A6	Q921A6 mus musculus
32	327	26.4	97	11	Q9JL76	Q9JL76 mus musculus
33	320.5	25.9	104	11	Q9JL82	Q9JL82 mus musculus
34	305	24.7	109	6	Q9N0W5	Q9N0W5 oryctolagus
35	296	23.9	107	11	Q9JL84	Q9JL84 mus musculus
36	274.5	22.2	218	11	Q925S1	Q925S1 mus musculus
37	244	19.7	107	4	Q9UL82	Q9UL82 homo sapien
38	239.5	19.4	107	4	Q9NSD6	Q9NSD6 homo sapien
39	235.5	19.0	108	4	Q96SB0	Q96SB0 homo sapien
40	231	18.7	130	4	Q9NE29	Q9NE29 homo sapien
41	225	18.2	130	11	Q9B8W4	Q9B8W4 mus musculus
42	214	17.3	112	4	Q96JDI	Q96JDI homo sapien
43	211	17.1	267	13	Q90529	Q90529 ginglymosto
44	207.5	16.8	112	4	Q96JD2	Q96JD2 homo sapien
45	206.5	16.7	116	4	Q96JD0	Q96JD0 homo sapien

ALIGNMENTS

RESULT	1
Q99M37	
ID	Q99M37
AC	Q99M37; PRELIMINARY; PRT; 238 AA.
DT	01-JUN-2001 (TREMBLrel. 17, Created)
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	HYPOTHETICAL 26.3 KDA PROTEIN.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
RC	TISSUE.;
RA	Strausberg R.;
RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BC002035; AAH02035.1; -
DR	HSSP; P01679; 2FBJ
DR	InterPro; IPR003599; Ig.
DR	InterPro; IPR003597; Ig_cl.
DR	InterPro; IPR003600; Ig_like.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF00047; ig; 2.
DR	SMART; SM00409; IG; 2.
DR	SMART; SM00407; IGC1; 1.
DR	SMART; SM00406; IGV; 1.
DR	SMART; SM00410; IG_Like; 1.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW	Hypothetical protein.
SQ	SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 60.3%; Score 745.5; DB 11; Length 238;  
Best Local Similarity 58.1%; Pred. No. 9.1e-58;  
Matches 136; Conservative 41; Mismatches 56; Indels 1; Gaps 1;

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QY 6 ILLVLLVWPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDY-DGDSYMNWYQOKP 64
DB 5 VRLVLMFWIPASSVDVWTTQTLPSLVSLGDAQISCRSSQSIHVHSGNTYLEWYQKP 64
QY 65 GKAPKLLIYAASNLGSGIPSRFSGSGTDTFTLTITSSLOPEDFATYYCOQSNEDPRTFG 124
DB 65 GQSPFKLIYKVSNRFGVDPDRFSGSGTDTFTLKISRVAEDLGVYFCGSHVPTFGS 124
QY 125 GTKVEIKRTVAAPSVFIPTSPSLSASVGDRTVITCKASQSDY-DGDSYMNWYQOKP 184
DB 125 GTKLEIKRADAAPTIFPPSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVL 184
QY 185 ESVTEQSDKSTYSLSTLTSLKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238
DB 185 NSWTQDQSDKSTYSLSTLTSLKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238

RESULT 2
Q91WF8 PRELIMINARY; PRT; 234 AA.
AC Q91WF8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE HYPOTHETICAL 25.9 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC015292; AAH15292.1; -.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6B7812D2 CRC64;

Query Match 59.7%; Score 738; DB 11; Length 234;
Best Local Similarity 59.7%; Pred. No. 4.1e-57;
Matches 142; Conservative 34; Mismatches 58; Indels 4; Gaps 1;

QY 1 METDTILLVLLVWPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDY-DGDSYMNWY 60
DB 1 MWSSAQFLGILLLCFOGTRCDIQMTQTSSLSASLGDRVTISCRASQDI----SNLYNWY 56
QY 61 QOKPKAPKLLIYAASNLGSGIPSRFSGSGTDTFTLTITSSLOPEDFATYYCOQSNEDPR 120
DB 57 QOKPDGTVKLLIYTSRLYGLVPSRFSGSGTDTFTLTITSSLOPEDFATYYCOQSNEDPR 116
QY 121 TFGQGTVEIKRTVAAPSVFIPTSPSLSASVGDRTVITCKASQSDY-DGDSYMNWY 180
DB 117 TFGSGTKLEVKRADAAPTIFPPSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQ 176
QY 181 GNSQSVTEQSDKSTYSLSTLTSLKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238
DB 177 NGVLSNWTQDQSDKSTYSLSTLTSLKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 234

RESULT 3
Q91WS9 PRELIMINARY; PRT; 233 AA.
AC Q91WS9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE HYPOTHETICAL 25.8 KDA PROTEIN (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC015292; AAH15292.1; -.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6B7812D2 CRC64;

Query Match 59.7%; Score 738; DB 11; Length 234;
Best Local Similarity 59.7%; Pred. No. 4.1e-57;
Matches 142; Conservative 34; Mismatches 58; Indels 4; Gaps 1;

QY 1 METDTILLVLLVWPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDY-DGDSYMNWY 60
DB 1 MWSSAQFLGILLLCFOGTRCDIQMTQTSSLSASLGDRVTISCRASQDI----SNLYNWY 56
QY 61 QOKPKAPKLLIYAASNLGSGIPSRFSGSGTDTFTLTITSSLOPEDFATYYCOQSNEDPR 120
DB 57 QOKPDGTVKLLIYTSRLYGLVPSRFSGSGTDTFTLTITSSLOPEDFATYYCOQSNEDPR 116
QY 121 TFGQGTVEIKRTVAAPSVFIPTSPSLSASVGDRTVITCKASQSDY-DGDSYMNWY 180
DB 117 TFGSGTKLEVKRADAAPTIFPPSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQ 176
QY 181 GNSQSVTEQSDKSTYSLSTLTSLKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238
DB 177 NGVLSNWTQDQSDKSTYSLSTLTSLKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 234

RESULT 4
Q91A5 PRELIMINARY; PRT; 214 AA.
AC Q91A5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scFv).";
RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF152371; AAD40242.1; -.
DR HSP; P01679; 2FBJ
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; Igv; 1.
DR SMART; SM00410; Ig_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 58.5%; Score 724; DB 11; Length 214;
Best Local Similarity 62.8%; Pred. No. 6.1e-56;
Matches 137; Conservative 31; Mismatches 46; Indels 4; Gaps 1;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSDY-DGDSYMNWYQOKPKAPKLLIYAASNLG 80
DB 1 DIQLTQSPSSMWYASLGERVITCKASQDI----NSVLSWFQKPGKSPKTLIYRANLVD 56
QY 81 GIPSRFSGSGTDTFTLTITSSLOPEDFATYYCOQSNEDPRTFGQGTVEIKRTVAAPSVF 140
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RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC013496; AAH13496.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match 59.6%; Score 737; DB 11; Length 233;
Best Local Similarity 62.7%; Pred. No. 4.9e-57;
Matches 143; Conservative 29; Mismatches 52; Indels 4; Gaps 1;

QY 11 LLLVWPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDY-DGDSYMNWYQOKPKAPKL 70
DB 10 LLLCFOGSRCDIQMTQTSSLSASLGDRVTISCSQGI----ANVLYWYQOKPDGTVKL 65
QY 71 LIYAASNLGSGIPSRFSGSGTDTFTLTITSSLOPEDFATYYCOQSNEDPRTFGQGTVEI 130
DB 66 LIYTSLSHSGVPSRFSGSGTDTFTLTITSSLOPEDFATYYCOQRYLPWTFGGTKLEI 125
QY 131 KRTVAAPSVFIPTSPSLSASVGDRTVITCKASQSDY-DGDSYMNWYQOKPKAPKL 190
DB 126 KRADAAPTIFPPSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTQ 185
QY 191 DSKDSTYSLSTLTSLKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238
DB 186 DSKDSTYSLSTLTSLKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 233

RESULT 4
Q91A5 PRELIMINARY; PRT; 214 AA.
AC Q91A5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scFv).";
RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF152371; AAD40242.1; -.
DR HSP; P01679; 2FBJ
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; Igv; 1.
DR SMART; SM00410; Ig_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 58.5%; Score 724; DB 11; Length 214;
Best Local Similarity 62.8%; Pred. No. 6.1e-56;
Matches 137; Conservative 31; Mismatches 46; Indels 4; Gaps 1;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSDY-DGDSYMNWYQOKPKAPKLLIYAASNLG 80
DB 1 DIQLTQSPSSMWYASLGERVITCKASQDI----NSVLSWFQKPGKSPKTLIYRANLVD 56
QY 81 GIPSRFSGSGTDTFTLTITSSLOPEDFATYYCOQSNEDPRTFGQGTVEIKRTVAAPSVF 140
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Db 57 GVPFRFGSGSGQDYSLTISSEYEDAGIYCYLOYDEFFTFGSGTKLEIKRADAAPTVS 116
.QY 141 IFPPSDEQLKSGTASVVCCLNNFYPREAKVQWVDNALQSGNSOESVTEQDSKDSYSL 200
Db 117 IFPPSDEQLKSGTASVVCCLNNFYPREAKVQWVDNALQSGNSOESVTEQDSKDSYSL 176
.QY 201 STLFLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 177 STLTLTKDEYERHNSYTCATHKTSTSPIVKCFNRNEC 214

RESULT 5
Q91W12 PRELIMINARY; PRT; 235 AA.
AC Q91W12;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE UNKNOWN (PROTEIN FOR MGC:65842).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BREAST TUMOR;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC006643; AA006643.1; - 5FC73BDEBD5E8FEF CRC64;
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;

Query Match 57.0%; Score 704.5; DB 11; Length 235;
Best Local Similarity 60.5%; Pred. No. 3.6e-54;
Matches 134; Conservative 33; Mismatches 50; Indels 5; Gaps 1;

.QY 18 STGDIVITQSPSSLSASVGRVTTTCASQSDVDGSDYNNWYQKPGKAPKLIYAASN 77
Db 20 SRGQIVLTQSPAIMSASGERVTTTCASQSDVDGSDYNNWYQKPGKAPKLIYAASN 74
.QY 78 LESGIPRFGSGSGTDFTLTISLQPEDFATYCCQSDNEDPRTFGGQTKVEIKRTYAAP 137
Db 75 LTSVGPDRFGSGSGTDFTLTISLQPEDFATYCCQSDNEDPRTFGGQTKVEIKRTYAAP 134
.QY 138 SVTFFPDSDEQLKSGTASVVCCLNNFYPREAKVQWVDNALQSGNSOESVTEQDSKDSY 197
Db 135 TVSIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWVDNALQSGNSOESVTEQDSKDSY 194
.QY 198 SLSTLFLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 195 SMSSTLTLTKDEYERHNSYTCATHKTSTSPIVKCFNRNEC 235

RESULT 6
Q91XL0 PRELIMINARY; PRT; 211 AA.
AC Q91XL0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE ADULT MALE KIDNEY CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE CLONE:0610010P20, FULL INSERT SEQUENCE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
RA Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Horii F.,
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RA Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y.,
RA Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T.,
RA Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D.,
RA Shibata K., Shibata Y., Shinagawa A., Shiraki T., Soabe Y.,
RA Suzuki H., Tagami Y., Tagawa A., Takahashi F., Tanaka T., Tejima Y.,
RA Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsumai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multipillar sequencer.";
RL Genome Res. 10:1757-1771(2000).
DR EMBL: AK002514; BAB22154.1; -.
SQ SEQUENCE 211 AA; 23182 MW; 1A5FFA0F8BA50163 CRC64;

Query Match 56.8%; Score 703; DB 11; Length 211;
Best Local Similarity 61.3%; Pred. No. 4.2e-54;
Matches 133; Conservative 33; Mismatches 43; Indels 8; Gaps 2;

.QY 24 LTQSPSSLSASVGRVTTTCASQSDVDGSDYNNWYQKPGKAPKLIYAASNLESG 81
Db 1 MTQSPASLSVSVGTVTITTCRASENI-----YSLAWYQQRQKSPOLLVTAANLADG 54
.QY 82 IPRFSGSGSGTDFTLTISLQPEDFATYCCQSDNEDPRTFGGQTKVEIKRTYAAPSVFI 141
Db 55 VPSRFGSGSGTQYSLKINSLSQSEDFGSGYFCQHFQWGTPTFGGQTKLEIKRADAAPTYSI 114
.QY 142 FPPSDEQLKSGTASVVCCLNNFYPREAKVQWVDNALQSGNSOESVTEQDSKDSYSL 201
Db 115 FPPSDEQLKSGTASVVCCLNNFYPREAKVQWVDNALQSGNSOESVTEQDSKDSYSL 174
.QY 202 TLTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 175 TLTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 211

RESULT 7
Q9UL77
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ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 108 108
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 38.0%; Score 470; DB 4; Length 108;
Best Local Similarity 82.1%; Pred. No. 5.4e-34;
Matches 92; Conservative 8; Mismatches 8; Indels 4; Gaps 1;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGKAPKLLIYAASNL 80
Db 1 DIQMTQSPSSLSASVGDRTVITCKASQSI-----SSVLNYYQKPGKAPKLLIYAAS 56
QY 81 GIPSRFSGSGGTDFLTITSSLPQEDFATYYCQSNEDPRTFGQGTKEIKR 132
Db 57 GVPFRFSGSGGTDFLTITSSLPQEDFATYYCQSS-YSTLTFGGTKEIKR 107

RESULT 9
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 108 108
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SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 36.3%; Score 449; DB 4; Length 108;
Best Local Similarity 77.7%; Pred. No. 3.8e-32;
Matches 87; Conservative 9; Mismatches 12; Indels 4; Gaps 1;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGKAPKLLIYAASNL 80
Db 1 DIQMTQSPSSLSASVGDRTVITCKASQSI-----SNLAWYQKPGKAPKLLIYAAS 56
QY 81 GIPSRFSGSGGTDFLTITSSLPQEDFATYYCQSNEDPRTFGQGTKEIKR 132
Db 57 GVPFRFSGSGGTDFLTITSSLPQEDFATYYCQKYNAPRTFGGTKEIKR 108

RESULT 10
Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
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RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035033; AAD56269.1; -.  
DR HSP; P01607; IREI.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
FT NON\_TER 107 107  
FT SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 35.4%; Score 437.5; DB 4; Length 107;  
Best Local Similarity 77.7%; Pred. No. 3.9e-31;  
Matches 87; Conservative 10; Mismatches 10; Indels 5; Gaps 2;  
  
QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYVDYDGDSYMNYQKPGKAPKLLIYAASNL80  
Db 1 DIQMTQSPSSLSASVGDRTVITCKASQSI-----SYLWNVYQKPGKAPKLLIYAASLQ56  
  
QY 81 GIPSRFSGSGGTDFTLTISLQPEDFATYYCQSNEDPRTFGQGTKEIKR 132  
Db 57 GVPFRSGSGGTDFTLTISGLQAEDEFATYYCQSS-YSALTGPGTKVDIR 107

RESULT 11  
Q9UL79  
ID Q9UL79 PRELIMINARY; PRT; 108 AA.  
AC Q9UL79;  
DT 01-MAY-2000 (TremBLrel. 13, Created)  
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)  
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;  
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035035; AAD56271.1; -.  
DR HSP; P01607; IREI.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
FT NON\_TER 108 108  
FT SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 35.2%; Score 436; DB 4; Length 108;  
Best Local Similarity 76.8%; Pred. No. 5.3e-31;  
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QY 81 GIPSRFSGSGGTDFTLTISLQPEDFATYYCQSNEDPRTFGQGTKEIKR 132  
Db 57 GVPFRSGSGGTDFTLTISCLQSEDEFATYYCQYYSPPTFGQGTKEIKR 108

RESULT 12

Query Match 34.8%; Score 430.5; DB 11; Length 235;

Q96PF6  
ID Q96PF6 PRELIMINARY; PRT; 116 AA.  
AC Q96PF6;  
DT 01-DEC-2001 (TremBLrel. 19, Created)  
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)  
DE KAPPA 1 LIGHT CHAIN VARIABLE REGION (FRAGMENT).  
GN SDNK1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21361171; PubMed=11468171;  
RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;  
RT "The tropism of organ involvement in primary systemic amyloidosis: contributions of Ig V(L) germ line gene use and clonal plasma cell burden.";  
RT burden.";  
RL Blood 98:714-720(2001).  
DR EMBL; AF361758; AAK51465.1; -.  
FT NON\_TER 116 116  
FT SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;

Query Match 34.9%; Score 432; DB 4; Length 116;  
Best Local Similarity 70.0%; Pred. No. 1.3e-30;  
Matches 84; Conservative 15; Mismatches 17; Indels 4; Gaps 1;  
  
QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYVDYDGDSYMNYQKPGKAPKLLIYAASNL80  
Db 1 DIQMTQSPSSLSASVGDRTVITCQASQDI----ANHLNWKYQKPGAPKFLIYDGSFLKT 56  
  
QY 81 GIPSRFSGSGGTDFTLTISLQPEDFATYYCQSNEDPRTFGQGTKEIKRTVAAPSVF 140  
Db 57 GVPFRSGSGSATNFTVTISSLQPEDFATYYCQYHLLPFTFGPGTKVDKRTVAAPSVF 116

RESULT 13  
Q99M11  
ID Q99M11 PRELIMINARY; PRT; 235 AA.  
AC Q99M11;  
DT 01-JUN-2001 (TremBLrel. 17, Created)  
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)  
DE HYPOTHETICAL 25.4 KDA PROTEIN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC002129; AAH0219.1; -.  
DR HSP; P01703; 7FAB.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003600; Ig\_like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; IGV; 2.  
DR SMART; SM00407; IGV; 1.  
DR SMART; SM00406; IGV; 1.  
DR SMART; SM00410; IGV; 1.  
DR SMART; SM00410; IGV; 2.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 235 AA; 25403 MW; 39807BFE6782A3FB CRC64;

Best Local Similarity 42.2%; Pred. No. 4.5e-30;  
Matches 100; Conservative 38; Mismatches 86; Indels 13; Gaps 7;

QY 7 LLWVLLWVPGSGDIVLTQSPSLSASVGDRTVITCKASQSDYDGDSDYNNWYQOKPGK 66  
Db 6 LLLVFLHLLTGSQAQLVLTQ-PSVSTSLGSAKLPCKA--STGNIGDSYNNWYQYQYMR 62  
QY 67 APKLLIYAASNLGSGIPRSFGSGS--GSGTDFLTITISLQPEDFATYCCQSNEDPRTFGQ 124  
Db 63 SPINMIYGDLLRSGVDFSGSDSSNSAFLTIQNVQADDEADYCCQSSGIRVFGG 122  
QY 125 GTKVEI-KRTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNEYPREAKVQWKVDNALQSGNS 183  
Db 123 GTRLTVLSPQKTSPTVLPFPSPSEELTKATLVCTISDFPGVTVDMKADG---TPVT 179  
QY 184 QESVTEQDSK--DSTVSLSTLTLKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238  
Db 180 QGVETTPQSKQNNKYNMASSYLTLAKAWETHSSYSCQVTHEG--HTVEKSLRADC 234

RESULT 14  
Q96E61 PRELIMINARY; PRT; 236 AA.  
AC Q96E61;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE UNKNOWN (PROTEIN FOR MGC:17259).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN, AND GLIOBLASTOMA WITH EGFR AMPLIFICATION;  
RA Strausberg R.;  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC012876; AAH12876.1; -  
SQ SEQUENCE 236 AA; 24712 MW; 7EC9FB3622FED957 CRC64;

Query Match 34.6%; Score 428; DB 4; Length 236;  
Best Local Similarity 41.9%; Pred. No. 7.4e-30;  
Matches 99; Conservative 40; Mismatches 87; Indels 10; Gaps 7;

QY 7 LLWVLLWVPGSGDIVLTQSPSLSASVGDRTVITCKASQSDYDGDSDYNNWYQOKPGK 66  
Db 6 LLLTLLAHCTGSAQSVLAQ-PFSVSGAPGQTVTISCTGS-STNIGAGYAVHWYQFPGA 63  
QY 67 APKLLIYAASNLGSGIPRSFGSGSGTDFLTITISLQPEDFATYCCQ--OSNEDPRTFGQ 124  
Db 64 APKVLIVGNYNRPGVPDRFSGSGKSGTSASLAITLQAEADYCCQSDGSLSGSVFGA 123  
QY 125 GTKVEI-KRTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNEYPREAKVQWKVDNA-LOSNG 182  
Db 124 GTKVTILGQKANTPTVLPFPSPSEELQANKATLVCLISDFPGAVTVAMKADGSPVKG- 182  
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Db 183 -VETTPKSKQNNKYAASSYLSLTPQWKSRSYSCQVTHEG--STVEKTVAPTEC 235

RESULT 15  
Q920E9 PRELIMINARY; PRT; 111 AA.  
AC Q920E9;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE PTERIN-MIMICKING ANTI-IDIOTOPE KAPPA CHAIN VARIABLE REGION (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;  
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307935; AAL09419.1; -  
FT NON\_TER 111  
FT NON\_TER 111  
SQ SEQUENCE 111 AA; 12046 MW; 1E46988AA6858526 CRC64;

Query Match 33.5%; Score 414; DB 11; Length 111;  
Best Local Similarity 71.2%; Pred. No. 4.7e-29;  
Matches 79; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

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Db 1 DIVLTQSPASLAVSLGORATISCRASKSVSTSGYSYHWHYQOKPGPKLLIYLASNLG 60  
QY 81 GIPSRFSGSGSGTDFLTITISLQPEDFATYCCQSNEDPRTFGOGTKVEIK 131  
Db 61 GVPARFSGSGSGTDFLTINHPVEEADAATYCOHSRELPTFTGGGTKEIK 111

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Job time: 683 sec



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09/447,662

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

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Perfect score: 246  
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Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	246	100.0	145	AAW83038	Anti-Fas humanised
2	246	100.0	145	AA14775	Fragment of humani
3	246	100.0	145	AAW90925	Humanised anti-Fas
4	246	100.0	464	AAW83041	Anti-Fas MAB HFE7A
5	246	100.0	464	AA14747	Mouse anti-Fas an
6	246	100.0	464	AAW90897	Murine anti-Fas an
7	246	100.0	470	AAW83036	Anti-Fas humanised
8	246	100.0	470	AAW83037	Anti-Fas humanised
9	246	100.0	470	AA14776	Humanised anti-Fas
10	246	100.0	470	AA14779	Humanised anti-Fas
11	246	100.0	470	AAW90926	Humanised HFE7A de

12	246	100.0	470	21	AAW90929	Humanised HFE7A de
13	246	100.0	470	21	AAW90933	Humanised anti-Fas
14	246	100.0	470	21	AAW90934	Humanised anti-Fas
15	246	100.0	470	21	AAW90935	Humanised anti-Fas
16	246	100.0	470	21	AAW90936	Humanised HFE7A de
17	176	71.5	119	16	AAW90936	Anti-EGFR antibody
18	176	71.5	119	16	AAW90936	Anti-EGFR antibody
19	164	66.7	111	18	AAW90936	Anti-DNA antibody
20	164	66.7	111	18	AAW90936	Anti-DNA antibody
21	164	66.7	111	18	AAW90936	Anti-DNA antibody
22	161	65.4	119	21	AAW90936	Murine 15B8 heavy
23	160	65.0	111	18	AAW90936	Anti-DNA antibody
24	158	64.2	309	22	AAW90936	SNV-env leader/hum
25	157.5	64.0	240	16	AAW90936	ScFv(FWP51). Synt
26	157.5	64.0	241	13	AAW90936	FWP51 fusion prote
27	157.5	64.0	637	13	AAW90936	(FRP51)-ETA fusion
28	157	63.8	111	18	AAW90936	Anti-DNA antibody
29	156	63.4	137	19	AAW90936	Protein sequence o
30	156	63.4	140	19	AAW90936	Murine Act-1 heavy
31	156	63.4	144	19	AAW90936	Consensus protein
32	156	63.4	180	19	AAW90936	Heavy chain of a h
33	155	63.0	117	20	AAW90936	Murine 6G425 heavy
34	155	63.0	117	20	AAW90936	Humanised 6G425 F(
35	155	63.0	117	21	AAW90936	Humanised murine 6
36	155	63.0	117	21	AAW90936	Murine 6G425 heavy
37	155	63.0	117	21	AAW90936	Humanised 6G425 F(
38	155	63.0	117	21	AAW90936	Single chain Fv an
39	154	62.6	262	22	AAW90936	Anti-gp54 MAB T16
40	153	62.2	119	19	AAW90936	Anti-gp54 MAB T16
41	153	62.2	245	19	AAW90936	Monoclonal antibod
42	148.5	60.4	125	20	AAW90936	Anti-IL-8 MAB 6G4
43	147.5	60.0	135	16	AAW90936	Anti IL-8 antibody
44	147.5	60.0	135	18	AAW90936	Anti IL-8 monoclon
45	147.5	60.0	135	18	AAW90936	

ALIGNMENTS

RESULT 1  
AAW83038  
ID AAW83038 standard; Protein; 145 AA.  
AC AAW83038;  
XX  
XX  
XX 15-MAR-1999 (first entry)  
XX  
XX Anti-Fas humanised antibody HFE7A heavy chain variable region.  
XX  
XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;  
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;  
KW systemic lupus erythematosus; graft versus host disease;  
KW Sjogren syndrome; pernicious anaemia; Addison's disease;  
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
KW rheumatoid arthritis; autoimmune haemolytic anaemia;  
KW myasthenia gravis; multiple sclerosis; Basedow's disease;  
KW thrombopenia purpura; insulin-dependent diabetes; allergy;  
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
KW transplant rejection; therapy.  
XX  
XX Homo sapiens.  
OS  
OS Synthetic.  
XX  
XX  
XX Key Location/Qualifiers  
XX Peptide 1..19  
XX Protein /label= Sig\_peptide  
XX Protein 20..145  
XX Region /label= Mat\_protein  
XX Region 50..54  
XX /label= CDR\_H1  
XX /note= "Claim 9"  
XX Region 69..84

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FT FT /label= CDR_H2
FT FT /note= "claim 9"
FT FT 118..129
FT FT /label= CDR_H3
FT FT /note= "claim 9"
XX AU9859701-A.
XX 08-OCT-1998.
XX 30-MAR-1998; 98AU-0059701.
XX 08-OCT-1997; 97JP-0276064.
XX 01-APR-1997; 97JP-0082953.
XX 25-JUN-1997; 97JP-0169088.
XX (SANY ) SANKYO CO LTD.
XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
XX Masahiko O, Nobufusa S, Shin Y, Tohru T;
XX WPI; 1998-543440/47.
XX N-PSDB; AAV70104.
XX New antibodies and proteins bind conserved epitope of Fas antigen -
XX used to evaluate drugs in animal models and to treat Fas-associated
XX diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
XX myocarditis, hepatitis and AIDS
XX Example 3; Page 207; 292pp; English.
XX This is the amino acid sequence of the VD type humanised heavy
XX chain variable region of murine anti-human Fas monoclonal antibody
XX HFE7A. It was utilised in a claimed humanised HFE7A heavy chain
XX (see AAV70079). The invention provides methods for producing humanised
XX antibodies by culturing host cells. Humanised versions of HFE7A (see
XX AAV83031-37) are capable of inducing apoptosis in abnormal cells
XX expressing Fas, and of inhibiting Fas-induced apoptosis in normal
XX cells. Humanised antibodies are used to evaluate, in animal models,
XX treatments of diseases that involve Fas/Fas ligand interactions, and
XX also to treat such diseases, including autoimmune disease (e.g.
XX systemic lupus erythematosus, Hashimoto's disease, graft versus host
XX disease, Sjogren syndrome, pernicious anaemia, Addison's disease,
XX scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid
XX arthritis, autoimmune haemolytic anaemia, sterility, myasthenia
XX gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura
XX and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
XX myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
XX anaemia, hepatitis, AIDS and transplant rejection (all claimed).
XX SQ Sequence 145 AA;

Query Match 100.0%; Score 246; DB 19; Length 145;
Best Local Similarity 42.5%; Pred. NO. 1.4e-11;
Matches 34; Conservative 46; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMQXXXXXXXXXXEIDPSDTYNQFKGXXXXXXXXXXXXXXXXXXXXX 60
Db 50 symqvwkqapgrlwmgeidpsdtytnqkfkgtlvtstastaymelsirs 109
QY 61 XXXXXXXXNRDYSNNWYFDV 80
Db 110 tavyyccarnrdysnnwfydv 129

RESULT 2
AAB14775
ID AAB14775 standard; peptide; 145 AA.
XX AC AAB14775;
XX 24-NOV-2000 (first entry)

```

```

XX DE Fragment of humanised anti-Fas antibody heavy chain, SEQ ID NO:75.
XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
KW murine; humanised antibody; complementarity determining region; CDR;
KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
KW hepatitis; AIDS; graft rejection; heavy chain.
XX OS Chimeric - Mus musculus.
XX OS Chimeric - Homo sapiens.
XX PN JP2000169393-A.
XX 20-JUN-2000.
XX 30-SEP-1999; 99JP-0278301.
XX 30-SEP-1998; 98JP-0276883.
XX (SANY ) SANKYO CO LTD.
XX WPI; 2000-485645/43.
XX N-PSDB; AAV72146.
XX Preventive or treating agent for the diseases caused by an abnormality
XX in the Fas/Fas ligand system e.g. autoimmune diseases, contains
XX anti-Fas antibody.
XX Example 15; Page 88; 139pp; Japanese.
XX The invention relates to compositions for the prevention or treatment
XX or diseases caused by an abnormality in the Fas/Fas ligand system
XX containing an anti-Fas antibody as the active component. The anti-Fas
XX antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
XX or a humanised version of HFE7A containing identical CDRs
XX (complementarity determining regions) to antibody HFE7A. Via its
XX interaction with Fas, the antibody of the invention acts as a modulator
XX of apoptosis. The compositions of the invention may therefore be used in
XX the treatment or prevention of conditions such as autoimmune diseases,
XX allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
XX glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
XX and organ graft rejection. Sequences AAB14775-B14776 and AAB14779
XX represent the heavy chains (or fragments thereof) of various humanised
XX HFE7A-derived anti-Fas antibodies.
XX SQ Sequence 145 AA;

Query Match 100.0%; Score 246; DB 21; Length 145;
Best Local Similarity 42.5%; Pred. NO. 1.4e-11;
Matches 34; Conservative 46; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMQXXXXXXXXXXEIDPSDTYNQFKGXXXXXXXXXXXXXXXXXXXXX 60
Db 50 symqvwkqapgrlwmgeidpsdtytnqkfkgtlvtstastaymelsirs 109
QY 61 XXXXXXXXNRDYSNNWYFDV 80
Db 110 tavyyccarnrdysnnwfydv 129

RESULT 3
AAW90925
ID AAW90925 standard; Protein; 145 AA.
XX AC AAW90925;
XX 08-AUG-2000 (first entry)
XX Humanised anti-Fas antibody HFE7A heavy chain protein.
XX

```

KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
 KW dermatologic; anti-arthritis; antiviral; immunomodulatory; cardiac;  
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
 KW nephrotropic; antifertility; neuroprotective; antiartherosclerotic;  
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
 XX  
 OS Synthetic.  
 XX  
 XX EP990663-A2.  
 XX  
 XX  
 XX PD 05-APR-2000.  
 XX  
 XX PF 29-SEP-1999; 99EP-0307711.  
 XX  
 XX PR 30-SEP-1998; 98JP-0276881.  
 XX PR 30-SEP-1998; 98JP-0276882.  
 XX  
 XX (SANY ) SANKYO CO LTD.  
 XX  
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 PI WPI; 2000-258930/23.  
 DR N-PSDB; AAA11584.  
 XX  
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems  
 PS Example reference 15; Page 126-127; 263pp; English.  
 XX  
 CC This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatologic, immunosuppressive, thyromimetic,  
 CC antirheumatic, nephrotropic, antilinfertility, neuroprotective,  
 CC antiartherosclerotic, cardiac and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody HFE7A heavy chain which is used in  
 CC the method described in the invention.  
 XX  
 XX Sequence 145 AA;

Query Match 100.0%; Score 246; DB 21; Length 145;  
 Best Local Similarity 42.5%; Pred. No. 1.4e-11;  
 Matches 34; Conservative 46; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMQXXXXXXXXXXXXXIDPSDSTYNQKFKGXXXXXXXXXXXXXXXXXXXXX 60  
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Db 50 sywmqvwkgapqgqlwmggeidpsdsytynqkfkgtatltvdsastaymelslrsd 109  
 QY 61 XXXXXXXXNRDYSNNWYFDV 80  
 Db 110 tavyycarnrdysnnwfydv 129  
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 AAW83041  
 ID AAW83041 standard; Protein; 464 AA.  
 XX  
 AC AAW83041;  
 XX  
 XX 15-MAR-1999 (first entry)  
 XX  
 XX Anti-Fas MAB HFE7A heavy chain.  
 XX  
 KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;  
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;  
 KW systemic lupus erythematosus; graft versus host disease;  
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;  
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;  
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;  
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;  
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
 KW transplant rejection; therapy; complementarity determining region;  
 KW CDR.  
 XX  
 OS Mus musculus.  
 XX  
 XX Key Location/Qualifiers  
 FT Peptide 1..19  
 FT Protein /label= Sig\_peptide  
 FT /label= 20..464  
 FT /label= Mat\_protein  
 FT Region 20..140  
 FT /label= Variable  
 FT Region 141..464  
 FT /label= Constant  
 FT Region 50..54  
 FT /label= CDR\_H1  
 FT /note= "claim 9"  
 FT Region 69..84  
 FT /label= CDR\_H2  
 FT /note= "claim 9"  
 FT Region 118..128  
 FT /label= CDR\_H3  
 FT /note= "claim 9"  
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 AU9859701-A.  
 XX  
 PD 08-OCT-1998.  
 XX  
 XX 30-MAR-1998; 98AU-0059701.  
 XX  
 XX 08-OCT-1997; 97JP-0276064.  
 XX 01-APR-1997; 97JP-0082953.  
 XX 25-JUN-1997; 97JP-0169088.  
 XX  
 XX (SANY ) SANKYO CO LTD.  
 XX  
 XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;  
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;  
 XX  
 XX WPI; 1998-543440/47.  
 DR N-PSDB; AAV71029.  
 XX  
 PT New antibodies and proteins bind conserved epitope of Fas antigen -  
 PT used to evaluate drugs in animal models and to treat Fas-associated  
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
 PT myocarditis, hepatitis and AIDS





XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
PT inflammatory or autoimmune disease, induces apoptosis selectively in  
PT cells with abnormal Fas-Fas ligand systems -  
XX  
PS Example reference 4; Page 100-102; 263pp; English.  
XX  
CC This invention describes a novel humanized anti-Fas antibody-like  
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
CC ligand system, by binding to Fas on the cell surface, and prevents  
CC apoptosis in cells with a normal system, by inhibiting binding between  
CC Fas and its ligand. The products of the invention have anti-inflammatory,  
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,  
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
CC antirheumatic, nephrotropic, antinfertility, neuroprotective,  
CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce  
CC inhibition of ligand binding. (I) are used to treat and/or prevent  
CC diseases associated with the Fas/Fas ligand system, especially systemic  
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
CC cells. They bind to both human and murine Fas, so can be evaluated in  
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
CC the native ligand, do not induce liver disease, and have reduced risk of  
CC inducing a human anti-murine antibody response. This sequence represents  
CC a murine anti-Fas monoclonal antibody HFE7A heavy chain described in the  
CC method of the invention.  
XX  
SQ Sequence 464 AA;

Query Match 100.0%; Score 246; DB 21; Length 464;  
Best Local Similarity 42.5%; Pred. No. 3.9e-10;  
Matches 34; Conservative 46; Mismatches 0; Indels 0; Gaps 0;

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Db 50 SYWMQVKGKPGGKLGIDPSDYSYNYNQKFGKATLTVDSSSTAYMQLSLTSD 109  
QY 61 XXXXXXXXNRDYSNNWYFDV 80  
Db 110 SAVVYCARNDYSNNWYFDV 129

RESULT 7  
ID AAW83036 standard; Protein: 470 AA.  
XX  
AC AAW83036;  
XX  
DT 15-MAR-1999 (first entry)  
XX  
DE Anti-Fas humanised antibody HFE7A heavy chain.  
XX  
KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;  
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;  
KW systemic lupus erythematosus; graft versus host disease;  
KW Sjogren syndrome; pernicious anaemia; Addison's disease;  
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
KW rheumatoid arthritis; autoimmune haemolytic anaemia;  
KW myasthenia gravis; multiple sclerosis; Basedow's disease;  
KW thrombopenia purpura; insulin-dependent diabetes;  
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
KW transplant rejection; therapy.  
XX

OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key  
FT Peptide  
FT 1..19  
FT /label= Sig\_peptide  
FT 20...470  
FT /label= Mat\_protein  
FT 20...140  
FT /label= Variable  
FT 141..464  
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FT 50...54  
FT /label= CDR\_H1  
FT /note= "claim 9"  
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FT /note= "claim 9"  
FT 118..129  
FT /label= CDR\_H3  
FT /note= "claim 9"  
XX  
AU9859701-A.  
XX  
PD 08-OCT-1998.  
XX  
PF 30-MAR-1998; 99AU-0059701.  
XX  
PR 08-OCT-1997; 97JP-0276064.  
PR 01-APR-1997; 97JP-0082953.  
PR 25-JUN-1997; 97JP-0169088.  
XX  
XX (SANY ) SANKYO CO LTD.  
XX  
PI Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;  
PI Masahiko O, Nobufusa S, Shin Y, Tohru T;  
XX  
DR WPI: 1998-543440/47.  
DR N-PSDB; AAV70079.  
XX  
PT New antibodies and proteins bind conserved epitope of Fas antigen -  
PT used to evaluate drugs in animal models and to treat Fas-associated  
PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
PT myocarditis, hepatitis and AIDS  
XX  
PS Claim 22; Page 212-213; 292pp; English.  
XX  
CC This is the amino acid sequence of the VD type humanised heavy  
CC chain of murine anti-human Fas monoclonal antibody HFE7A. E. coli  
CC pgHSL7A62 SANK 73397 harbors plasmid pgHSL7A62 carrying a fusion  
CC fragment of the humanised VD type HFE7A heavy chain and DNA  
CC encoding human IgG1 constant region (see AAV70079), and is deposited  
CC as FERM BP-6074 (claimed). The invention provides methods for  
CC producing humanised antibodies by culturing host cells. Humanised  
CC versions of HFE7A (see AAW83031-37), like native HFE7A, are capable  
CC of inducing apoptosis in abnormal cells expressing Fas, and of  
CC inhibiting Fas-induced apoptosis in normal cells. The humanised  
CC antibodies are used to evaluate, in animal models, treatments of  
CC diseases that involve Fas/Fas ligand interactions, and also to  
CC treat such diseases, including autoimmune disease (e.g. systemic  
CC lupus erythematosus, Hashimoto's disease, graft versus host disease,  
CC Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,  
CC Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,  
CC autoimmune haemolytic anaemia, sterility, myasthenia gravis,  
CC multiple sclerosis, Basedow's disease, thrombopenia purpura and  
CC insulin-dependent diabetes), allergies, atopy, arteriosclerosis,  
CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic  
CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).  
XX  
SQ Sequence 470 AA;

Query Match 100.0%; Score 246; DB 19; Length 470;

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Best Local Similarity 42.5%; Pred. No. 4.le-10;
Matches 34; Conservative 46; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWMQXXXXXXXXXXEIDPSDYTNYNQKFGXXXXXXXXXXXXXXXXXXXXX 60
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    | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
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    : : : : : | | | | | : : : : : | | | | | : : : : : | | | | |
Qy 61 XXXXXXXXNRDYSNNWYFDV 80
    : : : : : | | | | | : : : : : | | | | | : : : : : | | | | |
Db 110 tavvyccarnrdysnnwyfdv 129
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RESULT 8
AAW83037
ID AAW83037 standard; Protein; 470 AA.
AC AAW83037;
XX
XX 15-MAR-1999 (first entry)
DE
DE Anti-Fas humanised antibody HFE7A heavy chain.
XX
XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
KW systemic lupus erythematosus; graft versus host disease;
KW Sjogren syndrome; pernicious anaemia; Addison's disease;
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KW rheumatoid arthritis; autoimmune haemolytic anaemia;
KW myasthenia gravis; multiple sclerosis; Basedow's disease;
KW thrombopenia purpura; insulin-dependent diabetes; allergy;
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy; AIDS;
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KW transplant rejection; therapy.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Sig_peptide
FT Protein 20..470
FT /label= Mat_protein
FT Region 20..140
FT /label= Variable
FT Region 141..464
FT /label= Constant
FT Region 50..54
FT /label= CDR_H1
FT /note= "claim 9"
FT Region 69..84
FT /label= CDR_H2
FT /note= "claim 9"
FT Region 118..129
FT /label= CDR_H3
FT /note= "claim 9"
XX
XX AU9859701-A.
XX
XX 08-OCT-1998.
XX
XX 30-MAR-1998; 98AU-0059701.
XX
XX 08-OCT-1997; 97JP-0276064.
XX 01-APR-1997; 97JP-0082953.
XX 25-JUN-1997; 97JP-0169088.
XX
XX (SANY ) SANKYO CO LTD.
XX
XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
XX Masahiko O, Nobufusa S, Shin Y, Tohru T;
XX
XX WPI; 1998-543440/47.
XX N-PSDB; AAV70080.

```

XX New antibodies and proteins bind conserved epitope of Fas antigen -  
 PT used to evaluate drugs in animal models and to treat Fas-associated  
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
 PT myocarditis, hepatitis and AIDS  
 XX  
 PS Claim 22; Page 225-227; 292pp; English.

XX This is the amino acid sequence of the HV type humanised heavy  
 CC chain of murine anti-human Fas monoclonal antibody HFE7A. It  
 CC includes humanising R44G and A76T amino acid substitutions that are  
 CC conserved in the human IgG heavy chain. Host Escherichia coli  
 CC pGHPDHV3 SANK 70298 harbors plasmid pGHPDHV3 carrying a fusion  
 CC fragment of the humanised HV type HFE7A heavy chain and DNA  
 CC encoding human IgG1 constant region (see AAV70080), and is deposited  
 CC as FERM BP-6273 (claimed). The invention provides methods for  
 CC producing humanised antibodies by culturing host cells. Humanised  
 CC versions of HFE7A (see AAW83031-37), like native HFE7A, are capable  
 CC of inducing apoptosis in abnormal cells expressing Fas, and of  
 CC inhibiting Fas-induced apoptosis in normal cells. The humanised  
 CC antibodies are used to evaluate, in animal models, treatments of  
 CC diseases that involve Fas/Fas ligand interactions, and also to  
 CC treat such diseases, including autoimmune disease (e.g. systemic  
 CC lupus erythematosus, Hashimoto's disease, graft versus host disease,  
 CC Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,  
 CC Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,  
 CC autoimmune haemolytic anaemia, sterility, myasthenia gravis,  
 CC multiple scleritis, Basedow's disease, thrombopenia purpura and  
 CC insulin-dependent diabetes), allergies, atopy, arteriosclerosis,  
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic  
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).  
 XX  
 SQ Sequence 470 AA;

Query Match 100.0%; Score 246; DB 19; Length 470;  
 Best Local Similarity 42.5%; Pred. No. 4.le-10;  
 Matches 34; Conservative 46; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMQXXXXXXXXXXEIDPSDYTNYNQKFGXXXXXXXXXXXXXXXXXXXXX 60  
 . | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :  
 Db 50 symwqvwkqpgqqlwemgeidpsdytnynqkfkgtatltvdsastaymelsslrds 109  
 : : : : : | | | | | : : : : : | | | | | : : : : : | | | | |  
 QY 61 XXXXXXXXNRDYSNNWYFDV 80  
 : : : : : | | | | | : : : : : | | | | | : : : : : | | | | |  
 Db 110 tavvyccarnrdysnnwyfdv 129

RESULT 9  
 AAB14776  
 ID AAB14776 standard; Protein; 470 AA.  
 XX  
 AC AAB14776;  
 XX  
 XX 24-NOV-2000 (first entry)  
 XX  
 XX Humanised anti-Fas antibody heavy chain, SEQ ID NO:89.

XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;  
 KW murine; humanised antibody; complementarity determining region; CDR;  
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;  
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;  
 KW hepatitis; AIDS; graft rejection; heavy chain.

OS Chimeric - Mus musculus.  
 OS Chimeric - Homo sapiens.

XX JP2000169393-A.  
 PN  
 XX 20-JUN-2000.  
 PD  
 XX 30-SEP-1999; 99JP-0278301.

```

XX 30-SEP-1998; 98JP-0276883.
XX (SANY ) SANKYO CO LTD.
XX WPI; 2000-485645/43.
XX DR N-PSDB; AAA72159.
XX PT Preventive or treating agent for the diseases caused by an abnormality
XX in the Fas/Fas ligand system e.g. autoimmune diseases, contains
XX anti-Fas antibody -
XX Claim 21; Page 95-96; 139pp; Japanese.
XX The invention relates to compositions for the prevention or treatment
XX of diseases caused by an abnormality in the Fas/Fas ligand system
XX containing an anti-Fas antibody as the active component. The anti-Fas
XX antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
XX or a humanised version of HFE7A containing identical CDRs
XX (complementarity determining regions) to antibody HFE7A. Via its
XX interaction with Fas, the antibody of the invention acts as a modulator
XX of apoptosis. The compositions of the invention may therefore be used in
XX the treatment or prevention of conditions such as autoimmune diseases,
XX allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
XX glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
XX and organ graft rejection. Sequences AAB14775-B14776 and AAB14779
XX represent the heavy chains (or fragments thereof) of various humanised
XX HFE7A-derived anti-Fas antibodies.
XX Sequence 470 AA;
SQ
Query Match 100.0%; Score 246; DB 21; Length 470;
Best Local Similarity 42.5%; Pred. No. 4.1e-10;
Matches 34; Conservative 46; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYWMQXXXXXXXXXXXXXIDPDSYTNQKFGKXXXXXXXXXXXXXXXXXXXXX 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 50 sywmqvwkqpgqlwmgeldpsdsytnqkfgkatltvdtstaysaimelsslrse 109
QY 61 XXXXXXXXNRDYSNNWYFDV 80
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 110 tavyyccarnrdysnnwyfdv 129
RESULT 10
AAB14779
ID AAB14779 standard; Protein; 470 AA.
XX AC AAB14779;
XX DT 24-NOV-2000 (first entry)
XX DE Humanised anti-Fas antibody heavy chain, SEQ ID NO:117.
XX KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
XX murine; humanised antibody; complementarity determining region; CDR;
XX human Fas; Fas ligand; apoptosis modulator; programmed cell death;
XX autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
XX cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
XX hepatitis; AIDS; graft rejection; heavy chain.
XX OS Chimeric - Mus musculus.
XX OS Chimeric - Homo sapiens.
XX PN JP2000169393-A.
XX PD 20-JUN-2000.
XX PF 30-SEP-1999; 99JP-0278301.
XX PR 30-SEP-1998; 98JP-0276883.

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```

PA (SANY ) SANKYO CO LTD.
XX WPI; 2000-485645/43.
XX DR N-PSDB; AAA72184.
XX PT Preventive or treating agent for the diseases caused by an abnormality
XX in the Fas/Fas ligand system e.g. autoimmune diseases, contains
XX anti-Fas antibody -
XX Claim 21; Page 108-109; 139pp; Japanese.
XX The invention relates to compositions for the prevention or treatment
XX of diseases caused by an abnormality in the Fas/Fas ligand system
XX containing an anti-Fas antibody as the active component. The anti-Fas
XX antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
XX or a humanised version of HFE7A containing identical CDRs
XX (complementarity determining regions) to antibody HFE7A. Via its
XX interaction with Fas, the antibody of the invention acts as a modulator
XX of apoptosis. The compositions of the invention may therefore be used in
XX the treatment or prevention of conditions such as autoimmune diseases,
XX allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
XX glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
XX and organ graft rejection. Sequences AAB14775-B14776 and AAB14779
XX represent the heavy chains (or fragments thereof) of various humanised
XX HFE7A-derived anti-Fas antibodies.
XX Sequence 470 AA;
SQ
Query Match 100.0%; Score 246; DB 21; Length 470;
Best Local Similarity 42.5%; Pred. No. 4.1e-10;
Matches 34; Conservative 46; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYWMQXXXXXXXXXXXXXIDPDSYTNQKFGKXXXXXXXXXXXXXXXXXXXXX 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 50 sywmqvwkqpgqlwmgeldpsdsytnqkfgkatltvdtstaysaimelsslrse 109
QY 61 XXXXXXXXNRDYSNNWYFDV 80
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 110 tavyyccarnrdysnnwyfdv 129
RESULT 11
AAW90926
ID AAW90926 standard; Protein; 470 AA.
XX AC AAW90926;
XX DT 08-AUG-2000 (first entry)
XX DE Humanised HFE7A designed heavy chain protein.
XX KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
XX anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
XX dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
XX nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
XX hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
XX Hashimoto disease; rheumatoid arthritis; graft versus host disease;
XX Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
XX Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
XX multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
XX insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
XX cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX OS Synthetic.
XX PN EP990663-A2.
XX PD 05-APR-2000.
XX PF 29-SEP-1999; 99EP-0307711.
XX PR 30-SEP-1998; 98JP-0276881.

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PR 30-SEP-1998; 98JP-0276882.  
XX (SANY ) SANKYO CO LTD.  
XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
XX WPI: 2000-258930/23.  
DR N-PSDB; AAA11597.  
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
PT inflammatory or autoimmune disease, induces apoptosis selectively in  
PT cells with abnormal Fas-Fas ligand systems -  
XX  
XX Example reference 15; Page 134-136; 263pp; English.  
XX This invention describes a novel humanized anti-Fas antibody-like  
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
CC ligand system, by binding to Fas on the cell surface, and prevents  
CC apoptosis in cells with a normal system, by inhibiting binding between  
CC Fas and its ligand. The products of the invention have anti-inflammatory,  
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
CC antirheumatic, nephrotropic, cardiatic and hepatotropic activity. (I) induce  
CC antiarteriosclerotic, cardiatic and hepatotropic activity. (I) induce  
CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
CC inhibition of ligand binding. (I) are used to treat and/or prevent  
CC diseases associated with the Fas/Fas ligand system, especially systemic  
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
CC cells. They bind to both human and murine Fas, so can be evaluated in  
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
CC the native ligand, do not induce liver disease, and have reduced risk of  
CC inducing a human anti-murine antibody response. This sequence represents  
CC a humanised anti-Fas antibody HFE7A designed heavy chain which is used in  
CC the method described in the invention.  
XX  
SQ Sequence 470 AA;  
Query Match 100.0%; Score 246; DB 21; Length 470;  
Best Local Similarity 42.5%; Pred. NO. 4.1e-10; Indels 0; Gaps 0;  
Matches 34; Conservative 46; Mismatches 0;  
QY 1 SYWMQXX 60  
Db 50 symwqvwkqapggqlwemgeidpsdysytnyngkfkgkatltvdtstastymelssrsd 109  
QY 61 XXXXXXXXXNRDYSNNWYFDV 80  
Db 110 tavyyccarnrdysnnwfydv 129  
RESULT 12  
AAW90929  
ID AAW90929 standard; Protein; 470 AA.  
XX  
XX AAW90929;  
AC  
XX  
DT 08-AUG-2000 (first entry)  
DE  
DE Humanised HFE7A designed heavy chain protein #2.  
XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
XX anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiatic;  
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;

KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
XX Synthetic.  
XX EP990663-A2.  
XX 05-APR-2000.  
XX 29-SEP-1999; 99EP-0307711.  
XX 30-SEP-1998; 98JP-0276881.  
XX 30-SEP-1998; 98JP-0276882.  
XX (SANY ) SANKYO CO LTD.  
XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
XX WPI: 2000-258930/23.  
XX N-PSDB; AAA11622.  
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
PT inflammatory or autoimmune disease, induces apoptosis selectively in  
PT cells with abnormal Fas-Fas ligand systems -  
XX  
XX Example reference 22; Page 150-152; 263pp; English.  
XX This invention describes a novel humanized anti-Fas antibody-like  
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
CC ligand system, by binding to Fas on the cell surface, and prevents  
CC apoptosis in cells with a normal system, by inhibiting binding between  
CC Fas and its ligand. The products of the invention have anti-inflammatory,  
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,  
CC antiarteriosclerotic, cardiatic and hepatotropic activity. (I) induce  
CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
CC inhibition of ligand binding. (I) are used to treat and/or prevent  
CC diseases associated with the Fas/Fas ligand system, especially systemic  
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
CC cells. They bind to both human and murine Fas, so can be evaluated in  
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
CC the native ligand, do not induce liver disease, and have reduced risk of  
CC inducing a human anti-murine antibody response. This sequence represents  
CC a humanised anti-Fas antibody HFE7A designed heavy chain which is used in  
CC the method described in the invention.  
XX  
SQ Sequence 470 AA;  
Query Match 100.0%; Score 246; DB 21; Length 470;  
Best Local Similarity 42.5%; Pred. NO. 4.1e-10; Indels 0; Gaps 0;  
Matches 34; Conservative 46; Mismatches 0;  
QY 1 SYWMQXX 60  
Db 50 symwqvwkqapggqlwemgeidpsdysytnyngkfkgkatltvdtstastymelssrsd 109  
QY 61 XXXXXXXXXNRDYSNNWYFDV 80  
Db 110 tavyyccarnrdysnnwfydv 129

Db 110 tavyycarnrdysnnwyfdv 129

RESULT 13  
AAW90933  
ID AAW90933 standard; Protein: 470 AA.  
XX AC AAW90933;  
XX DT 08-AUG-2000 (first entry)  
XX DE Humanised anti-Fas designed heavy chain Heu 1 protein.  
XX KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;  
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;  
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
KW Goodpasture syndrome; Crohn's disease; myasthenia gravis;  
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
XX OS Synthetic.  
XX EP990663-A2.  
XX PN 05-APR-2000.  
XX PD  
XX PF 29-SEP-1999; 99EP-0307711.  
XX PR 30-SEP-1998; 98JP-0276881.  
XX PR 30-SEP-1998; 98JP-0276882.  
XX PA (SANY ) SANKYO CO LTD.  
XX PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
XX WPI: 2000-258930/23.  
XX N-PSDB; AAA11644.  
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
XX inflammatory or autoimmune disease, induces apoptosis selectively in  
XX cells with abnormal Fas-Fas ligand systems -  
XX Claim 2; Page 169-170; 263pp; English.  
XX This invention describes a novel humanized anti-Fas antibody-like  
XX molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
XX ligand system, by binding to Fas on the cell surface, and prevents  
XX apoptosis in cells with a normal system, by inhibiting binding between  
XX Fas and its ligand. The products of the invention have anti-inflammatory,  
XX anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
XX immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
XX antirheumatic, nephrotropic, antiinfertility, neuroprotective,  
XX antiarteriosclerotic, cardiac and hepatropic activity. (I) induce  
XX apoptosis by binding to cell surface Fas or inhibit it by competitive  
XX inhibition of ligand binding. (I) are used to treat and/or prevent  
XX diseases associated with the Fas/Fas ligand system, especially systemic  
XX lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
XX versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
XX anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
XX disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
XX multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
XX dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
XX cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
XX (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
XX inhibit apoptosis in normal cells but selectively induce it in abnormal  
XX cells. They bind to both human and murine Fas, so can be evaluated in  
XX murine disease models. (I) act on the active site of Fas, i.e. they mimic  
XX the native ligand, do not induce liver disease, and have reduced risk of

CC inducing a human anti-murine antibody response. This sequence represents  
CC a humanised anti-Fas antibody heavy chain construct designated Heu 1  
CC which is described in the method of the invention.  
XX SQ Sequence 470 AA;  
Query Match 100.0%; Score 246; DB 21; Length 470;  
Best Local Similarity 42.5%; Pred. No. 4.1e-10;  
Matches 34; Conservative 46; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 SYWMQXXXXXXXXXXXXXXXXXEDPSDSTYNKQFGXXXXXXXXXXXXXXXXXXXXX 60  
Db 50 sywmqvwkqpgqglwmgeidpsdystnyngkfkgkatltvdtststaysmelslrsd 109  
Qy 61 XXXXXXXXNRDYSNNWYFDV 80  
Db 110 tavyycarnrdysnnwyfdv 129  
RESULT 14  
AAW90934  
ID AAW90934 standard; Protein: 470 AA.  
XX AC AAW90934;  
XX DT 08-AUG-2000 (first entry)  
XX DE Humanised anti-Fas designed heavy chain Heu 2 protein.  
XX KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;  
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;  
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
KW Goodpasture syndrome; Crohn's disease; myasthenia gravis;  
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
XX OS Synthetic.  
XX EP990663-A2.  
XX PN 05-APR-2000.  
XX PD  
XX PF 29-SEP-1999; 99EP-0307711.  
XX PR 30-SEP-1998; 98JP-0276881.  
XX PR 30-SEP-1998; 98JP-0276882.  
XX PA (SANY ) SANKYO CO LTD.  
XX PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
XX WPI: 2000-258930/23.  
XX N-PSDB; AAA11645.  
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
XX inflammatory or autoimmune disease, induces apoptosis selectively in  
XX cells with abnormal Fas-Fas ligand systems -  
XX Claim 2; Page 174-176; 263pp; English.  
XX This invention describes a novel humanized anti-Fas antibody-like  
XX molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
XX ligand system, by binding to Fas on the cell surface, and prevents  
XX apoptosis in cells with a normal system, by inhibiting binding between  
XX Fas and its ligand. The products of the invention have anti-inflammatory,  
XX anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
XX immunomodulatory, dermatological, immunosuppressive, thyromimetic,

antirheumatic, nephrotropic, antinfertility, neuroprotective,  
arteriosclerotic, cardiant and hepatotropic activity. (I) induce  
apoptosis by binding to cell surface Fas or inhibit it by competitive  
inhibition of ligand binding. (I) are used to treat and/or prevent  
diseases associated with the Fas/Fas ligand system, especially systemic  
lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
(B, C or D) or alcoholic), and transplant rejection. (I) selectively  
inhibit apoptosis in normal cells but selectively induce it in abnormal  
cells. They bind to both human and murine Fas, so can be evaluated in  
murine disease models. (I) act on the active site of Fas, i.e. they mimic  
the native ligand, do not induce liver disease, and have reduced risk of  
inducing a human anti-murine antibody response. This sequence represents  
a humanised anti-Fas antibody heavy chain construct designated Heu 2  
which is described in the method of the invention.

Sequence	470 AA:
xx	
xx	
xx	

WPI; 2000-258930/23.  
N-PSDB; AAA11646.

New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems -

Claim 2; Page 180-182; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral, immunomodulatory, dermatological, immunosuppressive, thymimetic, antineumatic, nephrotropic, antifertility, neuroprotective, antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody heavy chain construct designated Heu 3 which is described in the method of the invention.

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## ALIGNMENTS

## RESULT

TELEFAX: 703-243-6410  
INFORMATION FOR SEO ID NO



QY 61 XXXXXXXXNR 70  
Db 83 SAVIYCAKGR 92

RESULT 4

US-08-881-037-16  
; Sequence 16, Application US/08881037  
; Patent No. 6080588  
; GENERAL INFORMATION:  
; APPLICANT: Glick, Gary D.  
; APPLICANT: Swanson, Patrick C.  
; TITLE OF INVENTION: DNA BINDING ANTIBODIES  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/881,037  
; FILING DATE: 23-JUN-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/443,540  
; FILING DATE: 18-MAY-1995  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kanski, Antoinette F.  
; REGISTRATION NUMBER: 34,202  
; REFERENCE/DOCKET NUMBER: 203442110710  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 813-5600  
; TELEFAX: (650) 494-0792  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 111 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-881-037-16

Query Match 66.7%; Score 164; DB 3; Length 111;  
Best Local Similarity 30.0%; Pred. No. 7.7e-06;  
Matches 21; Conservative 46; Mismatches 3; Indels 0; Gaps 0;

QY 1 SYNMQXXXXXXXXXXEIDPSDSTNNQKFKGXXXXXXXXXXXXXXXXXXXXX 60  
Db 23 SYNMHWKQPGQGLEWIGEDPSDYTYNNQKFKGKATLTVDKSSSTAYMQLSLTSED 82

QY 61 XXXXXXXXNR 70  
Db 83 SAVIYCAKGR 92

RESULT 5

US-08-881-037-61  
; Sequence 61, Application US/08881037  
; Patent No. 6080588  
; GENERAL INFORMATION:  
; APPLICANT: Glick, Gary D.  
; APPLICANT: Swanson, Patrick C.  
; TITLE OF INVENTION: DNA BINDING ANTIBODIES  
; NUMBER OF SEQUENCES: 113

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/881,037  
; FILING DATE: 23-JUN-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/443,540  
; FILING DATE: 18-MAY-1995  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kanski, Antoinette F.  
; REGISTRATION NUMBER: 34,202  
; REFERENCE/DOCKET NUMBER: 203442110710  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 813-5600  
; TELEFAX: (650) 494-0792  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 61:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-881-037-61

Query Match 66.7%; Score 164; DB 3; Length 119;  
Best Local Similarity 30.0%; Pred. No. 9.5e-06;  
Matches 21; Conservative 46; Mismatches 3; Indels 0; Gaps 0;

QY 1 SYNMQXXXXXXXXXXEIDPSDSTNNQKFKGXXXXXXXXXXXXXXXXXXXXX 60  
Db 31 SYNMHWKQPGQGLEWIGEDPSDYTYNNQKFKGKATLTVDKSSSTAYMQLSLTSED 90  
QY 61 XXXXXXXXNR 70  
Db 91 SAVIYCAKGR 100

RESULT 6

US-08-881-037-62  
; Sequence 62, Application US/08881037  
; Patent No. 6080588  
; GENERAL INFORMATION:  
; APPLICANT: Glick, Gary D.  
; APPLICANT: Swanson, Patrick C.  
; TITLE OF INVENTION: DNA BINDING ANTIBODIES  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/881,037

; FILING DATE: 23-JUN-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/443,540  
; FILING DATE: 18-MAY-1995  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Konski, Antoinette F.  
; REGISTRATION NUMBER: 34,202  
; REFERENCE/DOCKET NUMBER: 203442110710  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 813-5600  
; TELEFAX: (650) 494-0792  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 62:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-881-037-62

Query Match 66.7%; Score 164; DB 3; Length 119;  
Best Local Similarity 30.0%; Pred. No. 9.5e-06;  
Matches 21; Conservative 46; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 SYWMQXXXXXXXXXXEIDPSDSTYNNQKFGXXXXXXXXXXXXXXXXXXXXXXXXX 60  
DB 31 SYWMHWKQPGQGLEWIGEDPSDSTYNNQKFGKATLTVDKSSYAYMQLSLTSED 90  
  
QY 61 XXXXXXXXNR 70  
DB 91 SAVYYCAKGR 100

RESULT 7  
US-08-881-037-17  
; Sequence 17, Application US/08881037  
; Patent No. 6080588  
; GENERAL INFORMATION:  
; APPLICANT: Glick, Gary D.  
; APPLICANT: Swanson, Patrick C.  
; TITLE OF INVENTION: DNA BINDING ANTIBODIES  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/881,037  
; FILING DATE: 23-JUN-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/443,540  
; FILING DATE: 18-MAY-1995  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Konski, Antoinette F.  
; REGISTRATION NUMBER: 34,202  
; REFERENCE/DOCKET NUMBER: 203442110710  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 813-5600  
; TELEFAX: (650) 494-0792  
; TELEX:

; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 111 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-881-037-17

Query Match 65.0%; Score 160; DB 3; Length 111;  
Best Local Similarity 29.0%; Pred. No. 1.7e-05;  
Matches 20; Conservative 46; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 YWMQXXXXXXXXXXEIDPSDSTYNNQKFGXXXXXXXXXXXXXXXXXXXXXXXXX 61  
DB 24 YWMHWKQPGQGLEWIGEDPSDSTYNNQKFGKATLTVDKSSYAYMQLSLTSED 83  
  
QY 62 XXXXXXXXNR 70  
DB 84 AVYYCAKGR 92

RESULT 8  
US-08-881-037-63  
; Sequence 63, Application US/08881037  
; Patent No. 6080588  
; GENERAL INFORMATION:  
; APPLICANT: Glick, Gary D.  
; APPLICANT: Swanson, Patrick C.  
; TITLE OF INVENTION: DNA BINDING ANTIBODIES  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/881,037  
; FILING DATE: 23-JUN-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/443,540  
; FILING DATE: 18-MAY-1995  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Konski, Antoinette F.  
; REGISTRATION NUMBER: 34,202  
; REFERENCE/DOCKET NUMBER: 203442110710  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 813-5600  
; TELEFAX: (650) 494-0792  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-881-037-63

Query Match 65.0%; Score 160; DB 3; Length 119;  
Best Local Similarity 29.0%; Pred. No. 2.1e-05;  
Matches 20; Conservative 46; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 YWMQXXXXXXXXXXEIDPSDSTYNNQKFGXXXXXXXXXXXXXXXXXXXXXXXXX 61

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Db 32 YMHVWVQKPGQGLEWIGEDPSDYTYNQKFKGKATLTVDKSTTAYMQLSLTSDS 91
Qy 62 XXXXXXXXNR 70
Db 92 AVYYCAKGR 100

RESULT 9
US-08-881-037-59
; Sequence 59, Application US/08881037
; Patent No. 6080588
; GENERAL INFORMATION:
; APPLICANT: Click, Gary D.
; APPLICANT: Swanson, Patrick C.
; TITLE OF INVENTION: DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,037
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/443,540
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Konski, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442110710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX:
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-881-037-59

Query Match 64.6%; Score 159; DB 3; Length 98;
Best Local Similarity 29.4%; Pred. No. 1.5e-05;
Matches 20; Conservative 46; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SYWMQXXXXXXXXXXEIDPSDYTYNQKFKGXXXXXXXXXXXXXXXXXXXXXXXXXXXX 60
Db 31 SYMHVWVQKPGQGLEWIGEDPSDYTYNQKFKGKATLTVDKSSSTAYMQLSLTSED 90
Qy 61 XXXXXXXX 68
Db 91 SAVYYCAK 98

RESULT 10
US-08-235-838-11
; Sequence 11, Application US/08235838
; Patent No. 5571894
; GENERAL INFORMATION:
; APPLICANT: Weis, Winfried S.
```

```
; APPLICANT: Hynes, Nancy E.
; APPLICANT: Harwerth, Ina-Maria
; APPLICANT: Groner, Bernd
; APPLICANT: Hardman, No. 5571894man
; APPLICANT: Zwickl, Markus
; TITLE OF INVENTION: Recombinant Antibodies Specific for a
; TITLE OF INVENTION: Growth Factor Receptor
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,838
; FILING DATE: TBA
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/828,832
; FILING DATE: 31-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 91-810079.3
; FILING DATE: 05-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-235-838-11

Query Match 64.0%; Score 157.5; DB 1; Length 241;
Best Local Similarity 27.5%; Pred. No. 0.00031;
Matches 22; Conservative 47; Mismatches 10; Indels 1; Gaps 1;

Qy 1 SYWMQXXXXXXXXXXEIDPSDYTYNQKFKGXXXXXXXXXXXXXXXXXXXXXXXXXXXX 60
Db 32 SYMHVWVQKPGQGLEWIGMIDPSDSEYQNMFKKAALTVDKSSNTAYMQLSLTSED 91
Qy 61 XXXXXXXXNRDYSNNWYFDV 80
Db 92 SAVYYCAKG-GASGDWYFDV 110

RESULT 11
US-08-465-473B-11
; Sequence 11, Application US/08465473B
; Patent No. 5939531
; GENERAL INFORMATION:
; APPLICANT: Weis, Winfried S.
; APPLICANT: Hynes, Nancy E.
; APPLICANT: Harwerth, Ina-Maria
; APPLICANT: Groner, Bernd
; APPLICANT: Hardman, No. 5939531man
; APPLICANT: Zwickl, Markus
; TITLE OF INVENTION: Recombinant Antibodies Specific for a
; TITLE OF INVENTION: Growth Factor Receptor
; NUMBER OF SEQUENCES: 34
```



RESULT 14  
US-08-881-037-15  
; Sequence 15, Application US/08881037  
; Patent No. 6080588  
; GENERAL INFORMATION:  
; APPLICANT: Glick, Gary D.  
; APPLICANT: Swanson, Patrick C.  
; TITLE OF INVENTION: DNA BINDING ANTIBODIES  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/881,037  
; FILING DATE: 23-JUN-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/443,540  
; FILING DATE: 18-MAY-1995  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kanski, Antoinette F.  
; REGISTRATION NUMBER: 34,202  
; REFERENCE/DOCKET NUMBER: 20342110710  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 813-5600  
; TELEFAX: (650) 494-0792  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 15:

```

STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-JUN-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kotski, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX:
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-881-037-60

Query Match 63.8%; Score 157; DB 3; Length 119;
Best Local Similarity 27.1%; Pred. No. 4e-05;
Matches 19; Conservative 48; Mismatches 3; Indels 0; Gaps 0;

QY      1 SYWMQXXXXXXXXXXEIPDSYTNYNQKFGXXXXXXXXXXXXXXXXXXXXX 60
||||| : ::::::::::::::::::::|||::||| ||| ::::::::::::::::::::

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Search completed: August 14, 2002, 15:17:02  
Job time: 685 sec





Matches 21; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMQXXXXXXXXXXEIDPSDSTYNQKFGKXXXXXXXXXXXXXXXXXXXXXXXXX 60  
Db 31 NYWMQVVKRPGGLEWIGIDPSDSTYNQKFGKATLTVDTSSTAYMQLSLTSED 90

QY 61 XXXXXXXX 68  
Db 91 SAVVYCAR 98

RESULT 3  
S26463  
Ig heavy chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S26463  
R:Kavaler, J.  
submitted to the EMBL Data Library, April 1991  
A:Reference number: S26459  
A:Accession: S26463  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-111 <KAV>  
A:Cross-references: EMBL:X59113; NID:g51922; PIDN:CAA41839.1; PID:g51923  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 68.1%; Score 167.5; DB 2; Length 111;  
Best Local Similarity 28.8%; Pred. No. 3.2e-05;  
Matches 23; Conservative 48; Mismatches 8; Indels 1; Gaps 1;

QY 1 SYWMQXXXXXXXXXXEIDPSDSTYNQKFGKXXXXXXXXXXXXXXXXXXXXXXXXX 60  
Db 23 SYWMQVVKRPGGLEWIGIHPDSSTYNQKFGKATLTVDKSSSTAYMQLSLTSED 81

QY 61 XXXXXXXXNRDYSNNWYFDV 80  
Db 82 DSAVYCTRYGYWYFDV 101

RESULT 4  
PH1162  
Ig heavy chain V region (clone 10C.2A) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C:Accession: PH1162  
R:Schitteck, B.; Rajewsky, K.  
J. Exp. Med. 176, 427-438, 1992  
A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.  
A:Reference number: PH1105; MUID:92364545  
A:Accession: PH1162  
A:Molecule type: DNA  
A:Residues: 1-87 <SCH>  
A:Experimental source: B cell  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;6-87/Domain: immunoglobulin homology <IMM>

Query Match 67.1%; Score 165; DB 2; Length 87;  
Best Local Similarity 31.8%; Pred. No. 3.7e-05;  
Matches 21; Conservative 44; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYWMQXXXXXXXXXXEIDPSDSTYNQKFGKXXXXXXXXXXXXXXXXXXXXXXXXX 60  
Db 22 SYWMQVVKRPGGLEWIGIDPSDSTYNQKFGKATLTVDKSSSTAYMQLSLTSED 81

QY 61 XXXXXX 66  
Db 82 SAVFYC 87

RESULT 5  
PH1161  
Ig heavy chain V region (clone 13B.2A) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C:Accession: PH1161  
R:Schitteck, B.; Rajewsky, K.  
J. Exp. Med. 176, 427-438, 1992  
A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.  
A:Reference number: PH1105; MUID:92364545  
A:Accession: PH1161  
A:Molecule type: DNA  
A:Residues: 1-88 <SCH>  
A:Experimental source: B cell  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;7-88/Domain: immunoglobulin homology <IMM>

Query Match 66.3%; Score 163; DB 2; Length 88;  
Best Local Similarity 31.8%; Pred. No. 5.6e-05;  
Matches 21; Conservative 44; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYWMQXXXXXXXXXXEIDPSDSTYNQKFGKXXXXXXXXXXXXXXXXXXXXXXXXX 60  
Db 23 SYWMQVVKRPGGLEWIGIHPDSSTYNQKFGKATLTVDKSSSTAYMQLSLTSED 82

QY 61 XXXXXX 66  
Db 83 SAVFYC 88

RESULT 6  
PL0089  
Ig heavy chain V region (12S18-1) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 04-Mar-2000  
C:Accession: PL0089  
R:Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.;  
J. Exp. Med. 169, 519-533, 1989  
A:Title: Structural characterization of antidiotypic antibodies; evidence that Ab25  
A:Reference number: PL0080; MUID:89094248  
A:Accession: PL0089  
A:Molecule type: mRNA  
A:Residues: 1-119 <MEE>  
A:Cross-references: GB:X58580; GB:Y00794; NID:g51591; PIDN:CAA41456.1; PID:g930150  
A:Note: the sequence shown here is from the VH region of an antidiotypic monoclonal  
A:Note: sequences from two other clones (18S28-16 and 12S84-3) were almost identical  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 66.3%; Score 163; DB 2; Length 119;  
Best Local Similarity 27.5%; Pred. No. 8.9e-05;  
Matches 22; Conservative 47; Mismatches 9; Indels 2; Gaps 1;

QY 1 SYWMQXXXXXXXXXXEIDPSDSTYNQKFGKXXXXXXXXXXXXXXXXXXXXXXXXX 60  
Db 31 NYWMQVVKRPGGLEWIGIHPDSSTYNQKFGKATLTVDTSSTAYMQLSLTSED 90

QY 61 XXXXXXXXNRDYSNNWYFDV 80  
Db 91 SAVYICARNEGVA -WYFDV 108

RESULT 7  
B22769  
Ig heavy chain V region (B1-8.V1/V2) - mouse (tentative sequence)  
C:Species: Mus musculus (house mouse)  
C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 16-Aug-1996

A;Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-120 <VAR>  
C:A/Cross-references: EMBL:X67620; NID:g51856; PIDN:CAA47878.1; PID:g938260  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

F;15-98/domain: immunoglobulin homology <IMM>

Query Match            64.8%; Score 159.5; DB 2; Length 120;  
Best Local Similarity   29.1%; Pred.No. 0.00018;  
Matches         23; Conservative    47; Mismatches      8; Indels          1; Gaps

OY    1 SYMWQXXXXXXXXXXEIDPSDYSYNYNQKFKGXXXXXXXXXXXXXXX 60  
      IIII : ::::: : ||||| | : ::::: : ||||| | : ::::: :  
Db    31 SYNHWVQRPGGLEWGEIDPSDYTYNQKFKGRATLVDSSTAYMQFSSLTSED 90

OY    61 XXXXXXXXNRDYSNNWFYD 79  
      : ::::: : I : : I  
Db    91 SAVYYCAR-RYYGSRVSM D 108

RESULT    10  
PHI426  
Ig heavy chain V region (clone P2-57) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000  
C:Accession: PHI426  
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.  
J. Exp. Med. 177, 99-107, 1993  
A;Title: Molecular evolution of the human immunoglobulin E response: High information content in the hypervariable regions of the variable domains  
A:Reference number: PHI409; MUID:93115676  
A:Accession: PHI426  
A:Molecule type: mRNA  
A:Residues: 1-122 <VAN>  
A:Experimental source: PBMC  
C:A>Note: the authors translated the codon AAA for residue 28 as Ser and GTA as Cys  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

F;15-98/domain: immunoglobulin homology <IMM>

Query Match            64.6%; Score 159; DB 2; Length 122;  
Best Local Similarity   24.4%; Pred.No. 0.00021;  
Matches         19; Conservative    53; Mismatches      6; Indels          0; Gaps

OY    1 SYMWQXXXXXXXXXXEIDPSDYSYNYNQKFKGXXXXXXXXXXXXXXX 60  
      IIII : ::::: : ||||| | : ::::: : ||||| | : ::::: :  
Db    31 SYTWISVRQPQGKGLEWMGRIDPSDYTNYPSPFGHVTISADKSINTAYLOWSSLKASD 90

OY    61 XXXXXXXXNRDYSNNWFY 78  
      : ::::: : III : : I  
Db    91 TAIYYCAHOMYSNDIYW 108

RESULT    11  
S25175  
Ig heavy chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C:Accession: S25175  
R;Novick, M.J.; Novick, K.E.; Muller, S.  
submitted to the EMBL Data Library, July 1992  
A:Description: Structure and binding properties of monoclonal antibodies to rat IgG2b myeloma protein fused with anti-phage antibody  
A:Reference number: S25174  
A:Accession: S25175  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-120 <NON>  
C:A/Cross-references: EMBL:X67620; NID:g51856; PIDN:CAA47878.1; PID:g938260  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin

0:

Job time: 685 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 15:11:47 ; Search time 53.64 Seconds  
(without alignments)  
57.747 Million cell updates/sec

Title: 2\_g\_3\_g\_4  
Perfect score: 246  
Sequence: 1 SYWMQXXXXXXXXXXE.....XXXXXXXXXXNNWYFDV 80

Scoring table:  
BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues  
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	150	61.0	117	1	HV12_MOUSE
2	147.5	60.0	120	1	HV50_MOUSE
3	146	59.3	117	1	HV13_MOUSE
4	145	58.9	117	1	HV06_MOUSE
5	140	56.9	120	1	HV03_MOUSE
6	139.5	56.7	139	1	HV07_MOUSE
7	133.5	54.3	138	1	HV48_MOUSE
8	133	54.1	140	1	HV02_MOUSE
9	132	53.7	117	1	HV05_MOUSE
10	130	52.8	121	1	HV01_MOUSE
11	125.5	51.0	118	1	HV51_MOUSE
12	125	50.8	117	1	HV04_MOUSE
13	124	50.4	117	1	HV09_MOUSE
14	124	50.4	117	1	HV10_MOUSE
15	124	50.4	117	1	HV49_MOUSE
16	121	49.2	117	1	HV42_MOUSE
17	113.5	46.1	119	1	HV38_MOUSE
18	111	45.1	117	1	HV41_MOUSE
19	110	44.7	136	1	HV15_MOUSE
20	109.5	44.5	118	1	HV39_MOUSE
21	109.5	44.5	137	1	HV11_MOUSE
22	109	44.3	117	1	HV16_MOUSE
23	108.5	44.1	323	1	CO3_XENLA
24	108	43.9	117	1	HV18_MOUSE
25	107	43.5	119	1	HV40_MOUSE
26	105	42.7	117	1	HV52_MOUSE
27	105	42.7	119	1	HV37_MOUSE
28	104.5	42.5	123	1	HV24_MOUSE
29	104	42.3	114	1	HV00_MOUSE
30	103.5	42.1	123	1	HV18_MOUSE
31	103.5	42.1	142	1	HV01_RAT
32	103.5	42.1	144	1	HV26_MOUSE
33	103	41.9	116	1	HV36_MOUSE

34	103	41.9	122	1	HV20_MOUSE
35	103	41.9	275	1	EPI2_STAEP
36	102.5	41.7	657	1	CNI6_HAEIN
37	101.5	41.3	123	1	HV19_MOUSE
38	100.5	40.9	123	1	HV22_MOUSE
39	99.5	40.4	123	1	HV23_MOUSE
40	99.5	40.4	740	1	KRB6_CANAL
41	99	40.2	552	1	API_SCHPO
42	99	40.2	1097	1	DPOD_YEAST
43	98	39.8	147	1	HVIC_HUMAN
44	97.5	39.6	652	1	CNI6_YEREN
45	97.5	39.6	720	1	KRB6_YEAST

ALIGNMENTS

RESULT 1					
HV12_MOUSE					
ID	HV12_MOUSE	STANDARD;	PRT;	117 AA.	
AC	P01756;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig heavy chain V region MOPC 104E.				
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE=83075344; PubMed=6816276;				
RA	Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,				
RA	Hood L.E.;				
RT	"Complete amino acid sequence of a mouse mu chain: homology among				
RT	heavy chain constant region domains.";				
RL	Biochemistry 21:5415-5424(1982).				
CC	- - MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA				
CC	PROTEIN HAS ALSO BEEN DETERMINED.				
CC	- - MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.				
DR	PIR; A02039; MHMS4E.				
DR	InterPro; IPR003006; Iq.MHC.				
DR	InterPro; IPR003596; Iq_v.				
DR	Pfam; PF00047; ig; 1.				
DR	SMART; SM00406; Igv; 1.				
KW	Immunoglobulin V region; Glycoprotein.				
FT	DISULFID 22 96 BY SIMILARITY.				
FT	CARBOHYD 55 55 N-LINKED (GLCNAC. . .).				
FT	NON_TER 117 117				
SQ	SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;				
Query Match	61.0%;	Score	150;	DB 1;	Length 117;
Best Local Similarity	25.3%;	Pred. No.	0.00043;		
Matches	20;	Conservative	53;	Mismatches	2;
Indels	4;	Gaps	2;		
QY	2	YWMQXXXXXXXXXXEIDPSDSTYNQKFKGXXXXXXXXXXXXXXXXXXXXXXX 61			
Db	32	YIMKWKQSHGKSLWIGDINPNNGTSTYNQKFKGKATLTVDKSSSTAYVQLSLTSEDS 91			
QY	62	XXXXXXNRDYSNNWYFDV 80			
Db	92	AVTYCA--RDY--DWYFDV 106			
RESULT 2					
HV50_MOUSE					
ID	HV50_MOUSE	STANDARD;	PRT;	120 AA.	
AC	P06329;				
DT	01-JAN-1988 (Rel. 06, Created)				
DT	01-JAN-1988 (Rel. 06, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig heavy chain V region AC38 15.3.				

P01789	mus musculus
P30193	staphylococ
P44764	haemophilus
P01788	mus musculus
P01791	mus musculus
P01792	mus musculus
P87023	candida alb
Q00163	saccharomyc
P15436	saccharomyc
P01744	homo sapien
P53052	versinia en
P32486	saccharomyc

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=84182519; PubMed=6201362;  
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;  
RT "A V region determinant (idiotope) expressed at high frequency in B  
lymphocytes is encoded by a large set of antibody structural genes.";  
RL EMBO J. 3:517-523(1984).  
DR PIR; A02037; MHMS15.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IgV; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 98  
FT DOMAIN 99 105  
FT DOMAIN 106 120  
FT DISULFID 22 96  
FT NON\_TER 120 120  
SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match 60.0%; Score 147.5; DB 1; Length 120;  
Best Local Similarity 25.0%; Pred. No. 0.00073;  
Matches 20; Conservative 50; Mismatches 9; Indels 1; Gaps 1;  
QY 1 SYWMQXXXXXXXXXXEIDPSDSTYNQKFKGXXXXXXXXXXXXXXXXXXXXX 60  
DB 31 SYMHVIRPQGQLEWIGGINSGTNYNEKFK-SKATLTVDKSSATYMQLSLTPE 89  
QY 61 XXXXXXXXNRDYSNNWYFDV 80  
DB 90 DSAVYICARWDYEGDRYFDV 109

RESULT 3  
HV13\_MOUSE  
ID HV13\_MOUSE STANDARD; PRT; 117 AA.  
AC P01757;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region J558.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=80078170; PubMed=6765983;  
RA Schilling J., Clevinger B., Davie J.M., Hood L.;  
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA  
rearrangements in heavy chain V-region gene segments.";  
RL Nature 283:35-40(1980).  
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO  
BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF  
WHICH OCCUR IN THE D AND J SEGMENTS.  
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.  
DR PIR; A26242; MHMSJ5.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IgV; 1.  
KW Immunoglobulin V region.  
FT DISULFID 22 96  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447B41 CRC64;

Query Match 59.3%; Score 146; DB 1; Length 117;

Best Local Similarity 22.8%; Pred. No. 0.00094;  
Matches 18; Conservative 54; Mismatches 3; Indels 4; Gaps 1;  
QY 2 YWMQXXXXXXXXXXEIDPSDSTYNQKFKGXXXXXXXXXXXXXXXXXXXXX 61  
DB 32 YMKVVKQSHGKSLWIGDINPNNGGTSYNQKFKGKATLTVDKSSATYMQLSLTSEDS 91  
QY 62 XXXXXXXXNRDYSNNWYFDV 80  
DB 92 AVYICARDR----YWFYFDV 106  
RESULT 4  
HV06\_MOUSE  
ID HV06\_MOUSE STANDARD; PRT; 117 AA.  
AC P01750;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region 102 precursor.  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RX MEDLINE=81234548; PubMed=6788376;  
RA Bothwell A.L.M., Faskind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
RA Baltimore D.;  
RT "Heavy chain variable region contribution to the NpB family of  
antibodies: somatic mutation evident in a gamma 2a variable region.";  
RL Cell 24:625-637(1981).  
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY  
RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.  
DR PIR; A02032; HVMS02.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IgV; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.  
FT DOMAIN 20 49 FRAMEWORK-1.  
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 55 68 FRAMEWORK-2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 86 117 FRAMEWORK-3.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FCA8C CRC64;

Query Match 58.9%; Score 145; DB 1; Length 117;  
Best Local Similarity 26.5%; Pred. No. 0.0011;  
Matches 18; Conservative 46; Mismatches 4; Indels 0; Gaps 0;  
QY 1 SYWMQXXXXXXXXXXEIDPSDSTYNQKFKGXXXXXXXXXXXXXXXXXXXXX 60  
DB 50 SYMHVIRPQGQLEWIGGINSGTNYNEKFKGKATLTVDKSSATYMQLSLTSEDS 109  
QY 61 XXXXXXXX 68  
DB 110 SAVYICAI 117  
RESULT 5  
HV03\_MOUSE  
ID HV03\_MOUSE STANDARD; PRT; 120 AA.  
AC P01747;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)



[illegible]



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OX NCBI_TaxID=10090;
RP [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81053741; PubMed=6253904;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
RL region of immunoglobulin heavy chain MPC11.";
RL Nucleic Acids Res. 8:3591-3601(1980).
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840(1980).
CC -!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
DR PIR; A02027; GVMS11.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR Immunoglobulin V region.
KW NON_TER 121
FT SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;
SQ

Query Match 52.8%; Score 130; DB 1; Length 121;
Best Local Similarity 17.7%; Pred. No. 0.024;
Matches 14; Conservative 53; Mismatches 12; Indels 0; Gaps 0;

Qy 1 SYWMQXXXXXXXXXXEIDPSDSTYNQKFGKXXXXXXXXXXXXXXXXXXXXXXXXX 60
Db 31 NWIGWVKRPGHGLEWIDIPGGGFTYNDNLGKATLTADTSSSTAYTQLSLTSED 90

Qy 61 XXXXXXXXNRDYSNNWYFD 79
Db 91 SAIYHCARGIYNSPYFD 109

RESULT 11
HV51_MOUSE
ID HV51_MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMO J. 3:517-523(1984).
DR PIR; A02040; MHMS38.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 51.08; Score 125.5; DB 1; Length 118;
Best Local Similarity 20.3%; Pred. No. 0.055;
Matches 16; Conservative 52; Mismatches 8; Indels 3; Gaps 1;
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Qy 2 YWMQXXXXXXXXXXEIDPSDSTYNQKFGKXXXXXXXXXXXXXXXXXXXXXXXXX 61
Db 32 YMNWVKQSHGKSLWIDINPNNGTSTYNQKFGKATLTVDKSSSTAYTMELRSLTSED 91

Qy 62 XXXXXXXXNRDYSNNWYFD 80
Db 92 AVYICARGYGYDP---FDV 107

RESULT 12
HV04_MOUSE
ID HV04_MOUSE STANDARD; PRT; 117 AA.
AC P01748;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 23 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR PIR; A02030; HVMS23.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 50.8%; Score 125; DB 1; Length 117;
Best Local Similarity 19.1%; Pred. No. 0.06;
Matches 13; Conservative 49; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SYWMQXXXXXXXXXXEIDPSDSTYNQKFGKXXXXXXXXXXXXXXXXXXXXXXXXX 60
Db 50 SYWMHWVKRPGGLEWIGNPNNGTSTYNQKFGKATLTVDKSSSTAYTQLSLTSED 109

Qy 61 XXXXXXXX 68
Db 110 SAVIYCAR 117

RESULT 13
HV09_MOUSE
ID HV09_MOUSE STANDARD; PRT; 117 AA.
AC P01753; P11271;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 186-1 precursor.
OS Mus musculus (Mouse).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA MEDLINE=81234548; PubMed=6788376;
RX Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies; somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
DR PIR; B02034; HVMS61.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;

Query Match 50.4%; Score 124; DB 1; Length 117;
Best Local Similarity 19.1%; Pred. No. 0.073; 7; Indels 0; Gaps 0;
Matches 13; Conservative 48; Mismatches 7; Indels 0; Gaps 0;

QY 1 SYWMQXXXXXXXXXXEIDPSDYTNQFKGXXXXXXXXXXXXXXXXXXXXX 60
DB 50 SYWMHVQKPGRGLEWIGRIDPSNGGTYNEKFKSKATLTVDTSSSTAYMQLSLTSED 109
QY 61 XXXXXXXX 68
DB 110 SAVYYCAR 117

RESULT 14
HV10_MOUSE STANDARD; PRT; 117 AA.
AC P01754; P11270;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain v region 145 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies; somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
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CC
DR EMBL; M13788; AAA38506.1; -.
DR PIR; A02035; MHMSB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 B4.
FT DOMAIN 20 49 FRAMEWORK-1.
```

```
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CC
DR EMBL; J00533; AAA38602.1; -.
DR PIR; C02034; HVMS45.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 145.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12921 MW; D37DE8A3F543E996 CRC64;

Query Match 50.4%; Score 124; DB 1; Length 117;
Best Local Similarity 19.1%; Pred. No. 0.073; 7; Indels 0; Gaps 0;
Matches 13; Conservative 48; Mismatches 7; Indels 0; Gaps 0;

QY 1 SYWMQXXXXXXXXXXEIDPSDYTNQFKGXXXXXXXXXXXXXXXXXXXXX 60
DB 50 SYWMHVQKPGRGLEWIGRIDPSNGGTYNEKFKSKATLTVDKPSTAYMQLSLTSED 109
QY 61 XXXXXXXX 68
DB 110 SAVYYCAR 117

RESULT 15
HV49_MOUSE STANDARD; PRT; 117 AA.
AC P06328;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain v region VH558 B4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8509340; PubMed=2578321;
RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RT unrearranged VH gene segments.";
RL Cell 40:271-281(1985).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; M13788; AAA38506.1; -.
DR PIR; A02035; MHMSB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 B4.
FT DOMAIN 20 49 FRAMEWORK-1.
```

FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 55 68 FRAMEWORK-2.  
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 86 117 FRAMEWORK-3.  
FT DISULFID 41 115 BY SIMILARITY.  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 12834 MW; B8862FAC67ABD345 CRC64;

Query Match 50.4%; Score 124; DB 1; Length 117;  
Best Local Similarity 19.1%; Pred. No. 0.073; 7; Indels 0; Gaps 0;  
Matches 13; Conservative 48; Mismatches 7; Indels 0; Gaps 0;

Qy 1 SYWMQXXXXXXXXXXEIDPSDSTYNNQKFGXXXXXXXXXXXXXXXXXXXXX 60  
Db 50 SYWMHWKQRPGRGLEWIGNIDPNSGGTKYNEKFKSKATLVDPSPSTAYMQLSLTSED 109

Qy 61 XXXXXXXX 68  
Db 110 SAVICTR 117

Search completed: August 14, 2002, 15:23:12  
Job time: 685 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:10:52 ; Search time 187.61 Seconds  
(without alignments)  
73.768 Million cell updates/sec

Title: 2\_g\_3\_g\_4  
Perfect score: 246  
Sequence: 1 SYWMQXXXXXXXXXXXXX.....XXXXXXXXXXNNWYFDV 80

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database :
- 1: sp\_archaea.\*
  - 2: sp\_bacteria.\*
  - 3: sp\_fungi.\*
  - 4: sp\_human.\*
  - 5: sp\_invertebrate.\*
  - 6: sp\_mammal.\*
  - 7: sp\_mhc.\*
  - 8: sp\_organelle.\*
  - 9: sp\_phase.\*
  - 10: sp\_plant.\*
  - 11: sp\_rodent.\*
  - 12: sp\_virus.\*
  - 13: sp\_vertebrate.\*
  - 14: sp\_unclassified.\*
  - 15: sp\_rvirus.\*
  - 16: sp\_bacteriap.\*
  - 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	186.5	75.8	143	11	Q91V67 mus musculus
2	175	71.1	143	11	Q924P9 mus musculus
3	159.5	64.8	142	11	Q924Q2 mus musculus
4	159.5	64.8	481	11	Q91WT3 mus musculus
5	158.5	64.4	145	11	Q924R3 mus musculus
6	147.5	60.0	114	11	Q924R1 mus musculus
7	146	59.3	144	11	Q924P5 mus musculus
8	143.5	58.3	143	11	Q924Q5 mus musculus
9	143	58.1	117	11	Q924P8 mus musculus
10	142	57.7	140	11	Q924P8 mus musculus
11	140.5	57.1	278	11	Q924K1 mus musculus
12	140	56.9	146	11	Q924R8 mus musculus
13	139.5	56.7	145	11	Q924Q7 mus musculus
14	136.5	55.5	110	11	Q91L77 mus musculus
15	135.5	55.1	143	11	Q924Q0 mus musculus
16	134	54.5	117	11	Q924Q9 mus musculus

17	133.5	54.3	143	11	Q924R7	Q924r7 mus musculus
18	133.5	54.3	143	11	Q91VA2	Q91va2 mus musculus
19	132.5	53.9	145	11	Q924R4	Q924r4 mus musculus
20	131.5	53.5	143	11	Q924R0	Q924r0 mus musculus
21	130.5	53.0	141	11	Q924Q4	Q924q4 mus musculus
22	130	52.8	170	11	Q925S2	Q925s2 mus musculus
23	129	52.4	142	11	Q924Q1	Q924q1 mus musculus
24	128.5	52.2	118	11	Q921C4	Q921c4 mus musculus
25	128	52.0	119	5	Q9GVZ2	Q9gyz2 schistosoma
26	128	52.0	146	11	Q924Q3	Q924q3 mus musculus
27	127	51.6	140	11	Q924R2	Q924r2 mus musculus
28	126.5	51.4	145	11	Q924P7	Q924p7 mus musculus
29	125	50.8	145	11	Q924Q9	Q924q9 mus musculus
30	125	50.8	145	11	Q924Q6	Q924q6 mus musculus
31	125	50.8	146	11	Q924Q8	Q924q8 mus musculus
32	124	50.4	137	11	Q924R6	Q924r6 mus musculus
33	124	50.4	139	11	Q924R5	Q924r5 mus musculus
34	124	50.4	145	11	Q924R1	Q924r1 mus musculus
35	120	48.8	111	11	Q9D9B8	Q9d9b8 mus musculus
36	120	48.8	481	11	Q91WT1	Q91wt1 mus musculus
37	119	48.4	488	11	Q91WR1	Q91wr1 mus musculus
38	116.5	47.4	117	11	Q921C6	Q921c6 mus musculus
39	114.5	46.5	473	11	Q9D8L4	Q9d8l4 mus musculus
40	114	46.3	109	11	Q9JL75	Q9jl75 mus musculus
41	113	45.9	143	11	Q924P6	Q924p6 mus musculus
42	111	45.1	147	11	Q925S3	Q925s3 mus musculus
43	111	45.1	298	11	Q9QYF0	Q9qyf0 mus musculus
44	110.5	44.9	116	4	Q9UL89	Q9ul89 homo sapien
45	110.5	44.9	120	11	Q920E8	Q920e8 mus musculus

ALIGNMENTS

RESULT 1

Q91V67

ID Q91V67 PRELIMINARY; PRT; 143 AA.

AC Q91V67; 2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE VHL86.2-D-J-C MU PROTEIN (V304-D-J-C MU PROTEIN) (FRAGMENT).

GN V304-D-J-C MU.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Theria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6;

RA Kozono Y., Kozono H., Azuma T.;

RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals Affinity Maturation of B Cell Antigen Receptors in Response to (4-Hydroxy-3-Nitrophenyl)Acetyl (NP)."

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB069912; BAB6328.1; -

DR EMBL; AB069914; BAB63930.1; -

FT NON\_TER 1

FT NON\_TER 143

SQ SEQUENCE 143 AA; 15775 MW; 91BC6012B44FEFEBF CRC64;

Query Match 75.8%; Score 186.5; DB 11; Length 143;  
Best Local Similarity 32.5%; Pred. No. 1.8e-05;  
Matches 26; Conservative 47; Mismatches 4; Indels 3; Gaps 1;

Qy 1 SYWMQXXXXXXXXXXXXXDEIDPSDSTYNQKFKGXXXXXXXXXXXXXXXXXXXXX 60  
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :  
Db 31 SYMHVWKRPQGLEWIGVIDPSDSTYNQKFKGKATLVDTSSSTAYMQLSL\*SED 90  
Qy 61 XXXXXXXXXNRDYSNNWYFDV 80  
: : : : : | : | | | |  
Db 91 SAVIYCPTVD---DWYFDV 107





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QY 1 SYWMQXXXXXXXXXXEIDPDSYNYNOKFKGXXXXXXXXXXXXXXXXXXXXXXXXX 60
    ||||| : : : : : ||| : ||| : : : : : : : : : : : : : : : : : :
Db 31 SYMHWVKQRPGRGLEWIGRIDPNSSGGTKYNEKFKSKATLTVDKPSSTAYMQLSPTSED 90
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 XXXXXXXXNRDY-SNNWYFDV 80
    : : : : : : : : : : : |||||
Db 91 SAVYYCARGL-YDGNWYFDV 109
    : : : : : : : : : : : |||||

RESULT 6
Q9JL81 PRELIMINARY; PRT; 114 AA.
AC Q9JL81
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR HSSB; AF206025; AAF69323.1; -.
DR EMBL; P01810; 2FEJ.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1 114
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12829 MW; 404885FDE6BA56F8 CRC64;

Query Match 60.0%; Score 147.5; DB 11; Length 114;
Best Local Similarity 26.2%; Pred. NO. 0.013;
Matches 21; Conservative 49; Mismatches 9; Indels 1; Gaps 1;

QY 1 SYWMQXXXXXXXXXXEIDPDSYNYNOKFKGXXXXXXXXXXXXXXXXXXXXXXXXX 60
    ||||| : : : : : ||||| : ||||| : : : : : : : : : : : : : : : :
Db 23 SYMHWVKQRPQGLEWIGMIDPSDSETRLNQKFKDKATLTVDKSSSTAYMQLSPTSED 82
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 XXXXXXXXNRDY-SNNWYFDV 79
    : : : : : : : : : : : |||||
Db 83 SAVYYCARSNYGGSLYFD 102
    : : : : : : : : : : : |||||

RESULT 7
Q924P5 PRELIMINARY; PRT; 144 AA.
ID Q924P5
AC Q924P5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE VH186.2-D-J-C MU PROTEIN (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
```

```
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069920; BAB63936.1; -.
FT NON_TER 1 144
FT NON_TER 144 144
SQ SEQUENCE 144 AA; 15865 MW; CD07BE97E95C1B27 CRC64;

Query Match 59.3%; Score 146; DB 11; Length 144;
Best Local Similarity 24.7%; Pred. NO. 0.028;
Matches 20; Conservative 49; Mismatches 8; Indels 4; Gaps 2;

QY 1 SYWMQXXXXXXXXXXEIDPDSYNYNOKFKGXXXXXXXXXXXXXXXXXXXXXXXXX 60
    ||||| : : : : : ||| : ||| : : : : : : : : : : : : : : : : :
Db 31 SYMHWVKQRPGRGLEWIGRIDPNSSGGTKYNEKFKSKATLTVDKPSSTAYMQLSPTSED 90
    : : : : : : : : : : : ||| : ||| : : : : : : : : : : : : : : :
QY 61 XXXXXXXXNRDY-SNNWYFDV 80
    : : : : : : : : : : : ||| : |||
Db 91 SAVYYCAS---YGSIWYFDV 108
    : : : : : : : : : : : ||| : |||

RESULT 8
Q924Q5 PRELIMINARY; PRT; 143 AA.
ID Q924Q5
AC Q924Q5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE VH186.2-D-J-C MU PROTEIN (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067795; BAB63280.1; -.
FT NON_TER 1 143
FT NON_TER 143 143
SQ SEQUENCE 143 AA; 15908 MW; 55A2372870F0D568 CRC64;

Query Match 58.3%; Score 143.5; DB 11; Length 143;
Best Local Similarity 23.8%; Pred. NO. 0.044;
Matches 19; Conservative 48; Mismatches 10; Indels 3; Gaps 1;

QY 1 SYWMQXXXXXXXXXXEIDPDSYNYNOKFKGXXXXXXXXXXXXXXXXXXXXXXXXX 60
    ||||| : : : : : ||| : ||| : : : : : : : : : : : : : : : : :
Db 31 SYMHWVKQRPGRGLEWIGRIDPNSSGGTKYNEKFKSKATLTVDKPSSTAYMQLSPTSED 90
    : : : : : : : : : : : ||| : ||| : : : : : : : : : : : : : : :
QY 61 XXXXXXXXNRDY-SNNWYFDV 80
    : : : : : : : : : : : ||| : |||
Db 91 SAVYYCARFYDYE---YFDV 107
    : : : : : : : : : : : ||| : |||

RESULT 9
Q9QXF0 PRELIMINARY; PRT; 117 AA.
ID Q9QXF0
AC Q9QXF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
```



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DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE VHL86.2-D-J-C MU PROTEIN (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067793; BAB63278.1; -.
FT NON_TER 1
FT NON_TER 145
SQ SEQUENCE 145 AA; 16141 MW; 55A59A7908B2CD6A CRC64;

Query Match 56.7%; Score 139.5; DB 11; Length 145;
Best Local Similarity 22.8%; Pred. No. 0.094;
Matches 18; Conservative 49; Mismatches 11; Indels 1; Gaps 1;

Qy 1 SYWMQXXXXXXXXXXXXXIDPSDSTYNQKFGXXXXXXXXXXXXXXXXXXXXX 60
Db 31 SYWMHWKQPGQGLEWIGRIDPNPGSGTKYNEKFK-SKATLTVDKPSSTAYMQLSLTSE 89
Qy 61 XXXXXXXXNRDYSNNWYFD 79
Db 90 DSAVIYICARYDYGSSYFD 108

RESULT 14
ID Q9JL77 PRELIMINARY; PRT; 110 AA.
AC Q9JL77;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808 (2000).
DR EMBL; AF206029; AAF69327.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 110
SQ SEQUENCE 110 AA; 12138 MW; 2EDE81FB5862C9AF CRC64;

Query Match 55.5%; Score 136.5; DB 11; Length 110;
Best Local Similarity 20.5%; Pred. No. 0.092;
Matches 16; Conservative 54; Mismatches 7; Indels 1; Gaps 1;

Qy 1 SYWMQXXXXXXXXXXXXXIDPSDSTYNQKFG-XXXXXXXXXXXXXXXXXXXXX 59
Db 23 SSMHWAKQPGQGLEWIGEIHPNSGHTYNEKFKGKATLTVDTSSTAYVDLSLTS 82

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Qy 60 XXXXXXXXNRDYSNNWY 77
Db 83 SAVYYCARQRRNYAMDY 100

RESULT 15
Q924Q0
ID Q924Q0 PRELIMINARY; PRT; 143 AA.
AC Q924Q0;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE V165-D-J-C MU PROTEIN (FRAGMENT).
GN V165-D-J-C MU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069915; BAB63931.1; -.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 15704 MW; C99D2433F2BAD8A0 CRC64;

Query Match 55.1%; Score 135.5; DB 11; Length 143;
Best Local Similarity 21.5%; Pred. No. 0.19;
Matches 17; Conservative 51; Mismatches 8; Indels 3; Gaps 1;

Qy 1 SYWMQXXXXXXXXXXXXXIDPSDSTYNQKFGXXXXXXXXXXXXXXXXXXXXX 60
Db 31 SYWITWVKQPGQGLEWIGDIYFGSGSTYNEKFKSKATLTVDKPSSTAYMQLSLTSED 90
Qy 61 XXXXXXXXNRDYSNNWYFD 79
Db 91 SAVYYICAPD---SNHLYFD 106

Search completed: August 14, 2002, 15:22:12
Job time: 680 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:15:35 ; Search time 230.21 Seconds  
(without alignments)  
226.770 Million cell updates/sec

Title: US-09-499-662-143  
Perfect score: 2517  
Sequence: 1 MGWSCIIFLVATATGVHSQ.....MHEALHNYTKSLSPCK 470

Scoring table: BLOSUM62DX  
Gap 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_032802.\*  
1: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.\*  
6: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.\*  
7: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.\*  
8: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.\*  
9: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.\*  
10: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.\*  
13: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.\*  
14: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.\*  
15: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.\*  
16: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.\*  
17: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2517	100.0	470	21	AAW90933 Humanised anti-Fas
2	2515	99.9	470	21	AAW90934 Humanised anti-Fas
3	2514	99.9	470	19	AAW83037 Anti-Fas humanised
4	2514	99.9	470	21	AA14779 Humanised anti-Fas
5	2514	99.9	470	21	AAW90929 Humanised HFE7A de
6	2514	99.9	470	21	AAW90935 Humanised anti-Fas
7	2501	99.4	470	19	AAW83036 Anti-Fas humanised
8	2501	99.4	470	21	AA14776 Humanised anti-Fas
9	2501	99.4	470	21	AAW90926 Humanised HFE7A de
10	2495	99.1	470	21	AAW90936 Humanised HFE7A de
11	2346.5	93.2	731	22	AAW52156 Humanised HMFG-1 h

12	2346.5	93.2	741	22	AAW52159 Humanised HMFG-1 h
13	2341.5	93.0	729	22	AAW52158 Humanised HMFG-1 h
14	2341.5	93.0	739	22	AAW52161 Humanised HMFG-1 h
15	2335.5	92.8	730	22	AAW52157 Humanised HMFG-1 h
16	2335.5	92.8	740	22	AAW52160 Humanised HMFG-1 h
17	2304	91.5	652	19	AAW48650 Heavy chain of hMA
18	2290.5	91.0	465	22	AAW72228 Humanised 323/A3 (
19	2287	90.9	470	21	AAW80826 A dimeric anti-CD2
20	2286	90.8	466	22	AAW03755 Chimeric 2403 IgG
21	2285.5	90.8	464	22	AAW72232 Humanised 323/A3 (
22	2255	89.6	476	20	AAW88464 Monoclonal antibody
23	2251.5	89.5	481	13	AAW24442 Sequence of antibody
24	2248	89.3	472	20	AAW50166 Human reshaped F19
25	2232	88.7	449	14	AAW43339 Completely humanis
26	2232	88.7	449	19	AAW49816 Amino acid sequenc
27	2230	88.6	476	14	AAW31023 Antibody D heavy c
28	2229.5	88.6	583	22	AAW83156 Ganglioside GM2 an
29	2202.5	87.5	467	22	AAW36210 Human immune syste
30	2200.5	87.4	452	20	AAW29458 Recombinant immuno
31	2200.5	87.4	452	21	AAW30322 Humanised anti-IL-
32	2200.5	87.4	452	21	AAW77766 Humanised anti-IL-
33	2200	87.4	472	20	AAW50157 Chimeric mouse/hum
34	2193	87.1	592	22	AAW83838 Amino acid sequenc
35	2191.5	87.1	452	19	AAW89316 Anti-IL-8 humanise
36	2190	87.0	595	20	AAW86003 Anti-5T4 single ch
37	2188.5	86.9	473	22	AAW64475 Human type antihum
38	2186	86.8	474	22	AAW14177 Human novel protei
39	2185.5	86.8	473	22	AAW64471 Human type antihum
40	2181.5	86.7	475	22	AAW63640 Amino acid sequenc
41	2180.5	86.5	473	22	AAW64469 Human type antihum
42	2177	86.5	468	20	AAW55689 D9D10 heavy chain
43	2177	86.5	711	20	AAW85692 MoAbII fusion pro
44	2173.5	86.4	473	22	AAW64473 Human type antihum
45	2162	85.9	470	13	AAW22757 Reshaped CAMPATH-1

ALIGNMENTS

RESULT 1  
AAW90933  
ID AAW90933 standard; Protein; 470 AA.  
AC AAW90933;  
DT 08-AUG-2000 (first entry)  
XX Humanised anti-Fas designed heavy chain Heu 1 protein.  
DE  
XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;  
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;  
KW hepatotoxic; humanized; apoptosis; systemic lupus erythematosus;  
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;  
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
XX Synthetic.  
OS  
XX EP990663-A2.  
XX  
PD 05-APR-2000.  
XX  
PF 29-SEP-1999; 99EP-0307711.  
XX  
PR 30-SEP-1998; 98JP-0276881.  
PR 30-SEP-1998; 98JP-0276882.  
XX  
PA (SANY ) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 XX WPI; 2000-258930/23.  
 DR N-PSDB; AAA11644.  
 XX  
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems -  
 PS Claim 2; Page 169-170; 263pp; English.  
 XX  
 CC This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis, myasthenia gravis,  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody heavy chain construct designated Heu 1  
 CC which is described in the method of the invention.  
 XX Sequence 470 AA;  
 SQ

Query Match  
 Best Local Similarity 100.0%; Score 2517; DB 21; Length 470;  
 Matches 470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVATATGVHSQVLQSGAEVKKPGASVKVSKRAGYFTFTSYWQWVKQAP 60  
 DB 1 mgwscililflvatatgvhsqvlqsgaevkpgasvkvsckasgytftsywmqvkkqap 60  
 QY 61 GQGLEWGMGIDPDSVTYNNQKFKGKATLTVDTSSTAYMELSSLRSEDTAVYYCARNRD 120  
 DB 61 gqglewgmgeidpsdytnynqfkqkatltvdtststaymelsslrse dtavyyca rnr d 120  
 QY 121 YSNNNYFDVWGOGTLVTYSSASTKGFSPVPLAPSSKSTSGGTAALGCLVKDYFPPFVTVS 180  
 DB 121 ysnnywfdv wgggtlvtvssastk gspvfplapsskstsggtaalgclvkd yfpe pvtvs 180  
 QY 181 WNSGALTSGVHFPFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHNKPSNTKVDKRVPE 240  
 DB 181 wns galtsgvhf pfpavlqssg lylssv tvpssslgtqt yicnv nhn kpsntkvd krve p 240  
 QY 241 KSCDKTHTCPPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300  
 DB 241 kscdkthtccp c p a p e l l g g p s v f l f p p k k d t l m i s r t p e v t c v v d v s h e d p e v k f n w 300  
 QY 301 YVDGEVHNAKTPREQYNSTYRVVSVLTVHLQDWLNGKEYCKVSKNALPAPIEKTLS 360  
 DB 301 yvdgevhna ktpre eqynst yr vvsv ltvhl qdwl ngkeyckvskn alpapi ektls 360  
 QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGYFPSDAVWEESNGQPPENNYKTTTPV 420

Db 361 kakgqprepyvtlppsreemtknqvsltclvkgyfypsdiavewesngppennykttppv 420  
 QY 421 LQSDGSFFLYSKLTVDKSRWQGNVFSCVMHEALHNHYTKQSLSLSPGK 470  
 DB 421 lqsdgsfflyskltvdksrwqgnvfscvmhealhnhytqksls spgk 470  
 RESULT 2  
 AAW90934  
 ID AAW90934 standard; Protein; 470 AA.  
 AC AAW90934;  
 XX  
 XX 08-AUG-2000 (first entry)  
 DT Humanised anti-Fas designed heavy chain Heu 2 protein.  
 DE  
 DE  
 XX  
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;  
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;  
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
 XX Synthetic.  
 OS  
 XX EP990663-A2.  
 PN  
 PD 05-APR-2000.  
 XX  
 XX 29-SEP-1999; 99EP-0307711.  
 PF  
 XX 30-SEP-1998; 98JP-0276881.  
 PR  
 PR 30-SEP-1998; 98JP-0276882.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 DR WPI; 2000-258930/23.  
 DR N-PSDB; AAA11645.  
 XX  
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems -  
 XX Claim 2 ; Page 174-176; 263pp; English.  
 PS  
 XX This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,  
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively

CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
CC cells. They bind to both human and murine Fas, so can be evaluated in  
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
CC the native ligand, do not induce liver disease, and have reduced risk of  
CC inducing a human anti-murine antibody response. This sequence represents  
CC a humanised anti-Fas antibody heavy chain construct designated Heu 2  
CC which is described in the method of the invention.  
XX  
SQ Sequence 470 AA;

Query Match 99.9%; Score 2515; DB 21; Length 470;  
Best Local Similarity 99.8%; Pred. No. 7e-143;  
Matches 469; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVATATGVHSGVQVLSGAEVKKPGASVKYCKRSGSYTFTSYMMQWVKQAP 60  
Db 1 mgwscililflvatatgvhsqvlvgsgaevkkpgasvkysckasgytftsymbqvkqap 60  
QY 61 GQGLEWMEGIDPSDSYTNYNQKFKGKATLVDTSTSTAYMELSSLRSEDTAVYICARNRD 120  
Db 61 gqglewmgeidpsdsytnynqkfkgkatitvdtststaymelsslrse dtavvycarnrd 120  
QY 121 YSNNNYFDWGGTTLVTSSASTKPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180  
Db 121 ysnnnfyfdwggttltvtssastkpsvfplapskstsaggtaalgclvkd yfpepvtvs 180  
QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKDKRVEP 240  
Db 181 wnsгалtsgvhtfpavlgssglyslssv tvpssslgtqtyicnvnhkpsntkdkrvep 240  
QY 241 KSCDKTHCPCCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300  
Db 241 kscdtkthccppapellggpsvflfppkpkdtlmisrtpevtcvvvdvsh edpevkfnw 300  
QY 301 YVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360  
Db 301 yvdgvevhnaktpreeqynstyrvvsvl tvlqhqwlngkeyckvsnkalpapiektis 360  
QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGYGSPDSIAVWESNGOPENNYKTTTPV 420  
Db 361 kakgqprepqv ytlppsreemtknqvs ltcvkgyfspdsiavwesngopennykttppv 420  
QY 421 LDSGSEFFLYSKLTVDKSRWQQGNVFCGVMHEALHNHYTQKSLSISPGK 470  
Db 421 ldsdgsfflyskltvdksrwqqgnvfscv mhealhnhytqkslsispgk 470

RESULT 3  
AAW83037  
ID AAW83037 standard; Protein: 470 AA.  
XX  
AC AAW83037;  
XX

DT 15-MAR-1999 (first entry)  
XX

DE Anti-Fas humanised antibody HFE7A heavy chain.  
XX

XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;  
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;  
KW systemic lupus erythematosus; graft versus host disease;  
KW Sjogren syndrome; pernicious anaemia; Addison's disease;  
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
KW rheumatoid arthritis; autoimmune haemolytic anaemia;  
KW myasthenia gravis; multiple sclerosis; Basedow's disease;  
KW thrombopenia purpura; insulin-dependent diabetes; allergy;  
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
KW transplant rejection; therapy.

XX Homo sapiens.  
OS  
OS Synthetic.

FH Key Location/Qualifiers  
FT Peptide 1..19  
FT Protein /label= Sig\_peptide 20..470  
FT /label= Mat\_protein 20..140  
FT Region /label= Variable 141..464  
FT Region /label= Constant 50..54  
FT /label= CDR\_H1 /note= "Claim 9"  
FT Region 69..84  
FT /label= CDR\_H2 /note= "claim 9"  
FT Region 118..129  
FT /label= CDR\_H3 /note= "Claim 9"

XX AU9859701-A.

XX 08-OCT-1998.

XX 30-MAR-1998; 98AU-0059701.

XX 08-OCT-1997; 97JP-0276064.

PR 01-APR-1997; 97JP-0082953.

PR 25-JUN-1997; 97JP-0169088.

XX (SANY ) SANKYO CO LTD.

XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;  
PI Masahiko O, Nobufusa S, Shin Y, Tohru T;  
XX WPI; 1998-543440/47.  
N-PSDB; AAV70080.

DR New antibodies and proteins bind conserved epitope of Fas antigen -  
XX used to evaluate drugs in animal models and to treat Fas-associated  
XX diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
XX myocarditis, hepatitis and AIDS

PS Claim 22; Page 225-227; 292pp; English.

XX This is the amino acid sequence of the HV type humanised heavy  
CC chain of murine anti-human Fas monoclonal antibody HFE7A. It  
CC includes humanising R44G and A76T amino acid substitutions that are  
CC are conserved in the human IgG heavy chain. Host Escherichia coli  
CC pgHPDHV3 SANK 70298 harbors plasmid pgHPDHV3 carrying a fusion  
CC fragment of the humanised HV type HFE7A heavy chain and DNA  
CC encoding human IgG1 constant region (see AAV70080), and is deposited  
CC as FERM BP-6273 (claimed). The invention provides methods for  
CC producing humanised antibodies by culturing host cells. Humanised  
CC versions of HFE7A (see AAW83031-37), like native HFE7A, are capable  
CC of inducing apoptosis in abnormal cells expressing Fas, and of  
CC inhibiting Fas-induced apoptosis in normal cells. The humanised  
CC antibodies are used to evaluate, in animal models, treatments of  
CC diseases that involve Fas/Fas ligand interactions, and also to  
CC treat such diseases, including autoimmune disease (e.g. systemic  
CC lupus erythematosus, Hashimoto's disease, graft versus host disease,  
CC Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,  
CC Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,  
CC autoimmune haemolytic anaemia, sterility, myasthenia gravis,  
CC multiple scl rosia, Basedow's disease, thrombopenia purpura and  
CC insulin-dependent diabetes), allergies, atopy, arteriosclerosis,  
CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic  
CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).

XX Sequence 470 AA;

Query Match 99.9%; Score 2514; DB 19; Length 470;  
Best Local Similarity 99.8%; Pred. No. 8.1e-143;

Matches	469;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0
Qy	1	MGWSCIIILFLVATATGVHSQVLQVSGAEVKKPGASVKSVCASGYTFTSYMMQWVKQAP	60						
Db	1	mgwsciiilflvatatgvhsqvlvgsgaevkkpgasvkscasgytftsywmqvwkqap	60						
Qy	61	GGLEWGEIDPDSSTYNNQFKGKATLTVDTSTSTAYMELSSLSRSEDVAVYYCARNRD	120						
Db	61	ggglewgeidpsdsytnyngkfkgkatltvdtststaymelsslsrsedtavyyccarnrd	120						
Qy	121	YSNNWYFDVWCGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS	180						
Db	121	ysnnwyfdvwegtltvssastkgpsvfp lapssksts ggtaalgcilvkdyfpeptvts	180						
Qy	181	WNSGALTSGVHTFPVAVLQSSGLYSLSSVTVTPSSSLGTGTICNVNHNKPSNTKVDKRVPE	240						
Db	181	wnsгалtsgvhtfpav lqssglyslssv tvpssslgtctyicnvnhkpsntkvdkrvpe	240						
Qy	241	KSCDKHTCTPCPAPELPGSPSVFLFPFKPKDITLISRPTVTCVVDVSHEDPEVKFNW	300						
Db	241	kscdkthctpcpapellgpsvflfpfpkpkdtl misrptevtcvvdvshedpevkfnw	300						
Qy	301	YVDGVEVHNATKPREEQYNTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS	360						
Db	301	yvdgvevhnaktpreeqyntyrvvsvltvlhqdwlngkeykckvsnkalpapiektis	360						
Qy	361	KAKGQPREPQVYVTLPPPSREEMTKNQVSLTCLVKGFYPSDIAVEHESGQPENNYKTTTPPV	420						
Db	361	kakgqprepqvtylppsreemtknqvslctclvkgyfypsdiavehsgqpennykttppv	420						
Qy	421	LDSGSEFLYSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK	470						
Db	421	ldsgsfflyskltdvksrwqggnvfscvnmhealhnhytqkslspsgk	470						
RESULT	4								
AAB14779									
ID	AA14779	standard; Protein; 470	AA.						
XX	AA14779;								
AC	XX								
XX	XX								
DT	24-NOV-2000	(first entry)							
XX	XX								
DE	DE								
XX	XX	Humanised anti-Fas antibody heavy chain, SEQ ID NO:117.							
KW	KW	Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;							
KW	KW	murine; humanised antibody; complementarity determining region; CDR;							
KW	KW	human Fas; Fas ligand; apoptosis modulator; programmed cell death;							
KW	KW	autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;							
KW	KW	cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;							
KW	KW	hepatitis; AIDS; graft rejection; heavy chain.							
XX	XX								
OS	OS	Chimeric - Mus musculus.							
OS	OS	Chimeric - Homo sapiens.							
XX	XX								
PN	PN	JP2000169393-A.							
XX	XX								
PD	PD	20-JUN-2000.							
XX	XX								
PF	PF	30-SEP-1999; 99JP-0278301.							
XX	XX								
PR	PR	30-SEP-1998; 98JP-0276883.							
XX	XX								
PA	PA	(SANY ) SANKYO CO LTD.							
XX	XX								
DR	DR	WPI; 2000-485645/43.							
DR	DR	N-PSDB; AAA72184.							
XX	XX								
PT	PT	Preventive or treating agent for the diseases caused by an abnormality							
PT	PT	in the Fas/Fas ligand system e.g. autoimmune diseases, contains							
PT	PT	anti-Fas antibody -							
XX	XX								
PS	PS	Claim 21; Page 108-109; 139pp; Japanese.							

XX	The invention relates to compositions for the prevention or treatment of diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFE7A, or a humanised version of HFE7A containing identical CDRs (complementarity determining regions) to antibody HFE7A. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14775-B14776 and AAB14779 represent the heavy chains (or fragments thereof) of various humanised HFE7A-derived anti-Fas antibodies.									
SQ	Sequence 470 AA;									
	Query Match	99.9%;	Score 2514;	DB 21;	Length 470;					
	Best Local Similarity	99.8%;	Pred. No. 8	1e-143;						
	Matches 469;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;					
Qy	1	MGWSCIIILFVATATGVHSGVQLVQSGAEVKKPGASVKYKSCASGYTFTSYWMQWKQAP	60							
Db	1	mgwsciiilfvatgvtghsgvqlvqsgaevkpgasvkysckasgytftcsymwqvkkqap	60							
Qy	61	GQGLEWNGEIDPSDSTNYNQKPKGKATLTVDSTSTAYMELSLRSEDATYYTCARNRD	120							
Db	61	ggglewngelidpsdscytnyngkfkgkatltvdststaymelsslrsestavyvycarnrd	120							
Qy	121	YSNNWYFDVWGQGLTVVSSASTKGSVFPLAPSSKSTSGTAALGCLVKDYFPEPTVTS	180							
Db	121	ysnnwyfdvwwgeglvtvssastkgsvfplapsskstsggtaalgclvkdyfpeptvs	180							
Qy	181	WNSGALTSGVHTFPVAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNWKPSNTKYDKRVEP	240							
Db	181	wnsгалtsgvhtfpavlqsgglyslssvvtvpssslgtqtyicnvnhkpsntckvdkrvep	240							
Qy	241	KSCDKHTCCPCPAPELLGGPSVFLPPLPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW	300							
Db	241	kscdkhtccpcpaelllggpsvflppkpkdtlmisrtpcvtcvvdvshedpevkfnw	300							
Qy	301	YVGDGEVHNARTKPREBOQYNTYRVYSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS	360							
Db	301	yvgdgevhnaktkpreeqynstyrvyvsltlvldqdwlngkeykckvsnkalpapiektis	360							
Qy	361	KAKGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPV	420							
Db	361	kakgqprepqvytlppsreemtknqvsllclvkgyfpsdiavewesngopennykttppv	420							
Qy	421	LDSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHHVTKQSLSLSPCK 470								
Db	421	ldsdgsfflyskltvdksrwqqgnvfscsvmhealhnhytqtslsispgk 470								
RESULT	5									
AAW90929										
ID	AAW90929 standard; Protein; 470 AA.									
XX										
AC	AAW90929;									
XX										
DT	08-AUG-2000 (first entry)									
XX										
DE	Humanised HFE7A designed heavy chain protein #2.									
XX										
KW	Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;									
KW	anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;									
KW	dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas									
KW	nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;									
KW	hepatotropic; humanized; apoptosis; systemic lupus erythematosus;									
KW	Hashimoto disease; rheumatoid arthritis; graft versus host disease;									
KW	Stjorden's syndrome; anemia; Addison's disease; scleroderma sterility;									



Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

Synthetic.

EP990663-A2.

05-APR-2000.

29-SEP-1999; 99EP-0307711.

30-SEP-1998; 98JP-0276881.

30-SEP-1998; 98JP-0276882.

(SANY ) SANKYO CO LTD.

Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
WPI; 2000-258930/23.  
N-PSDB; AAA11622.

New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems

Example reference 22; Page 150-152; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, cardiatic and hepatotropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody HFE7A designed heavy chain which is used in the method described in the invention.

Sequence 470 AA;

Query Match 99.9%; Score 2514; DB 21; Length 470;  
Best Local Similarity 99.8%; Pred. No. 8.1e-143;  
Matches 469; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCILFLVATGVHSGVQVLSGAEVKKPGASVKVSKASGYFTSYWMDVQKAP 60  
DB 1 mgwscilflvatgvhsgvqlvqsgaevkpgasvkvsckasgyfttsymgwkqap 60  
QY 61 GQGLEWMEIDPSYTNYNQKFKGKATLTVDSTSTAYMELSLRSDTAVYICARNRD 120  
DB 61 gqglewmeidpsdnytnqkfkgtltvdtststaymelslrdsdtavycarnrd 120  
QY 121 YSNWYFDVWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS 180

Db 121 ysnwytadvwgeglvtvssastkgpsvfplapssksts ggtaaigclvkdypfpvts 180  
QY 181 WNSGALTSGVTFPAVLQSSGLYSLSVYVTPSSSLGTOTYICNVNHNKPSNTKVDKRVPEP 240  
Db 181 wnsгалtsghvtfpavlqssglsyslvvtvpssslgltqctyicnvnhkpsntkvdkrvep 240  
QY 241 KCDKTHFCPCPCAPPELLGSPSVFLFPPPKDKTLMISTPTEVTVVDSHEDPEVKFNW 300  
Db 241 kscdkthtcpcpcapellgspsvflfppkpkdtlmiststpevtcvvdsvedpevkfnw 300  
QY 301 YVDGVEVHNAKTKPREQYNSTYRVVSVLTVLRHODMLNGKEYCKVSKNKPAPTEKRTS 360  
Db 301 yvdgvevhnaktkpreeqynstyrvvsvltvlrhodmlngkeyckvsknkalpapekrtis 360  
QY 361 KAKGQPREPQVYTLPPPSREEMTKNQVSLTCLVKGPYPDPDIAVWEWSNGQPENNYKTPPV 420  
Db 361 kagqprepqvtytlpppsreemtknqvslctclvkgyfypsdiavewesngqpennykttppv 420  
QY 421 LDSGSEFLYSLKLVNDRKRWQGNVFCVSMHEALHNHYTOKLSLSLSPGK 470  
Db 421 ldsdgsfflysklvtvdkerwqgnvfscvsmhealhnhytqkslsalspgk 470

## RESULT 6

AAW90935  
ID AAW90935 standard; Protein; 470 AA.

XX AC AAW90935;

XX DT 08-AUG-2000 (first entry)

XX DE Humanised anti-Fas designed heavy chain Heu 3 protein.

XX KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;  
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;  
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

XX OS Synthetic.

XX PN EP990663-A2.

XX PD 05-APR-2000.

XX PF 29-SEP-1999; 99EP-0307711.

XX PR 30-SEP-1998; 98JP-0276881.

XX PR 30-SEP-1998; 98JP-0276882.

XX PA (SANY ) SANKYO CO LTD.

XX PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

XX WPI; 2000-258930/23.

XX DR N-PSDB; AAA11646.

XX PT New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems

XX PS Claim 2; Page 180-182; 263pp; English.

XX CC This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents

CC apoptosis in cells with a normal system, by inhibiting binding between  
CC Fas and its ligand. The products of the invention have anti-inflammatory,  
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
CC antihematuric, nephrotropic, antiinfertility, neuroprotective,  
CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce  
CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
CC inhibition of ligand binding. (II) are used to treat and/or prevent  
CC diseases associated with the Fas/Fas ligand system, especially systemic  
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
CC cells. They bind to both human and murine Fas, so can be evaluated in  
CC murine disease models. (II) act on the active site of Fas, i.e. they mimic  
CC the native ligand, do not induce liver disease, and have reduced risk of  
CC inducing a human anti-murine antibody response. This sequence represents  
CC a humanised anti-Fas antibody heavy chain construct designated Heu 3  
CC which is described in the method of the invention.

XX SQ Sequence 470 AA;

Query Match 99.9%; Score 2514; DB 21; Length 470;  
Best Local Similarity 99.8%; Pred. No. 8.1e-143;  
Matches 469; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCIILFVATATGVHSQVLQSGAEGKPKGASVKYKSCASGYTFTSYWQWVKQAP 60  
Db 1 mgwsciiilfvatatghvqlvqsgaevkpkpgasvkscasgyftfsymwqwrqap 60  
QY 61 GGGLEWMEIDPSDSTNTNQPKGKATLTVDSTSTAYMELSSURSEDTAVYYCARNRD 120  
Db 61 ggglewmeidpsdsytnynqkfkgkatltvdtststaymeisslrsedtavyycarnrd 120  
QY 121 YSNWYFDVWGQGLTVTVSSASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVYS 180  
Db 121 ysnwfyfdwgggtlvtvssastkgsvpflapsskstsggtaalgclvkdypfpvptvs 180  
QY 181 WNSGALTSGVHTFPVAVLQSGGLYSLSVVTVPPSSSLGTQTYICNVNHPKSNTKVDKRVEP 240  
Db 181 wnsгалtsgvhtcfpavlqsgglyslsvvtvpssslgtqtyicnvnhpkpsntkvdkrvcp 240  
QY 241 KSCDKTHCTCPCPAPPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVVDSHEDPEVKFNM 300  
Db 241 kscdkthctcpcpapellggpsvfifppkpkdtlmisrtpevtcvvvdvshedpevkfnw 300  
QY 301 YVDGVEVHNAKTPREQNTYRVVSVLTVLHQDLNKGKCYKVSNNKALPAPIETKTS 360  
Db 301 yvdgvevhnaaktpreeqnystyrvvsvltvlhqdlngkyekyckvsnkalpapietkltis 360  
QY 361 KAKGQPREPVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420  
Db 361 kagqprepvvtlppsreemtknqvsltcclvkgyfypsdiavewesngqpennnykttppv 420  
QY 421 LQSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470  
Db 421 lqsdgsfflyskltdvksrwqgnvfscsvmhcalhnhytqkslsispkg 470

RESULT 7

AAW83036  
ID AAW83036 standard; Protein; 470 AA.

XX AC AAW83036;

XX DT 15-MAR-1999 (first entry)

XX

DE Anti-Fas humanised antibody HFE7A heavy chain.  
XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;  
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;  
KW systemic lupus erythematosus; graft versus host disease;  
KW Sjogren syndrome; pernicious anaemia; Addison's disease;  
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
KW rheumatoid arthritis; autoimmune haemolytic anaemia;  
KW myasthenia gravis; multiple sclerosis; Basedow's disease;  
KW thrombopenia purpura; insulin-dependent diabetes; allergy;  
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
KW transplant rejection; therapy.  
OS Homo sapiens.  
OS Synthetic.  
XX Key Location/Qualifiers  
FT Peptide 1..19 /label= Sig\_peptide  
FT Protein 20..470 /label= Mat\_protein  
FT Region 20..140 /label= Variable  
FT Region 141..464 /label= Constant  
FT Region 50..54 /label= CDR\_H1  
FT /note= "claim 9"  
FT Region 69..84 /label= CDR\_H2  
FT /note= "claim 9"  
FT Region 118..129 /label= CDR\_H3  
FT /note= "claim 9"  
XX AU9859701-A.  
PD 08-OCT-1998.  
XX 30-MAR-1998; 98AU-0059701.  
XX 08-OCT-1997; 97JP-0276064.  
PR 01-APR-1997; 97JP-0082953.  
PR 25-JUN-1997; 97JP-0169088.  
XX (SANY ) SANKYO CO LTD.  
XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;  
PI Masahiko O, Nobufusa S, Shin Y, Tohru T;  
XX WPI; 1998-543440/47.  
DR N-PSDB; AAV70079.  
XX New antibodies and proteins bind conserved epitope of Fas antigen -  
PT used to evaluate drugs in animal models and to treat Fas-associated  
PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
PT myocarditis, hepatitis and AIDS  
XX Claim 22; Page 212-213; 292pp; English.  
XX This is the amino acid sequence of the VD type humanised heavy  
CC chain of murine anti-human Fas monoclonal antibody HFE7A. E. coli  
CC pghSL7A62 SANK 73397 harbors plasmid pghSL7A62 carrying a fusion  
CC fragment of the humanised VD type HFE7A heavy chain and DNA  
CC encoding human IgG1 constant region (see AAV70079), and is deposited  
CC as FERM BP-6074 (claimed). The invention provides methods for  
CC producing humanised antibodies by culturing host cells. Humanised  
CC versions of HFE7A (see AAW83031-37), like native HFE7A, are capable  
CC of inducing apoptosis in abnormal cells expressing Fas, and of  
CC inhibiting Fas-induced apoptosis in normal cells. The humanised  
CC antibodies are used to evaluate, in animal models, treatments of  
CC diseases that involve Fas/Fas ligand interactions, and also to

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CC treat such diseases, including autoimmune disease (e.g. systemic
CC lupus erythematosus, Hashimoto's disease, graft versus host disease,
CC Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,
CC Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,
CC autoimmune haemolytic anaemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura and
CC insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
XX
SQ Sequence 470 AA;

Query Match 99.4%; Score 2501; DB 19; Length 470;
Best Local Similarity 99.4%; Pred. No. 4.8e-142;
Matches 467; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVATATGVHSGVQLVQSGAEVKPKGASVKVSKASGYTFTSYWMQWVKQAP 60
Db 1 MGWSCIILFLVATATGVHSGVQLVQSGAEVKPKGASVKVSKASGYTFTSYWMQWVKQAP 60
QY 61 GQGLEWMEIDPDSYSTNYNQKFKGKATLVDTSTSTAYMELSLRSEDATVYYCARNRD 120
Db 61 GQGLEWMEIDPDSYSTNYNQKFKGKATLVDTSTSTAYMELSLRSEDATVYYCARNRD 120
QY 121 YSNWYFDVWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAAALGCLVKDYFPEPTVS 180
Db 121 YSNWYFDVWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAAALGCLVKDYFPEPTVS 180
QY 181 WNSGALTSVHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKRVPE 240
Db 181 WNSGALTSVHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKRVPE 240
QY 241 KSCDKTHTCCPCPAPPELLGGPSVFLPAPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300
Db 241 KSCDKTHTCCPCPAPPELLGGPSVFLPAPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300
QY 301 YDGVVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 360
Db 301 YDGVVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 360
QY 361 KAKGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
Db 361 KAKGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
QY 421 LDSDGSFFLYSKLTVDKSRWQOGNVFSCSVMHREALHNYTKQSLSPGK 470
Db 421 LDSDGSFFLYSKLTVDKSRWQOGNVFSCSVMHREALHNYTKQSLSPGK 470

RESULT 8
AAB14776
ID AAB14776 standard; Protein; 470 AA.
XX
AC AAB14776;
XX
DT 24-NOV-2000 (first entry)
XX
DE Humanised anti-Fas antibody heavy chain, SEQ ID NO:89.
XX
KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5628;
KW murine; humanised antibody; complementarity determining region; CDR;
KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancyelophthisis;
KW hepatitis; AIDS; graft rejection; heavy chain.
XX
OS Chimeric - Mus musculus.
OS Chimeric - Homo sapiens.
XX
PN JP2000169393-A.
XX
PD 20-JUN-2000.
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XX 30-SEP-1999; 99JP-0278301.
XX 30-SEP-1998; 98JP-0276883.
XX (SANY ) SANKYO CO LTD.
XX WPI: 2000-485645/43.
XX N-PSDB; AAA72159.
XX Preventive or treating agent for the diseases caused by an abnormality
XX in the Fas/Fas ligand system e.g. autoimmune diseases, contains
XX anti-Fas antibody -
XX
XX Claim 21; Page 95-96; 139pp; Japanese.
XX The invention relates to compositions for the prevention or treatment
XX or diseases caused by an abnormality in the Fas/Fas ligand system
XX containing an anti-Fas antibody as the active component. The anti-Fas
XX antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
XX or a humanised version of HFE7A containing identical CDRs
XX (complementarity determining regions) to antibody HFE7A. Via its
XX interaction with Fas, the antibody of the invention acts as a modulator
XX of apoptosis. The compositions of the invention may therefore be used in
XX the treatment or prevention of conditions such as autoimmune diseases,
XX allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
XX glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
XX and organ graft rejection. Sequences AAB14775-B14776 and AAB14779
XX represent the heavy chains (or fragments thereof) of various humanised
XX HFE7A-derived anti-Fas antibodies.
XX
XX Sequence 470 AA;
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Query Match 99.4%; Score 2501; DB 21; Length 470;
Best Local Similarity 99.4%; Pred. No. 4.8e-142;
Matches 467; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVATATGVHSGVQLVQSGAEVKPKGASVKVSKASGYTFTSYWMQWVKQAP 60
Db 1 MGWSCIILFLVATATGVHSGVQLVQSGAEVKPKGASVKVSKASGYTFTSYWMQWVKQAP 60
QY 61 GQGLEWMEIDPDSYSTNYNQKFKGKATLVDTSTSTAYMELSLRSEDATVYYCARNRD 120
Db 61 GQGLEWMEIDPDSYSTNYNQKFKGKATLVDTSTSTAYMELSLRSEDATVYYCARNRD 120
QY 121 YSNWYFDVWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAAALGCLVKDYFPEPTVS 180
Db 121 YSNWYFDVWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAAALGCLVKDYFPEPTVS 180
QY 181 WNSGALTSVHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKRVPE 240
Db 181 WNSGALTSVHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKRVPE 240
QY 241 KSCDKTHTCCPCPAPPELLGGPSVFLPAPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300
Db 241 KSCDKTHTCCPCPAPPELLGGPSVFLPAPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300
QY 301 YDGVVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 360
Db 301 YDGVVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 360
QY 361 KAKGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
Db 361 KAKGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
QY 421 LDSDGSFFLYSKLTVDKSRWQOGNVFSCSVMHREALHNYTKQSLSPGK 470
Db 421 LDSDGSFFLYSKLTVDKSRWQOGNVFSCSVMHREALHNYTKQSLSPGK 470

RESULT 9
AAW90926
```

AAW90926 standard; Protein; 470 AA.  
 AAW90926;  
 08-AUG-2000 (first entry)  
 Humanised HFE7A designed heavy chain protein.  
 Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
 anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;  
 dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
 nephrotropic; antinfertility; neuroprotective; antiartherosclerotic;  
 hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
 Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
 Synthetic.  
 EP990663-A2.  
 05-APR-2000.  
 29-SEP-1999; 99EP-0307711.  
 30-SEP-1998; 98JP-0276881.  
 30-SEP-1998; 98JP-0276882.  
 (SANY ) SANKYO CO LTD.  
 Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 WPI: 2000-258930/23.  
 N-PSDB; AA11597.  
 New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 inflammatory or autoimmune disease, induces apoptosis selectively in  
 cells with abnormal Fas-Fas ligand systems -  
 Example reference 15; Page 134-136; 263pp; English.  
 This invention describes a novel humanized anti-Fas antibody-like  
 molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 ligand system, by binding to Fas on the cell surface, and prevents  
 apoptosis in cells with a normal system, by inhibiting binding between  
 Fas and its ligand. The products of the invention have anti-inflammatory,  
 anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 antirheumatic, nephrotropic, antinfertility, neuroprotective,  
 antiartherosclerotic, cardiac and hepatropic activity. (I) induce  
 apoptosis by binding to cell surface Fas or inhibit it by competitive  
 inhibition of ligand binding. (I) are used to treat and/or prevent  
 diseases associated with the Fas/Fas ligand system, especially systemic  
 lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 inhibit apoptosis in normal cells but selectively induce it in abnormal  
 cells. They bind to both human and murine Fas, so can be evaluated in  
 murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 the native ligand, do not induce liver disease, and have reduced risk of  
 inducing a human anti-murine antibody response. This sequence represents  
 a humanised anti-Fas antibody HFE7A designed heavy chain which is used in  
 the method described in the invention.

Sequence 470 AA;

Query Match 99.4%; Score 2501; DB 21; Length 470;  
 Best Local Similarity 99.4%; Pred No. 4.8e-142;  
 Matches 467; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVATATGVHSQVLQSGAEVKKPGASVKVSKASGTYFTSYWQWYKQAP 60  
 DB 1 mgwsciilflvatagvhsqvlvqsgaevkkpgasvkvsckasgyftfsymmqwvkqap 60  
 QY 61 GGLQEWGMDISDSVTNNQFKGKATLTDSTSTAYWELSLRSEDATAYYICARNRD 120  
 DB 61 gglqewmgeidpsdsvtnnqfkgtatldtstastaymelsslrsestavyycarnrd 120  
 QY 121 YNNNYFVDMVGOGTLTVVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYS 180  
 DB 121 ynnnyfvdwvgogtlvtvssastkgpsvflapsskstsggtaaalgclvdyfpeptvys 180  
 QY 181 WNSGALTSVGHFTFPAVLQSSGLYSLSVVTVPSSSSLGTQTYICNVNHNKPSNTKVDKRVPE 240  
 DB 181 wnsгалtsvghtfpavlgsglyslsvvtvpssslgtqtyicnvnhkpstntkvdkrvpe 240  
 QY 241 KSCDKTHCTPCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDYSHEDPEVKFNW 300  
 DB 241 kscdkthctpcpcpapeilggpsvflfppkpkdtlmisrtpevtcvvvdvshedepevkfnw 300  
 QY 301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKTIS 360  
 DB 301 yvdgvevhnaktkpreeqynstyrvvsvltvlhqdmngkeyckvsnkalpapiektis 360  
 QY 361 KAKGPQEPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPV 420  
 DB 361 kagqppepqvylppstreemtknqvsltclvkgyfypsdiavewesngqpennnykttppv 420  
 QY 421 LQSDGSFFLYSKLTVDKSRWQQGNVFCSMVHEALHNHYTQKSLSLSPGK 470  
 DB 421 ldsdgsfflyskltvdksrwqgnvfscsmvhealhnhytqkslsispgk 470

RESULT 10  
 AAW90936  
 ID AAW90936 standard; Protein; 470 AA.  
 XX AC AAW90936;  
 XX DT 08-AUG-2000 (first entry)  
 XX DE Humanised HFE7A designed heavy chain HHH type protein.  
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;  
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
 KW nephrotropic; antinfertility; neuroprotective; antiartherosclerotic;  
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
 XX Synthetic.  
 XX OS EP990663-A2.  
 XX PD 05-APR-2000.  
 XX PF 29-SEP-1999; 99EP-0307711.  
 XX PR 30-SEP-1998; 98JP-0276881.  
 XX PR 30-SEP-1998; 98JP-0276882.  
 XX PA (SANY ) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
XX WPI: 2000-2589930/23.  
DR N-PSDB; AAA11655.  
XX  
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
PT inflammatory or autoimmune disease, induces apoptosis selectively in  
XX cells with abnormal Fas-Fas ligand systems -  
XX Claim 2; Page 188-189; 263pp; English.  
XX  
XX This invention describes a novel humanized anti-Fas antibody-like  
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
CC ligand system, by binding to Fas on the cell surface, and prevents  
CC apoptosis in cells with a normal system, by inhibiting binding between  
CC Fas and its ligand. The products of the invention have anti-inflammatory,  
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
CC antirheumatic, nephrotropic, antifertility, neuroprotective,  
CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce  
CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
CC inhibition of ligand binding. (I) are used to treat and/or prevent  
CC diseases associated with the Fas/Fas ligand system, especially systemic  
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
CC cells. They bind to both human and murine Fas, so can be evaluated in  
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
CC the native ligand, do not induce liver disease, and have reduced risk of  
CC inducing a human anti-murine antibody response. This sequence represents  
CC a humanised anti-Fas antibody HFE7A heavy chain construct HHH type .  
XX which is described in the method of the invention.  
XX  
SQ Sequence 470 AA;

Query Match 99.1%; Score 2495; DB 21; Length 470;  
Best Local Similarity 98.7%; Pred. No. 1.1e-141;  
Matches 464; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MGWSCIIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAP 60  
DB 1 mgwsciiilflvatatgvhsqvlvqsgaevkpgasvkvsckasgytftsymbmqwvrqap 60  
QY 61 GQGLEWMGEIDPSDSTYNYNOKFKGKATLTVDSTSTAYMELSLRSDEDTAVYYCARNRD 120  
DB 61 gqglewmgeidpsdstynynokfkgtitrdtststaymelslrsedtaavyycarnrd 120  
QY 121 YSNWNVFDVWQCGILTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180  
DB 121 ysnwnyfdvwdqegtltvtvssastkgpsvfplapsskstsggtaalgclvkdypfepvtvs 180  
QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGQTQYICNVNHHKPSNTKVDKRVPE 240  
DB 181 wnsгалtsгvhtfpavlgssglyslssvttvtpssslgqtqyicnvnhkpstkvdkrvpe 240  
QY 241 KSCDKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300  
DB 241 kscdkhtccpcpaelggpsvflfppkpkdtlmisrtpevtcvvvdshedpevkfnw 300  
QY 301 YVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360  
DB 301 yvdgvevhnatkpreqynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektis 360  
QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420  
DB 361 kakgqprepqvtytlppsreemtknqvsltclvkgyfypsdiavewesngqpennnykttppv 420

DB 361 kakgqprepqvtytlppsreemtknqvsltclvkgyfypsdiavewesngqpennnykttppv 420  
QY 421 LDSGCSFFLYSKLTVDKSRWQGNVFCFSVMHEALHNHYTQKSLSLSPGK 470  
DB 421 ldsdgsfflyskltvdksrwqgnvfcsvmhealhnhytqkslslspgk 470  
RESULT 11  
AAM52156  
ID AAM52156 standard; Protein; 731 AA.  
XX  
XX AAM52156;  
AC  
XX 05-FEB-2002 (first entry)  
DT  
XX Humanised HMPG-1 heavy chain/DNase I fusion protein 1.  
DE  
XX Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;  
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.  
KW Homo sapiens.  
XX OS  
XX Synthetic.  
XX  
XX WO200174905-A1.  
PN  
XX 11-OCT-2001.  
PD  
XX 26-MAR-2001; 2001WO-GB01324.  
PR  
XX 03-APR-2000; 2000GB-0008049.  
PR 02-OCT-2000; 2000US-237159P.  
XX  
XX (ANTI-) ANTISOMA RES LTD.  
PI Young RJ;  
XX  
XX WPI: 2001-662969/76.  
DR  
XX Novel compound used to treat cancer has target cell-specific portion  
PT comprising humanised monoclonal antibody having specificity for  
PT polymorphic epithelial mucin, and cytotoxic portion having  
PT endonucleolytic activity -  
XX  
XX Claim 20; Figure 7; 176pp; English.  
PS  
XX The invention relates to a compound which comprises a target  
CC cell-specific portion, comprising an humanised monoclonal antibody,  
CC having specificity for polymorphic epithelial mucin (PEM) or its antigen  
CC binding fragment and a cytotoxic portion having endonucleolytic activity,  
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The  
CC compound has cytostatic activity useful for treating cancer and acting as  
CC a potential inducer of apoptosis.  
XX  
SQ Sequence 731 AA;

Query Match 93.2%; Score 2346.5; DB 22; Length 731;  
Best Local Similarity 93.0%; Pred. No. 1.4e-132;  
Matches 437; Conservative 20; Mismatches 10; Indels 3; Gaps 1;

QY 1 MGWSCIIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAP 60  
DB 1 mgwsciiilflvatatgvhsqvlvqsgaevkpgasvkvsckasgytftsymbwvrqap 60  
QY 61 GQGLEWMGEIDPSDSTYNYNOKFKGKATLTVDSTSTAYMELSLRSDEDTAVYYCARNRD 120  
DB 61 gqglewmgeidpsdstynynokfkgtitrdtststaymelslrsedtaavyycarsyd 120  
QY 121 YSNWNVFDVWQCGILTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180  
DB 121 fa---wfaywgggtltvtvssastkgpsvfplapsskstsggtaalgclvkdypfepvtvs 177  
QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGQTQYICNVNHHKPSNTKVDKRVPE 240

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Db 178 wnsгалtsгvhtfpavlgssglsysvvtvpsssgtqtyicnvnkpsntkvdckvpe 237
QY 241 KSCDKHTHTCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
Db 238 kscdkhtcpcpapellggpsvflfppkpkdtlmsrtpevtccvvdvshedpevkfnw 297
QY 301 YVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
Db 298 yvdgvevhnaktkpreeqynstyrvvsvltclvlgqdwlngkeyckvsnkalpapiektis 357
QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPV 420
Db 358 kagqprepqvylppsrdeitknqvsitclvkgfypsdiavwesngqpennnykttppv 417
QY 421 LDSGGSFFLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYTQKSLSLSPGK 470
Db 418 ldsdgsfflyskitvdksrwqgnvfscsvmhealhnhytqkslsispgk 467

RESULT 12
AAM52159
ID AAM52159 standard; Protein; 741 AA.
XX
AC AAM52159;
XX
DT 05-FEB-2002 (first entry)
XX
DE Humanised HMFG-1 heavy chain/DNase I fusion protein 4.
XX
KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200174905-A1.
XX
PD 11-OCT-2001.
XX
PF 26-MAR-2001; 2001WO-GB01324.
XX
PR 03-APR-2000; 2000GB-0008049.
PR 02-OCT-2000; 2000US-237159P.
XX
PA (ANTI-) ANTISOMA RES LTD.
XX
PI Young RJ;
XX
DR WPI; 2001-662969/76.
XX
PT Novel compound used to treat cancer has target cell-specific portion
PT comprising humanised monoclonal antibody having specificity for
PT polymorphic epithelial mucin, and cytotoxic portion having
PT endonucleolytic activity -
XX
PS Claim 20; Figure 10; 176pp; English.
XX
CC The invention relates to a compound which comprises a target
CC cell-specific portion, comprising an humanised monoclonal antibody,
CC having specificity for polymorphic epithelial mucin (PEM) or its antigen
CC binding fragment and a cytotoxic portion having endonucleolytic activity,
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
CC compound has cytostatic activity useful for treating cancer and acting as
CC a potential inducer of apoptosis.
XX
SQ Sequence 741 AA;

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Query Match          93.2%; Score 2346.5; DB 22; Length 741;
Best Local Similarity 93.0%; Pred. No. 1.4e-132;
Matches 437; Conservative 20; Mismatches 10; Indels 3; Gaps 1;

```

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QY 1 MGWSCILFLVATATGVHSQVLVQSGAEYKVPKASVYKVSCKASGYTFTSYMMQWVQKAP 60
Db 1 mgwscllflvatatgvhsqvlvqsgaevkpgasvkvsckasgytfsaywiewvqap 60
QY 61 GQGLEWNGEIDPSDSTYNQKFKGKATLIVDTSTSTAYMELSLSRSEDATVYYCARNRD 120
Db 61 gglewngeidpsdstynqkfkgrvtvtrdstntaymelslsrsedtavyycarsyd 120
QY 121 YSNWNVFDVMGQGTFLTVSSASTKGPSPVFLPAPSSKSTSGTAAALGCLVXDYFPPEVTVS 180
Db 121 ysnwnvfdvmgqgtflvtvssastkgpsvflpapskstsagttaalgclvxdyfpevtvs 177
QY 181 WNSGALTSГVHTFPVAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKRVPE 240
Db 178 wnsгалtsгvhtfpavlgssglsysvvtvpsssgtqtyicnvnkpsntkvdckvpe 237
QY 241 KSCDKHTHTCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
Db 238 kscdkhtcpcpapellggpsvflfppkpkdtlmsrtpevtccvvdvshedpevkfnw 297
QY 301 YVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
Db 298 yvdgvevhnaktkpreeqynstyrvvsvltclvlgqdwlngkeyckvsnkalpapiektis 357
QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPV 420
Db 358 kagqprepqvylppsrdeitknqvsitclvkgfypsdiavwesngqpennnykttppv 417
QY 421 LDSGGSFFLYSKLTVDKSRWQGNVFSVCSVMHEALHNHYTQKSLSLSPGK 470
Db 418 ldsdgsfflyskitvdksrwqgnvfscsvmhealhnhytqkslsispgk 467

RESULT 13
AAM52158
ID AAM52158 standard; Protein; 729 AA.
XX
AC AAM52158;
XX
DT 05-FEB-2002 (first entry)
XX
DE Humanised HMFG-1 heavy chain/DNase I fusion protein 3.
XX
KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200174905-A1.
XX
PD 11-OCT-2001.
XX
PF 26-MAR-2001; 2001WO-GB01324.
XX
PR 03-APR-2000; 2000GB-0008049.
PR 02-OCT-2000; 2000US-237159P.
XX
PA (ANTI-) ANTISOMA RES LTD.
XX
PI Young RJ;
XX
DR WPI; 2001-662969/76.
XX
PT Novel compound used to treat cancer has target cell-specific portion
PT comprising humanised monoclonal antibody having specificity for
PT polymorphic epithelial mucin, and cytotoxic portion having
PT endonucleolytic activity -
XX
PS Claim 20; Figure 9; 176pp; English.
XX
CC The invention relates to a compound which comprises a target
CC cell-specific portion, comprising an humanised monoclonal antibody,

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CC having specificity for polymorphic epithelial mucin (PEM) or its antigen  
CC binding fragment and a cytotoxic portion having endonucleolytic activity,  
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The  
CC compound has cytostatic activity useful for treating cancer and acting as  
CC a potential inducer of apoptosis.  
XX  
SQ Sequence 729 AA;

Query Match 93.0%; Score 2341.5; DB 22; Length 729;  
Best Local Similarity 93.0%; Pred. No. 2.7e-132;  
Matches 436; Conservative 20; Mismatches 10; Indels 3; Gaps 1;  
QY 1 MGWSCIILFVATGTVHSGVQLVQSGAEYKPGASVYKSCASGYTFTSYWQWVKQAP 60  
Db 1 mgwscilflivatgthsqvqlvqsgaevkpgasvkvsckasgytfsaywiewvraq 60  
QY 61 GQGLEWNGEIDPDSSTYNQKFKGKATLVDTSTAYMELSLRSEDVAVYCCARNRD 120  
Db 61 gkglewngellpgsnmsrynekfkgrvtvtrdtstntaymelslrsedtavyyccarsyd 120  
QY 121 YSNWYFDVMGQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVS 180  
Db 121 fa---wfaywgqglvtvssastkgpsvflapsskstsaggtaalgclvkdypcptvs 177  
QY 181 WNSGALTSVHTFPVAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKRVPE 240  
Db 178 wnsгалtsvhtfpavllqssglyslsvstvpssslgtqtyicnvnhkpsntkvdkkvpe 237  
QY 241 KSCDKHTCPCPCAPPELLGGPSVFLPAPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300  
Db 238 kscdkhtcpcpcapellggpsvflppkpkdtlmisrtpevtcvvvdvshedpevkfnw 297  
QY 301 YVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360  
Db 298 yvdgvevhnaktpreeqynstyrvvsvltvlhqdwlngkeyckvsnkalpapiectis 357  
QY 361 KAKQPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPV 420  
Db 358 kakqprepqvyltpprdeitknqvsitclvkgfypsdiavwesngqpennnykttppv 417  
QY 421 LDSGSEFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 469  
Db 418 ldsdgsfflyskltvdksrwqqgnvfscsvmhhealhnhytqkslsispg 466

RESULT 14  
AAM52161  
ID AAM52161 standard; Protein; 739 AA.  
XX  
AC AAM52161;  
XX  
DT 05-FEB-2002 (first entry)  
XX  
DE Humanised HMFG-1 heavy chain/DNase I fusion protein 6.  
XX  
KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;  
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN W0200174905-A1.  
XX  
PD 11-OCT-2001.  
XX  
PF 26-MAR-2001; 2001WO-GB01324.  
XX  
PR 03-APR-2000; 2000GB-0008049.  
PR 02-OCT-2000; 2000US-237159P.  
XX  
PA (ANTI-) ANTISOMA RES LTD.  
XX

PI Young RJ;  
DR WPI; 2001-662969/76.  
XX  
XX Novel compound used to treat cancer has target cell-specific portion  
PT comprising humanised monoclonal antibody having specificity for  
PT polymorphic epithelial mucin, and cytotoxic portion having  
PT endonucleolytic activity -  
XX  
XX Claim 20; Figure 12; 176pp; English.  
XX  
XX The invention relates to a compound which comprises a target  
CC cell-specific portion, comprising an humanised monoclonal antibody,  
CC having specificity for polymorphic epithelial mucin (PEM) or its antigen  
CC binding fragment and a cytotoxic portion having endonucleolytic activity,  
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The  
CC compound has cytostatic activity useful for treating cancer and acting as  
CC a potential inducer of apoptosis.  
XX  
SQ Sequence 739 AA;

Query Match 93.0%; Score 2341.5; DB 22; Length 739;  
Best Local Similarity 93.0%; Pred. No. 2.8e-132;  
Matches 436; Conservative 20; Mismatches 10; Indels 3; Gaps 1;  
QY 1 MGWSCIILFVATGTVHSGVQLVQSGAEYKPGASVYKSCASGYTFTSYWQWVKQAP 60  
Db 1 mgwscilflivatgthsqvqlvqsgaevkpgasvkvsckasgytfsaywiewvraq 60  
QY 61 GQGLEWNGEIDPDSSTYNQKFKGKATLVDTSTAYMELSLRSEDVAVYCCARNRD 120  
Db 61 gkglewngellpgsnmsrynekfkgrvtvtrdtstntaymelslrsedtavyyccarsyd 120  
QY 121 YSNWYFDVMGQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVS 180  
Db 121 fa---wfaywgqglvtvssastkgpsvflapsskstsaggtaalgclvkdypcptvs 177  
QY 181 WNSGALTSVHTFPVAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKRVPE 240  
Db 178 wnsгалtsvhtfpavllqssglyslsvstvpssslgtqtyicnvnhkpsntkvdkkvpe 237  
QY 241 KSCDKHTCPCPCAPPELLGGPSVFLPAPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300  
Db 238 kscdkhtcpcpcapellggpsvflppkpkdtlmisrtpevtcvvvdvshedpevkfnw 297  
QY 301 YVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360  
Db 298 yvdgvevhnaktpreeqynstyrvvsvltvlhqdwlngkeyckvsnkalpapiectis 357  
QY 361 KAKQPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPV 420  
Db 358 kakqprepqvyltpprdeitknqvsitclvkgfypsdiavwesngqpennnykttppv 417  
QY 421 LDSGSEFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 469  
Db 418 ldsdgsfflyskltvdksrwqqgnvfscsvmhhealhnhytqkslsispg 466

RESULT 15  
AAM52157  
ID AAM52157 standard; Protein; 730 AA.  
XX  
AC AAM52157;  
XX  
DT 05-FEB-2002 (first entry)  
XX  
DE Humanised HMFG-1 heavy chain/DNase I fusion protein 2.  
XX  
KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;  
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.  
XX  
OS Homo sapiens.







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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:17:04 ; Search time 82.88 Seconds  
(without alignments)  
138.514 Million cell updates/sec

Title: US-09-499-662-143  
Perfect score: 2517  
Sequence: 1 MGWSCILFLVATATGVHSQ.....MHEALNHVTKYKSLSPGK 470

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2232	88.7	449	1	US-08-458-516-13
2	2230	88.6	476	2	US-08-378-939-10
3	2202.5	87.5	467	4	US-09-049-672A-8
4	2200.5	87.4	452	3	US-09-027-449-71
5	2200.5	87.4	452	4	US-09-026-985-71
6	2177	86.5	468	4	US-09-026-985-71
7	2177	86.5	711	4	US-09-485-737B-67
8	2161.5	85.9	454	2	US-07-934-373C-22
9	2161.5	85.9	454	3	US-08-437-642B-22
10	2161.5	85.9	454	5	PCT-US93-07832-22
11	2144	85.2	472	4	US-08-793-450-8
12	2124	84.4	451	2	US-08-887-352B-14
13	2124	84.4	451	2	US-08-887-352B-16
14	2124	84.4	451	3	US-08-466-151-65
15	2124	84.4	451	4	US-09-109-207C-14
16	2124	84.4	451	4	US-09-109-207C-16
17	2124	84.4	451	4	US-09-296-005-14
18	2124	84.4	451	4	US-09-296-005-16
19	2121	84.3	478	3	US-08-487-550-8
20	2116	84.1	451	2	US-08-887-352B-18
21	2116	84.1	451	4	US-09-109-207C-18
22	2116	84.1	451	4	US-09-282-505-2
23	2116	84.1	451	4	US-09-054-255-2
24	2116	84.1	451	4	US-09-296-005-18
25	2105	83.6	453	3	US-08-466-151-8
26	2105	83.6	453	4	US-08-466-151-8
27	2103.5	83.6	467	2	US-07-916-098A-45

28	2102.5	83.5	449	4	US-09-679-397-2	Sequence 2, Appl
29	2099.5	83.4	552	5	PCT-US93-07832-23	Sequence 23, Appl
30	2096.5	83.3	469	2	US-07-934-373C-23	Sequence 23, Appl
31	2096.5	83.3	469	3	US-08-437-642B-23	Sequence 23, Appl
32	2096	83.3	451	4	US-09-247-352-3	Sequence 3, Appl
33	2090.5	83.1	459	1	US-08-157-101A-7	Sequence 7, Appl
34	2072.5	82.3	467	1	US-08-704-744-81	Sequence 81, Appl
35	2070.5	82.3	473	4	US-09-049-672A-4	Sequence 4, Appl
36	2060.5	81.9	445	4	US-08-341-560B-17	Sequence 17, Appl
37	2054.5	81.6	446	3	US-08-397-411-7	Sequence 7, Appl
38	2054	81.6	476	3	US-08-487-550-12	Sequence 12, Appl
39	2022	80.3	442	5	PCT-US96-10043-9	Sequence 9, Appl
40	2022	80.3	476	3	US-08-487-550-4	Sequence 4, Appl
41	2010	79.9	442	1	US-08-461-968A-5	Sequence 5, Appl
42	2010	79.9	442	2	US-08-462-571-5	Sequence 5, Appl
43	1995.5	79.3	450	2	US-08-788-800-12	Sequence 12, Appl
44	1986	78.9	442	1	US-08-480-036-2	Sequence 2, Appl
45	1986	78.9	442	1	US-08-461-968A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-08-458-516-13  
; Sequence 13, Application US/08458516  
; Patent No. 5777085  
; GENERAL INFORMATION:  
; APPLICANT: Co, Man Sung  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Humanized Antibodies Reactive with GPIIB/IIIA  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/458,516  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/059,159  
; FILING DATE: 03-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-37-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 449 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-458-516-13

Query Match 88.7%; Score 2232; DB 1; Length 449;  
Best Local Similarity 93.1%; Pred No. 2.8e-158;  
Matches 420; Conservative 14; Mismatches 15; Indels 2; Gaps 2;

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QY 20 QVQLVQSGAEVKKPGASVKVSCKRSGSYTFTSYNQWVKQAPGQGLEWMGIDPSDSYTN 79
Db 1 QVQLVQSGAEVKKPGSSVKVSCKRSGYAFNYLIEWVRQAPGQGLEWIGVYIPGSGGTNY 60
QY 80 NQKFKGKATLTDSTSTAYMELSSLRSEDTAVYICARNRDYNNWYFDVWGQGLTVTVS 139
Db 61 NEKFKGRTLTVDSTNTAYMELSSLRSEDTAVYFCAR-RDGYGW-FAYWGQGLTVTVS 118
QY 140 SASTKGPSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 199
Db 119 SASTKGPSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 178
QY 200 SGLYSLSVVTVTPSSSLGTQYICNVNHNKPSNTKVDKRPKSCDKTHTCCPPCAPPELLG 259
Db 179 SGLYSLSVVTVTPSSSLGTQYICNVNHNKPSNTKVDKVPKSCDKTHTCCPPCAPPELLG 238
QY 260 GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVVEVHNKTKPREEQY 319
Db 239 GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVVEVHNKTKPREEQY 298
QY 320 NSTYRVSVLTQLVHODWLNKKEYCKKVSNNKALPAPIEKTISKAKGQPREPVYTLPPSRE 379
Db 299 NSTYRVSVLTQLVHODWLNKKEYCKKVSNNKALPAPIEKTISKAKGQPREPVYTLPPSRE 358
QY 380 EMTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTPTPVLDSDGSFFLYSLKTVDKSR 439
Db 359 ELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTPTPVLDSDGSFFLYSLKTVDKSR 418
QY 440 WQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
Db 419 WQGNVFCSCVMHEALHNHYTQKSLSLSPGK 449
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RESULT 2
US-08-378-939-10
; Sequence 10, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
US-08-378-939-10
Query Match 88.6%; Score 2230; DB 2; Length 476;
Best Local Similarity 88.4%; Pred. No. 4.3e-158;
Matches 421; Conservative 21; Mismatches 28; Indels 6; Gaps 1;
QY 1 MGSCIIILFLVATATGVHISOVLQVSGAEVKKPGASVKVSCKRSGSYTFTSYNQWVKQAP 60
Db 1 MDWTWFLFVVAATGVQSQMQLVQSGAEVKKPGSSVTVSCKASGGTFSNVAISWVRQAP 60
QY 61 GQGLEWMEIDPSDSYTNYNQKFKGKATLFDVDTSTSTAYMELSSLRSEDTAVYICARNR- 119
Db 61 GQGLEWMEIDPSDSYTNYNQKFKGKATLFDVDTSTSTAYMELSSLRSEDTAVYICARNR- 120
QY 120 -----DYSNNWYFDVWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 174
Db 121 ROANFRARVGVDFPMGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 180
QY 175 EPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHNKPSNTKV 234
Db 181 EPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHNKPSNTKV 240
QY 235 DKRVEPKSCDKTHTCCPPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 294
Db 241 DKRVEPKSCDKTHTCCPPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
QY 295 EVKFNWYDGVVEVHNKTKPREEQYNSTYRVSVLTQLVHODWLNKKEYCKKVSNNKALPAP 354
Db 301 EVKFNWYDGVVEVHNKTKPREEQYNSTYRVSVLTQLVHODWLNKKEYCKKVSNNKALPAP 360
QY 355 IEKTISKAKGQPREPVYTLPPSREEMTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNY 414
Db 361 IEKTISKAKGQPREPVYTLPPSREEMTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNY 420
QY 415 KTTTPVLDSDGSFFLYSLKTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
Db 421 KTTTPVLDSDGSFFLYSLKTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476
RESULT 3
US-09-049-672A-8
; Sequence 8, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Cerrone, Michael C  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0497 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 467 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: LUNGTU11  
CLONE: 2747531  
US-09-049-672A-8

Query Match 87.5%: Score 2202.5; DB 4; Length 467;  
Best Local Similarity 89.28; Pred. No. 4.6e-156;  
Matches 414; Conservative 19; Mismatches 28; Indels 3; Gaps 1;  
Qy 7 ILFLVATATGHSQVQLVQSGAEYKPKGASVYKSKASGYTFTSYMMQWVQAPQGGLW 66  
Db 7 ILFLVAAATGHAQVQLVQSGAEYKPKGASVQVCTVSGFTLSDLSVHHVQAPQGGLW 66  
Qy 67 MGEIDPSDSTYNNQKFGKATLVDTSTAYMELSLRSEDYAVYICARNRYSNNWY 126  
Db 67 MGLAPENGAEVAYAKFLRLTSLDSTADTAYMFLNLSGSDSAIYYCARQH---YDF 123  
Qy 127 FDVWGQGLTVTVSSASVKGPSVFLAPSSKSTSGGTAALGCLVKDYRPPVTVSWNSGAL 186  
Db 124 FDFWGQGLTVTVSSASVKGPSVFLAPSSKSTSGGTAALGCLVKDYRPPVTVSWNSGAL 183  
Qy 187 TSGVHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKYDKRVEPKSCDKT 246  
Db 184 TSGVHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKYDKRVEPKSCDKT 243  
Qy 247 HTCPCPAPELLGSPVFLPPPKDLMISRTEVTCVVDVSHEDPEVFNKYVDGVE 306  
Db 244 HTCPCPAPELLGSPVFLPPPKDLMISRTEVTCVVDVSHEDPEVFNKYVDGVE 303  
Qy 307 VHNKTRPREQYNTYRVSVLVTLHODWLNKGYCKVSNKALPAPIEKTISKAKGQP 366  
Db 304 VHNKTRPREQYNTYRVSVLVTLHODWLNKGYCKVSNKALPAPIEKTISKAKGQP 363  
Qy 367 REPOVYTLPPSREMTKNQVSLTCLVKGFPSPDI AVEWESNGQPENNYKTPPVLDSDGS 426  
Db 364 REPOVYTLPPSREMTKNQVSLTCLVKGFPSPDI AVEWESNGQPENNYKTPPVLDSDGS 423  
Qy 427 FFLYSLKTVDSKRWQGNVFCSCVMHEALHNHYTQKLSLSPGK 470  
Db 424 FFLYSLKTVDSKRWQGNVFCSCVMHEALHNHYTQKLSLSPGK 467

RESULT 4  
US-09-027-449-71  
Sequence 71, Application US/09027449  
Patent No. 6025158  
GENERAL INFORMATION:  
APPLICANT: Gonzalez, Tania R.  
APPLICANT: Leong, Steven R.  
APPLICANT: Presta, Leonard G.  
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and  
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way

CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/027,449  
FILING DATE: 20-Feb-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/074,330  
FILING DATE: 22-Jan-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/038,664  
FILING DATE: 21-Feb-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: PI085R3-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5530  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 452 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-027-449-71

Query Match 87.4%: Score 2200.5; DB 3; Length 452;  
Best Local Similarity 90.08; Pred. No. 6.2e-156;  
Matches 407; Conservative 27; Mismatches 17; Indels 1; Gaps 1;  
Qy 20 QVQLVQSGAEYKPKGASVYKSKASGYTFTSYMMQWVQAPQGGLWGEIDPSDSTYNY 79  
Db 1 EVQLVQSGGLVQPGSLRLSCAASGYSFSSHYHMHVQAPGKGLWEVGYIDPSNGETTY 60  
Qy 80 NQKFGKATLVLDISTSTAYMELSLRSEDYAVYICAR-NRDYSNNWTFDVGQGLTVTV 138  
Db 61 NQKFGKRTLSRDNSKNTAYLQMNLSRAEDYAVYICARGDYRYNGDFDVGQGLTVTV 120  
Qy 139 SSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYRPPVTVSWNSGALTSGVHTFPVAVLQ 198  
Db 121 SSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYRPPVTVSWNSGALTSGVHTFPVAVLQ 180  
Qy 199 SSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKYDKRVEPKSCDKTHTCPCPAPELL 258  
Db 181 SSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKYDKRVEPKSCDKTHTCPCPAPELL 240  
Qy 259 GGPSVFLPPPKDLMISRTEVTCVVDVSHEDPEVFNKYVDGVEVHNKATKPREEQ 318  
Db 241 GGPSVFLPPPKDLMISRTEVTCVVDVSHEDPEVFNKYVDGVEVHNKATKPREEQ 300  
Qy 319 YNSTYRVSVLVTLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 378  
Db 301 YNSTYRVSVLVTLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 360  
Qy 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKTVDSK 438  
Db 361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKTVDSK 420  
Qy 439 RWQGNVFCSCVMHEALHNHYTQKLSLSPGK 470  
Db 421 RWQGNVFCSCVMHEALHNHYTQKLSLSPGK 452  
RESULT 5  
US-09-026-985-71

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: Sequence 71, Application US/09026985
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: GENERAL INFORMATION:
: APPLICANT: Gonzalez, Tania R.
: APPLICANT: Leong, Steven R.
: APPLICANT: presta, Leonard G.
: TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
: TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
: NUMBER OF SEQUENCES: 72
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/026,985
: FILING DATE: 20-Feb-1998
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Love, Richard B.
: REGISTRATION NUMBER: 34,659
: REFERENCE/DOCKET NUMBER: P1085R3-1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-5530
: TELEFAX: 650/953-9881
: INFORMATION FOR SEQ ID NO: 71:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 452 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
:
: US-09-026-985-71

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[illegible]

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|||||
Db 421 RMOQGVNFSVCWHEALHNHYTKRSLSPGR 452
|||||
RESULT 6
US-09-485-737B-67
; Sequence 67, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buysse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEA
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-67

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Query Match	86.5%	Score 2177;	DB 4;	Length 468;
Best Local Similarity	88.2%;	Pred. No. 3.6e-154;		
Matches 410;	Conservative 20;	Mismatches 31;	Indels 4;	Gaps 1;

Qy	6	IILFLVATATGVHSQVOLVOSGAEVKKPGASVKASGYFTSTWMDQWVQKAPQCGLE	55
Db	7	IFSFLISASVILSQVOLVOSGSELKKPGASVKISCKASGYFTDYGMDWVQKAPQCGLK	66
Qy	66	WMGEIDPSDSYTNQKFKGKATLVDTSTSTAYMELSLRGEDTAVYYCARNRDYSNMW	125
Db	67	WMGWINTYGESYVDFGRFVPSLDTSVSAAYLQISLKAEDTATYFCARRGFVA---	123
Qy	126	YFDWGGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVLDKDPPEPVTVSNWSGA	185
Db	124	-MDYWGQGTITVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVLDKDPPEPVTVSNWSGA	182
Qy	186	LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTTICNVNHKPSNTKVDKRVEPKSCDK	245
Db	183	LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTTICNVNHKPSNTKVDKRVEPKSCDK	242
Qy	246	THTCPCCPAPELLGGPSVFLFPKPKDPTLMISRTPEVTWVDVSHEDPEVKFNWYVDGV	305
Db	243	THTCPCCPAPELLGGPSVFLFPKPKDPTLMISRTPEVTWVDVSHEDPEVKFNWYVDGV	302
Qy	306	EVINAKTKPREEQYNSTYRVVSVLTVLHDWNLNGKEYCKVSKNALPAPLTIKSKAKGO	365
Db	303	EVINAKTKPREEQYNSTYRVVSVLTVLHDWNLNGKEYCKVSKNALPAPLTIKSKAKGO	362
Qy	366	PREPQVYTLTPPSREMTKQVSLTCLVKGFGYPSDIAVEMESNGQPENNYKTTTPVLVDSOG	425
Db	363	PREPQVYTLTPPSREMTKQVSLTCLVKGFGYPSDIAVEMESNGQPENNYKTTTPVLVDSOG	422
Qy	426	SFELYSKLTVDKSRWQOGNVFSCVMHEALHNHYTOKSLSLSPGK	470
Db	423	SFELYSKLTVDKSRWQOGNVFSCVMHEALHNHYTOKSLSLSPGK	467

RESULT 7  
US-09-485-737B-90  
: Sequence 90, Application US/09485737B

; Patent No. 6350860  
; GENERAL INFORMATION:  
; APPLICANT: Buysse, Marie-Ange  
; APPLICANT: Sablon, Erwin  
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,  
; FILE REFERENCE: INNS:015  
; CURRENT APPLICATION NUMBER: US/09/485,737B  
; CURRENT FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165  
; PRIOR FILING DATE: 1998-08-14  
; PRIOR APPLICATION NUMBER: EPO 98870139.7  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: EPO 97870122.5  
; PRIOR FILING DATE: 1997-08-18  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 90  
; LENGTH: 711  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC  
US-09-485-737B-90

Query Match 86.5%; Score 2177; DB 4; Length 711;  
Best Local Similarity 88.2%; Pred. No. 6.3e-154;  
Matches 410; Conservative 20; Mismatches 31; Indels 4; Gaps 1;

QY 6 IILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMQWVQKQAPGGGLE 65  
DB 7 IFGLLSASVILSQVQLVQSGSELKPKGASVKISCKASGYTFTDYGMNVVQKQAPGGGLK 66  
QY 66 WMGEIDPSDYTNVQKFKGKATLTVDSTSTAYMELSSRLSEDTAVYICARNRDYSNNW 125  
DB 67 WMGWINYTCESYVDDFKGRFVSLDTSVAAYLQISSLKAEDTATYFCARRGFYA-- 123  
QY 126 YFDVWGOGTLTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWSGA 185  
DB 124 -MDYWGOGTLTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWSGA 182  
QY 186 LTSVHTFPVAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVPEPKCDK 245  
DB 183 LTSVHTFPVAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVPEPKCDK 242  
QY 246 THTCPPCAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 305  
DB 243 THTCPPCAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 302  
QY 306 EVINAKTKPREQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKISKAKGQ 365  
DB 303 EVINAKTKPREQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKISKAKGQ 362  
QY 366 PREQVYTLPPSREEMTKNQVSLTCLVKGYGPPSDIAVWESNGQPENNYKTPPVLDSDG 425  
DB 363 PREQVYTLPPSREEMTKNQVSLTCLVKGYGPPSDIAVWESNGQPENNYKTPPVLDSDG 422  
QY 426 SFFLYSKLTVDKSRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 470  
DB 423 SFFLYSKLTVDKSRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 467

## RESULT 8

US-07-934-373C-22

; Sequence 22, Application US/07934373C

; Patent No. 5821337

; GENERAL INFORMATION:

; APPLICANT: Paul J. Carter

; APPLICANT: Leonard G. Presta

; TITLE OF INVENTION: Immunoglobulin Variants

; NUMBER OF SEQUENCES: 48

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA: US/07/934,373C  
; FILING DATE: 21-Aug-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05126  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/715272  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0709P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 454 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-07-934-373C-22

Query Match 85.9%; Score 2161.5; DB 2; Length 454;  
Best Local Similarity 89.4%; Pred. No. 4.9e-153;  
Matches 406; Conservative 17; Mismatches 28; Indels 3; Gaps 1;

QY 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMQWVQKQAPGQGLEWMGEIDPSDSYTN 79  
DB 1 QVQLQSGPELVKPGASVKISCKTSGYFTFTYTHMVKQSHGKSLWIGGPNKNGSSH 60  
QY 80 NQKPKGKATLTVDSTSTAYMELSSRLSEDTAVYICARNRDYSNNW---YFDVWGOGTLV 136  
DB 61 NQKPKGKATLTVDSTSTAYMELSSRLSEDTSGIYICARWGLNYGFDVRYFDVWGAGTV 120  
QY 137 TVSSASTKGPSVFLPAPSSKSTSGTAALGCLVKDYFPEPTVTVSNWSGALTSGVHTTTPAV 196  
DB 121 TVSSASTKGPSVFLPAPSSKSTSGTAALGCLVKDYFPEPTVTVSNWSGALTSGVHTTTPAV 180  
QY 197 LQSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVPEKSCDKTHTCPCPAPE 256  
DB 181 LQSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVPEKSCDKTHTCPCPAPE 240  
QY 257 LLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPRE 316  
DB 241 LLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAAKTKPRE 300  
QY 317 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKISKAKQPREPQVYTLPP 376  
DB 301 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKISKAKQPREPQVYTLPP 360  
QY 377 SREEMTKNQVSLTCLVKGYGPPSDIAVWESNGQPENNYKTPPVLDSDGSFSLSKLTVD 436  
DB 361 SREEMTKNQVSLTCLVKGYGPPSDIAVWESNGQPENNYKTPPVLDSDGSFSLSKLTVD 420  
QY 437 KSRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 470  
DB 421 KSRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 454

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RESULT 9
US-08-437-642B-22
; Sequence 22, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-22

Query Match 85.9%; Score 2161.5; DB 3; Length 454;
Best Local Similarity 89.4%; Pred. No. 4.9e-153;
Matches 406; Conservative 17; Mismatches 28; Indels 3; Gaps 1;

QY 20 QVLQVQSGAEVKKPGASVKVSCKASQVFTSYMMQWVKQAPQGGLFWMGEIDPDSYTN 79
Db 1 QVLQVQSGPELVKPGASVKISCKTSSYFTTEYTHMMKQSHGKSLGWGFPNKGSSH 60
QY 80 NQKFKGKATLTVDSTSTAYMELSLRSEDATVYYCARNRDYSNNW---YFDVWGQGLTV 136
Db 61 NQRFMDKATLAVDKSTSTAYMELSLRSEDGIYYCARWRLNGYDFVRYFDVWGAGTV 120
QY 137 TVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 196
Db 121 TVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 180
QY 197 LQSSGLYSLSSVTVTPSSSLGQTICNVNHRKPSNTKVDKVEPKSCDKTHTCPPCPAPE 256
Db 181 LQSSGLYSLSSVTVTPSSSLGQTICNVNHRKPSNTKVDKVEPKSCDKTHTCPPCPAPE 240
QY 257 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 316

Db 241 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 300
QY 317 EQYNSTYRVVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 376
Db 301 EQYNSTYRVVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 360
QY 377 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSGFFLYSKLTVD 436
Db 361 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSGFFLYSKLTVD 420
QY 437 KSRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 470
Db 421 KSRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 454

RESULT 10
PCT-US93-07832-22
; Sequence 22, Application PC/TUS9307832
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07832
; FILING DATE: 19930820
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 709P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX: 415/952-9881
; TELE: 910/371-7168
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US93-07832-22

Query Match 85.9%; Score 2161.5; DB 5; Length 454;
Best Local Similarity 89.4%; Pred. No. 4.9e-153;
Matches 406; Conservative 17; Mismatches 28; Indels 3; Gaps 1;

QY 20 QVLQVQSGAEVKKPGASVKVSCKASQVFTSYMMQWVKQAPQGGLFWMGEIDPDSYTN 79
Db 1 QVLQVQSGPELVKPGASVKISCKTSSYFTTEYTHMMKQSHGKSLGWGFPNKGSSH 60
QY 80 NQKFKGKATLTVDSTSTAYMELSLRSEDATVYYCARNRDYSNNW---YFDVWGQGLTV 136
QY 80 NQKFKGKATLTVDSTSTAYMELSLRSEDATVYYCARNRDYSNNW---YFDVWGQGLTV 136
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Db 61 NORFMDKATLAVDKSTSTAYMELSLTSEDGIIYCARWGLNYGFDVRYFDVWGAGTV 120  
Qy 137 TVSSASTKGPVFPPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSNWNGALTSVGHVTFPAV 196  
Db 121 TVSSASTKGPVFPPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSNWNGALTSVGHVTFPAV 180  
Qy 197 LQSSGLYSLSSVTVVPSSSLGTQYICNVNHPKSNKTKVDRKVPKSCDKTHTCPCPAPPE 256  
Db 181 LQSSGLYSLSSVTVVPSSSLGTQYICNVNHPKSNKTKVDRKVPKSCDKTHTCPCPAPPE 240  
Qy 257 LLGSPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 316  
Db 241 LLGSPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPRE 300  
Qy 317 EYNSTYRVVSVLTVLHODWLNKREYKCKVSNKALPAPIETKISKAKQPREPQVYTLPP 376  
Db 301 EYNSTYRVVSVLTVLHODWLNKREYKCKVSNKALPAPIETKISKAKQPREPQVYTLPP 360  
Qy 377 SREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTV 436  
Db 361 SREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTV 420  
Qy 437 KSRWQGNVFCSCVMHEALHNYTKQSLSPGK 470  
Db 421 KSRWQGNVFCSCVMHEALHNYTKQSLSPGK 454

RESULT 11  
US-08-793-450-8  
; Sequence 8, Application US/08793450  
; Patent No. 6312690  
; GENERAL INFORMATION:  
; APPLICANT: EDELMAN, LENA  
; APPLICANT: MARGARITTE, CHRISTEL  
; APPLICANT: KACZOREK, MICHEL  
; APPLICANT: CHABRIHL, HASSAN  
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/793,450  
; FILING DATE: 03-MAR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94/10566  
; FILING DATE: 02-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 472 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-793-450-8

Query Match 85.2%; Score 2144; DB 4; Length 472;  
Best Local Similarity 84.8%; Pred. No. 1e-151;  
Matches 403; Conservative 27; Mismatches 37; Indels 8; Gaps 3;  
Qy 1 MGWSCIILFLVATATGVHSGVQVLOVSGABVKKPGASVKVSKASGYTFYTSYWMQWQKAP 60  
Db 1 MGWSCIILFLVATATGVHSGVQVLOVSGABVKKPGASVKVSKASGYTFYTSYWMQWQKAP 60  
Qy 61 GCGLEWMEIDPSDSYTNKQFKGKATLTVDTSSTAYMELSSLRSEDTAVTYCARND 120  
Db 61 GCGLEWMEIDPSDSYTNKQFKGKATLTVDTSSTAYMELSSLRSEDTAVTYCARND 119  
Qy 121 YSNWNV----YFDVWQGTTLTVSSASTKGPVFPPLAPSSKSTSGTAAALGCLVKDYFPE 175  
Db 120 Y--KKYHCDWDFPWCQGTTVTVSSASTKGPVFPPLAPSSKSTSGTAAALGCLVKDYFPE 177  
Qy 176 PVTVSNWNGALTSVGHVTFPAVLQSSGLYSLSSVTVVPSSSLGTQYICNVNHPKSNKTKVD 235  
Db 178 PVTVSNWNGALTSVGHVTFPAVLQSSGLYSLSSVTVVPSSSLGTQYICNVNHPKSNKTKVD 237  
Qy 236 KVEPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE 295  
Db 238 KAEPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE 297  
Qy 296 VKFNMYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHODWLNKREYKCKVSNKALPAPI 355  
Db 298 VKFNMYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHODWLNKREYKCKVSNKALPAPI 357  
Qy 356 EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 415  
Db 358 EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 417  
Qy 416 TTPPVLDSDGSGFFLYSKLTVDRKSRWQGNVFCSCVMHEALHNYTKQSLSPGK 470  
Db 418 TTPPVLDSDGSGFFLYSKLTVDRKSRWQGNVFCSCVMHEALHNYTKQSLSPGK 472

RESULT 12  
US-08-887-352B-14  
; Sequence 14, Application US/08887352B  
; Patent No. 5994511  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,352B  
; FILING DATE: 03-Jul-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P1123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 14:



; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39, 044
; REFERENCE/DOCKET NUMBER: P0718P2CID1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-65

Query Match 84.4%; Score 2124; DB 3; Length 451;
Best Local Similarity 87.6%; Pred. No. 3e-150;
Matches 396; Conservative 24; Mismatches 30; Indels 2; Gaps 2;

Qy 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YVMQWVKQAPGQGLEWMGEIDPDSVTN 78
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYISITSGYSNNWIRQAPGKLEWVASI-TYDGSIN 59
Qy 79 YNQKFKGKATLTVDSTSTAYMELSSLRSEDTAVYYCARNRDYSNWYFDVWGQGLTVTV 138
Db 60 YNPSVKGRITISRDSDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHEFAVWGQGLTVTV 119
Qy 139 SSASTKGPSVPFLAPSSKSTSGGTAALGCLVKDYKPEPTVSWNSGALTSGVHTFPAVLQ 198
Db 120 SSASTKGPSVPFLAPSSKSTSGGTAALGCLVKDYKPEPTVSWNSGALTSGVHTFPAVLQ 179
Qy 199 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKRVKPKSCDKTHTCPPCPAPELL 258
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKRVKPKSCDKTHTCPPCPAPELL 239
Qy 259 GGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 318
Db 240 GGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299
Qy 319 YNSTYRVVSVLTVLDHQLWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
Db 300 YNSTYRVVSVLTVLDHQLWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359
Qy 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 438
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 419
Qy 439 RWQOGNVFSCSVMHHEALHNHYTQKSLSLSPGK 470
Db 420 RWQOGNVFSCSVMHHEALHNHYTQKSLSLSPGK 451

RESULT 15
US-09-109-207C-14
; Sequence 14, Application us/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide

; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-14

Query Match 84.4%; Score 2124; DB 4; Length 451;
Best Local Similarity 87.6%; Pred. No. 3e-150;
Matches 396; Conservative 24; Mismatches 30; Indels 2; Gaps 2;

Qy 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YVMQWVKQAPGQGLEWMGEIDPDSVTN 78
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYISITSGYSNNWIRQAPGKLEWVASI-TYDGSIN 59
Qy 79 YNQKFKGKATLTVDSTSTAYMELSSLRSEDTAVYYCARNRDYSNWYFDVWGQGLTVTV 138
Db 60 YNPSVKGRITISRDSDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHEFAVWGQGLTVTV 119
Qy 139 SSASTKGPSVPFLAPSSKSTSGGTAALGCLVKDYKPEPTVSWNSGALTSGVHTFPAVLQ 198
Db 120 SSASTKGPSVPFLAPSSKSTSGGTAALGCLVKDYKPEPTVSWNSGALTSGVHTFPAVLQ 179
Qy 199 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKRVKPKSCDKTHTCPPCPAPELL 258
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKRVKPKSCDKTHTCPPCPAPELL 239
Qy 259 GGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 318
Db 240 GGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299
Qy 319 YNSTYRVVSVLTVLDHQLWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
Db 300 YNSTYRVVSVLTVLDHQLWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359
Qy 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 438
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 419
Qy 439 RWQOGNVFSCSVMHHEALHNHYTQKSLSLSPGK 470
Db 420 RWQOGNVFSCSVMHHEALHNHYTQKSLSLSPGK 451

Search completed: August 14, 2002, 15:17:05
Job time: 688 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:18:59 ; Search time 108.64 Seconds  
(without alignments)  
415.703 Million cell updates/sec

Title: US-09-499-662-143

Perfect score: 2517

Sequence: 1 MGWSCIILFLVATATGVHSQ.....MHEALHNHYTKSLSLSPGK 470

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1758	69.8	330	1 GHU	Ig gamma-1 chain C
2	1639.5	65.1	377	2 A23511	Ig gamma-3 chain C
3	1637.5	65.1	377	2 A60764	Ig gamma-3 chain C
4	1613.5	64.1	469	2 S37483	Ig gamma-2a chain
5	1610	64.0	326	1 G2HU	Ig gamma-2 chain C
6	1599.5	63.5	327	1 G4HU	Ig gamma-4 chain C
7	1549	61.5	474	1 G2MS11	Ig gamma-2b chain
8	1547	61.5	446	2 S40295	Ig gamma-2a chain
9	1504.5	59.8	475	2 S01321	Ig gamma-2b chain
10	1474	58.6	470	2 S22080	Ig heavy chain pre
11	1467	58.3	472	2 S31459	Ig gamma-1 chain -
12	1432	56.9	374	2 S69339	Ig heavy chain v r
13	1426.5	56.7	444	2 PC4436	monoclonal antibod
14	1267	50.3	328	2 I47159	Ig gamma 2a chain
15	1261	50.1	328	2 I47160	Ig gamma 2b chain
16	1253	49.8	255	4 S31866	Ig gamma-1 chain C
17	1245	49.5	234	2 PT0207	Ig gamma chain C r
18	1235	49.1	328	2 I47158	Ig gamma 1 chain c
19	1231.5	48.9	323	1 GHRB	Ig gamma chain C r
20	1231	48.9	328	2 I47161	Ig gamma 3 chain c
21	1210.5	48.1	329	1 G2GP	Ig gamma-2 chain C
22	1165.5	46.3	308	2 C30554	Ig heavy chain C r
23	1157	46.0	289	1 G3HWU	Ig gamma-3 heavy c
24	1155	45.9	326	2 PS0017	Ig gamma-1 chain C
25	1150	45.7	329	1 G3MSC	Ig gamma-3 chain C
26	1145	45.5	324	1 G1MS	Ig gamma-1 chain C
27	1144.5	45.5	333	2 PS0018	Ig gamma-2b chain C
28	1140	45.3	393	1 G1MSM	Ig gamma-1 chain C
29	1139	45.3	398	1 G3MSM	Ig gamma-3 chain C

Ig gamma-2a chain  
Ig gamma-2c chain  
Ig gamma-2a chain  
Ig gamma-2a chain  
Ig gamma-2a chain  
Ig gamma-2 chain C  
Ig gamma-2b chain  
Ig gamma 4 chain c  
Ig epsilon chain C  
Ig mu chain precu  
Ig heavy chain pre  
Ig heavy chain (DO  
Ig gamma chain - m  
Ig gamma-1 heavy c  
Ig heavy chain VHI  
Ig Y heavy chain (

#### ALIGNMENTS

RESULT 1

GHU

Ig gamma-1 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 31-Jan-1981 #sequence\_revision 18-Aug-1982 #text\_change 16-Jul-1999  
C;Accession: A93433; S33887; B90563; A90564; B91668; A91723; A02146

R;Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A;Reference number: A93433; MUID:82274238

A;Accession: A93433

A;Molecule type: DNA

A;Residues: 1-330 <ELL>

A;Cross-references: EMBL:Z17370

A;Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) marker

A;Note: Lys-330 is removed after translation

R;Harris, L.J.

submitted to the EMBL Data Library, October 1992

A;Reference number: S33904

A;Accession: S36861

A;Molecule type: DNA

A;Residues: 2-330 <HAR>

A;Cross-references: EMBL:Z17370

R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A;Title: Structure of human immunoglobulin gamma genes: Implications for evolution of

A;Reference number: S33887; MUID:83001943

A;Accession: S33887

A;Molecule type: DNA

A;Residues: 88-113;235-330 <TAK>

A;Cross-references: EMBL:Z17370

R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman

Biochemistry 9, 3161-3170, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq

A;Reference number: A90563; MUID:71064024

A;Contents: myeloma protein Eu

A;Accession: B90563

A;Molecule type: protein

A;Residues: 1-96,'R',98-135 <CUN>

A;Note: this sequence has the G1m(3) marker, 97-Arg

R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se

A;Reference number: A90564; MUID:71064025

A;Contents: Eu

A;Accession: A90564

A;Molecule type: protein

A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',2

A;Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met

R;Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein NI

igen Primaerstruktur.  
A:Reference number: A91668; MUID:77070269  
A:Contents: myeloma protein Nie  
A:Accession: B91668  
A:Molecule type: protein  
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27  
A>Note: this sequence has the GIm(17) and GIm(1) markers  
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
A:Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL  
A:Reference number: A91723; MUID:83289131  
A:Contents: myeloma protein KOL; disulfide bonds  
A:Accession: A91723  
A:Molecule type: protein  
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH  
A>Note: this sequence has the GIm(3) and GIm(non-1) markers  
R:Call, W.E.; Edelman, G.M. 1970  
Biochemistry 9, 3188-3196, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid  
A:Reference number: A90565; MUID:71064027  
A:Contents: annotation; disulfide bonds  
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976  
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob  
endronide cleavage products, and the disulfide bridges.  
A:Reference number: A91667; MUID:77070267  
A:Contents: annotation; disulfide bonds  
C:Genetics:  
A:Gene: GDB:IGHG1  
A:Cross-references: GDB:120085; OMIM:147100  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1; 114/1; 224/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:137-206/Domain: immunoglobulin homology <IM2>  
F:243-310/Domain: immunoglobulin homology <IM3>  
F:27-93,144-204,250-308/Disulfide bonds: #status experimental  
F:103/Disulfide bonds: interchain (to light chain) #status experimental  
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 69.8%; Score 1758; DB 1; Length 330;  
Best Local Similarity 99.1%; Pred. No. 3 6e-93;  
Matches 327; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200  
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

QY 201 GLYSLSSVTVPSSSLGTTQYICNVNHKPSNTKVDKRVKDPKSCDKTHTCPPCPAPPELLGG 260  
Db 61 GLYSLSSVTVPSSSLGTTQYICNVNHKPSNTKVDKRVKDPKSCDKTHTCPPCPAPPELLGG 120

QY 261 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN 320  
Db 121 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN 180

QY 321 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRREE 380  
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

QY 381 MTKNQVSLTCLVKGFVPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 440  
Db 241 LTRNQVSLTCLVKGFVPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300

QY 441 QGQNVFSCSVMHAEALHNHYTQKSLSLSPGK 470  
Db 301 QGQNVFSCSVMHAEALHNHYTQKSLSLSPGK 330

RESULT 2  
A23511  
Ig gamma-3 chain C region (allotype G3m(b)) - human  
C:Species: Homo sapiens (man)  
C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 23-Jul-1999  
C:Accession: A23511  
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.  
Nucleic Acids Res. 14, 1779-1789, 1986  
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene.  
A:Reference number: A23511; MUID:86148507  
A:Accession: A23511  
A:Molecule type: DNA  
A:Residues: 1-377 <HUC>  
A:Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056  
C:Genetics:  
A:Gene: GDB:IGHG3  
A:Cross-references: GDB:119339; OMIM:147120  
A:Map position: 14q32.33-14q32.33  
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 65.1%; Score 1639.5; DB 2; Length 377;  
Best Local Similarity 82.8%; Pred. No. 2 3e-86;  
Matches 312; Conservative 7; Mismatches 11; Indels 47; Gaps 1;

QY 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200  
Db 1 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

QY 201 GLYSLSSVTVPSSSLGTTQYICNVNHKPSNTKVDKRV----- 238  
Db 61 GLYSLSSVTVPSSSLGTTQYICNVNHKPSNTKVDKRVKELKTPLOGTTHTCPCRPKPKSC 120

QY 239 -----EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKPKDT 273  
Db 121 DTPPC 180

QY 274 LMSRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVHL 333  
Db 181 LMSRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVHL 240

QY 334 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVK 393  
Db 241 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVK 300

QY 394 GFYPDSIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNFSCSVMH 453  
Db 301 GFYPDSIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNFSCSVMH 360

QY 454 ALHNHYTQKSLSLSPGK 470  
Db 361 ALHNHYTQKSLSLSPGK 377

RESULT 3  
A60764  
Ig gamma-3 chain C region, form LAT - human  
C:Species: Homo sapiens (man)  
C:Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 16-Jul-1999  
C:Accession: A60764  
R:Huck, S.; Lefranc, G.; Lefranc, M.P.  
Immunogenetics 30, 250-257, 1989  
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 conv  
A:Reference number: A60764; MUID:90007613  
A:Accession: A60764  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-377 <HUC>  
C:Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: immunoglobulin

F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 65.1%; Score 1637.5; DB 2; Length 377;  
Best Local Similarity 82.8%; Pred. No. 3e-86;  
Matches 312; Conservative 7; Mismatches 11; Indels 47; Gaps 1;

QY 141 ASTKGPSVFFPLAPSCKSTSGTAAALGCLVKDYFPEPVTVSNWNSGALTSVHTFPAVLQSS 200

Db 1 ASTKGPSVFFPLAPCSRSTSGTAAALGCLVKDYFPEPVTVSNWNSGALTSVHTFPAVLQSS 60

QY 201 GLXLSVVTVVSSSLGTQYICVNNHKPSNTKVKRV----- 238

Db 61 GLXLSVVTVVSSSLGTQYICVNNHKPSNTKVKRV----- 120

QY 239 -----EPKSCDKTHTCPCPAPELGGPSVFLFPKPKDT 273

Db 121 DTPPPCRCPKSCDTPPCPRCPKSCDTPPCPRCPAPELGGPSVFLFPKPKDT 180

QY 274 LMISRTPEVTCVVVDVSHEDPEVKFNRYVDGVEVHNAKTPREPOYNSTYRVVSVLTVLH 333

Db 181 LMISRTPEVTCVVVDVSHEDPEVQFKYVDGVEVHNAKTPREPOYNSTYRVVSVLTVLH 240

QY 334 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSREEMTKNQVSLTCLVK 393

Db 241 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSREEMTKNQVSLTCLVK 300

QY 394 GFYPESDIAREWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVWHE 453

Db 301 GFYPESDIAREWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVWHE 360

QY 454 ALHNHYTQKSLSLSPGK 470

Db 361 ALHNHYTQKSLSLSPGK 377

RESULT 4

S37483

Ig gamma-2a chain - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999

C;Accession: S37483

R;Ducancel, F.F.D.

submitted to the EMBL Data Library, February 1993

A;Reference number: S37483

A;Accession: S37483

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-469 <DUC>

A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: immunoglobulin

F;276-345/Domain: immunoglobulin homology <IMM>

Query Match 64.1%; Score 1613.5; DB 2; Length 469;  
Best Local Similarity 64.6%; Pred. No. 9e-85;  
Matches 305; Conservative 59; Mismatches 103; Indels 5; Gaps 4;

QY 1 MGWSCIIFLVATATGVHSGVOLVQSGAEVKKPGASVKVCKASGYFTTSYMMQWVKQAP 60

Db 1 MGWSWIFLLISGTAGVHCQIQLOQSGPELVKPGASVKISCKASGYFTTDYIYNKQKP 60

QY 61 GQGLEWGEIDPSDYSYNYNOKFKGKATLVDTSTAYMELSLRSDTAVYYCARNRD 120

Db 61 GQGLUKWIGWIYPASGNTRYENEFKGAATLVDTSSSTAYMQLSLTSDTAVYFCARAMG 120

QY 121 YSNWNYDVGWQGLTVTVSSASTKGPSVFLPASPCKSTSGTAAALGCLVKDYFPEPVTVS 180

Db 121 -ATATLDYWGQGTTLTVSSAKTAPSVYPLAPVCGDGTSSVTLGCLVKGYFPEPVTLT 179

QY 181 WNSGALTSVGHVTFPAVLQSSGLXSLSSVTVVPSSSLGTQTYICVNNHKPSNTKVKDRVPE 240

Db 180 WNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEP 238

QY 241 KSCDKTHTCPD--CPAPELGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298

Db 239 RG-PTIKPCPPCKCPAPNLGGPSVFIFPPAKIKDVLMLSLSPIVTCVVVDVSEDDPDVQI 297

QY 299 NWYVDGVEVHNAKTPREEOYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 358

Db 298 SWEVNNVEVHTAQOTHQREDYNSLTRVVVSALPIQHDWMSGKEFKCKVNNKDLPAPIERT 357

QY 359 ISKAKGQPREPOVYITLPPSREEMTKNQVSLTCLVKGYFPSDIAVEWESNGQPENNYKTP 418

Db 358 ISKPKGSRAPQVYVLPPEEETKKQVTLTCMTDFMPEDYVVEWTNNGTSLNKNTE 417

QY 419 PVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVWHEALHNHYTQKSLSLSPGK 470

Db 418 PVLDSGDSFYMYSKLRVEKKWVERNSYSCSVVHEGLNHHHTKSFSTPCK 469

RESULT 5

G2HU

Ig gamma-2 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 30-Apr-1981 #sequence\_revision 13-Jun-1983 #text\_change 21-Jul-2000

C;Accession: A93906; A92809; A90752; A93132; A02148

R;Ellison, J.; Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982

A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain

A;Reference number: A93906; MUID:82197621

A;Accession: A93906

A;Molecule type: DNA

A;Residues: 1-326 <ELL>

A;Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056

A;Note: Lys-326 is probably removed posttranslationally

R;Wang, A.C.; Tung, E.; Fudenberg, H.H.

J. Immunol. 125, 1048-1054, 1980

A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, an

A;Reference number: A92809; MUID:81007873

A;Contents: myeloma protein Til

A;Accession: A92809

A;Molecule type: protein

A;Residues: 1-19, Q',21-57, Z',59, A',61-193, D',195-325 <WAN>

A;Note: Trp-156 is at or near the complement-binding site

R;Connell, G.E.; Parr, D.M.; Hofmann, T.

Can. J. Biochem. 57, 758-767, 1979

A;Title: The amino acid sequences of the three heavy chain constant region domains of

A;Reference number: A90752; MUID:80001357

A;Contents: myeloma protein Zie

A;Accession: A90752

A;Molecule type: protein

A;Residues: 1-24, E',26-57, EV',60-85;132-171, ZZZ',175, B',177-193, D',195-196, Q',L

A;Note: this sequence has since been revised

R;Hofmann, T.; Parr, D.M.

Mol. Immunol. 16, 923-925, 1979

A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobul-

A;Reference number: A93132; MUID:80114419

A;Contents: Zie

A;Accession: A93132

A;Molecule type: protein

A;Residues: 238-275 <HOF>

R;Hofmann, T.; Parr, D.M.

submitted to the Atlas, March 1980

A;Reference number: A94591

A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268

A;Note: the revised sequence differs from that shown in having 60-Ala and in the amid

ned

R;Milstein, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.

A;Reference number: A90253; MUID:72033500

A;Contents: annotation; myeloma protein Sa, disulfide bonds

R;Frangione, B.; Milstein, C.; Pink, J.R.L.

Nature 221, 145-148, 1969  
A:Title: Structural studies of immunoglobulin G.  
A:Reference number: A93157; MUID:69064124  
A:Contents: annotation; Sa, disulfide bonds  
C:Genetics:  
A:Gene: IGHG2

A:Cross-references: GDB:119338; OMIM:147110  
A:Map position: 14q32.33-14q32.33  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 18

C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:133-202/Domain: immunoglobulin homology <IM1>  
F:133-202/Domain: immunoglobulin homology <IM2>  
F:239-306/Domain: immunoglobulin homology <IM3>

F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83,140-200,246-304/Disulfide bonds: #status experimental  
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 64.0%; Score 1610; DB 1; Length 326;  
Best Local Similarity 91.8%; Pred. No. 9.4e-85;  
Matches 303; Conservative 10; Mismatches 13; Indels 4; Gaps 2;

QY 141 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPVAVLQSS 200  
Db 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPVAVLQSS 60

QY 201 GLYSLSVVTVPSVSSSLGTQTYICNVNHPKNTKVDKRRVEPKSCDKTHTCPPCPAPPELLGG 260  
Db 61 GLYSLSVVTVPSVSSSLGTQTYICNVNHPKNTKVDKRRVEPKSCDKTHTCPPCPAPPELLGG 260

QY 261 PSVLEFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320  
Db 117 PSVLEFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 176

QY 321 STYRVVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTTISKAKGQPREPQVYTLPPSREE 380  
Db 177 STYRVVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTTISKAKGQPREPQVYTLPPSREE 236

QY 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 440  
Db 237 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 296

QY 441 QGQNFVSCVMHEALHNHYTQKSLSLSPGK 470  
Db 297 QGQNFVSCVMHEALHNHYTQKSLSLSPGK 326

RESULT 6  
G4HU

Ig gamma-4 chain C region - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 16-Jul-1999  
C:Accession: A90933; A90249; A02150

R:Ellison, J.; Buxbaum, J.; Hood, L.  
DNA 1, 11-18, 1981

A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.  
A:Reference number: A90933; MUID:83157104  
A:Accession: A90933

A:Molecule type: DNA  
A:Residues: 1-327 <ELL>  
A:Note: the sequence was determined from the germline gene

R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.  
Biochem. J. 117, 33-47, 1970

A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant  
A:Reference number: A90249; MUID:70207560  
A:Accession: A90249

A:Molecule type: protein  
A:Residues: 1-30;81-326 <PIN>  
C:Genetics:  
A:Gene: IGHG4

A:Cross-references: GDB:119340; OMIM:147130  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1; 111/1; 221/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 18

C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:133-202/Domain: immunoglobulin homology <IM1>  
F:133-202/Domain: immunoglobulin homology <IM2>  
F:239-306/Domain: immunoglobulin homology <IM3>

F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83,140-200,246-304/Disulfide bonds: #status experimental  
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 63.5%; Score 1599.5; DB 1; Length 327;  
Best Local Similarity 91.8%; Pred. No. 3.7e-84;  
Matches 303; Conservative 9; Mismatches 15; Indels 3; Gaps 1;

QY 141 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPVAVLQSS 200  
Db 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPVAVLQSS 60

QY 201 GLYSLSVVTVPSVSSSLGTQTYICNVNHPKNTKVDKRRVEPKSCDKTHTCPPCPAPPELLGG 260  
Db 61 GLYSLSVVTVPSVSSSLGTQTYICNVNHPKNTKVDKRRVEPKSCDKTHTCPPCPAPPELLGG 117

QY 261 PSVLEFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320  
Db 118 PSVLEFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 177

QY 321 STYRVVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTTISKAKGQPREPQVYTLPPSREE 380  
Db 178 STYRVVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTTISKAKGQPREPQVYTLPPSREE 237

QY 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 440  
Db 238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 297

QY 441 QGQNFVSCVMHEALHNHYTQKSLSLSPGK 470  
Db 298 QGQNFVSCVMHEALHNHYTQKSLSLSPGK 327

RESULT 7  
G2WSLI

Ig gamma-2b chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Mar-1980 #sequence\_revision 01-Dec-2000 #text\_change 01-Dec-2000  
C:Accession: S25057; A02157; A26235; A26232; A26233; A53598

R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.  
submitted to the EMBL Data Library, July 1992

A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific  
A:Reference number: S25057  
A:Accession: S25057

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-474 <FIS>

A:Cross-references: EMBL:X67210; NID:G54826; PIDN:CAA47649.1; PID:G54827  
R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.  
Nature 283, 786-789, 1980

A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned fr  
A:Reference number: A02157; MUID:80120716  
A:Contents: a allele

A:Molecule type: DNA  
A:Residues: 138-161, 'L', 163-189, 'Fp', 193-474 <YAM>  
A:Cross-references: GB:J00461

A:Note: the sequence was determined from the germline gene  
R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.  
Science 206, 1299-1303, 1979



A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b heavy chain  
A:Reference number: A26235; MUID:80081501  
A:Contents: MPC 11  
A:Accession: A26235  
A:Molecule type: mRNA  
A:Residues: 138-172, 'P', 174-189, 'PP', 193-376, 'T', 378-474 <TU1>  
A:Note: Lys-474 is probably removed posttranslationally.  
R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.  
Science 206, 1303-1306, 1979  
A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglobulin heavy chain  
A:Reference number: A26232; MUID:80081502  
A:Accession: A26232  
A:Molecule type: DNA  
A:Residues: 138-172, 'P', 174-189, 'PP', 193-376, 'T', 378-474 <TU2>  
R:Ollo, R.; Rougeon, F.  
Nature 296, 761-763, 1982  
A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma2b heavy chain genes  
A:Reference number: A26233; MUID:82173203  
A:Contents: b allele  
A:Accession: A26233  
A:Molecule type: DNA  
A:Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLL>  
R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi, J.  
J. Biol. Chem. 269, 12345-12350, 1994  
A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.  
A:Reference number: A53598; MUID:94216359  
A:Accession: A53598  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 234-251 <IKM>  
C:Comment: The a allele sequence is shown.  
C:Genetics:  
A:Introns: 138/1; 236/1; 258/1; 368/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (lambda) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin  
F:157-222/Domain: immunoglobulin homology <IM1>  
F:236-257/Region: hinge  
F:281-350/Domain: immunoglobulin homology <IM2>  
F:387-454/Domain: immunoglobulin homology <IM3>  
F:152/Disulfide bonds: interchain (to light chain) #status predicted  
F:164-220,288-348,394-452/Disulfide bonds: #status predicted  
F:247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted  
F:324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 61.58; Score 1549; DB 1; Length 474;  
Best Local Similarity 61.4%; Pred. No. 4.2e-81;  
Matches 293; Conservative 66; Mismatches 108; Indels 10; Gaps 3;

Qy 1 MGWSCILFLVATATGVSQVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKAP 60  
Db 1 MENSWIFLLGAGVHSEVQLQSGPELVNPGASVKMSCKASGYTFTSYMMHWKRP 60  
Qy 61 GQLEWMGIDPSYTNYNKFKGKAPLTVDTSSTAYMELSSLRSEDTAVYVCARNR 120  
Db 61 GQLEWIGYINPNKDGKFKNEKFKGKATLTSDKSNATYMESSLTSDSAVYVCARDYD 120  
Qy 121 YSNWYFDVWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTV 180  
Db 121 YD---WFAYMGQGLTVTVSSAAKTTTPPSVYPLAPGCGDTGTSVTSGLVKGYFPESVT 177  
Qy 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSTKVDKRV 240  
Db 178 WNSGSLSSSVHTLSQALLQSGLYTMSSSVTVTPSSVTSQVTCVAHPASSTTVDDKLEP 237  
Qy 241 KSCDKT-HTCPK-----CPAPELLGSPVFLPPKPKDTLMISRTPEVTCVVDVSHED 293  
Db 238 SGPSTINCPCKECKPCAPNLEGSPVFIFFPNKIDVLMISLTLPKVTCTVVDVSEDD 297  
Qy 294 PEVKFNWYDGVGVHNAKTKPREQYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPA 353

Db 298 PDVQISWPNVNVVEVHTAQTHREDYNTIRVSVTLPIQHODWMSGKEFKCKVNNKDLPS 357  
Qy 354 PIETISKAGKOPPEQVYITLPPSREEMTKNOVSLTCLVKGYFSPDIAVWEESNQEPNN 413  
Db 358 PIETISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVGENPGDISVEWTSNGHTEEN 417  
Qy 414 YKTPPVLDSDGSFFLYSKLTVDKSRWQGNVFSVMHEALHNHYTKSLSPGK 470  
Db 418 YKDTAPVLDSDGSFYISKLNKTKWEKTSFSCNVRHGLKKNLYLTKTISRSPGK 474

## RESULT

8  
Ig gamma-2a chain (mAb735) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 16-Jul-1999  
C:Accession: S40295  
R:Kiebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.  
submitted to the EMBL Data Library, January 1993  
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 again  
A:Reference number: S40295  
A:Accession: S40295  
A:Molecule type: protein  
A:Residues: 1-446 <KLE>  
C:Genetics:  
A:Map position: 12  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglyutamic acid  
F:1-446/Product: Ig gamma-2a chain #status experimental <KAT>  
F:1-117/Domain: V-D-J region <VDJ>  
F:118-446/Domain: C region <CHR>  
F:118-214/Domain: C1 region <CH1>  
F:215-230/Region: hinge  
F:231-340/Domain: C2 region <CH2>  
F:341-446/Domain: C3 region <CH3>  
F:360-427/Domain: immunoglobulin homology <IM>  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted  
F:132/Disulfide bonds: interchain (to light chain) #status predicted  
F:224,227,229/Disulfide bonds: interchain #status predicted  
F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 61.58; Score 1547; DB 2; Length 446;  
Best Local Similarity 64.6%; Pred. No. 5.1e-81;  
Matches 292; Conservative 58; Mismatches 94; Indels 8; Gaps 4;

Qy 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKAPQGGLEWMGEIDPSD 79  
Db 1 QIQLQSGPELVNPGASVKISCKASGYTFTDYIHWKQRPGEGLWIGWYPSGNTKY 60  
Qy 80 NQKFKGKATLVDTSTSTAYMELSSLRSEDTAVYVCARNRDYNNWYFDVWGQGLTVTV 139  
Db 61 NEKFKGKATLVDTSTSTAYMQLSSLTSDSAVYFCARGGKFA---MDYWGQGSVTV 116  
Qy 140 SASYKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 199  
Db 117 SAKTAPSVYPLAPVCGDTGTSVTLGCLVKGYFPEPTVTLWNSGSLSSGVHTFPAVL 176  
Qy 200 SGLYSLSSVTVTPSSSLGTQTYICNVNHPKSTKVDKRVKPEKSCDKTHTCPP-CPAPEL 257  
Db 177 D-LVTLSSTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPKCKPAPNL 234  
Qy 258 LGGSPVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPRE 317  
Db 235 LGGSPVFIFFPKIKIDVLMISLSPVTCVVDVSEDDPDVQISWPNVNVVEVHTAQTH 294  
Qy 318 QYNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPTEKTSKAKGPREQVYTLPPS 377  
Db 295 DYNSTLRVVSALPPIQHODWMSGKEFKCKVNNKDLPAPIERTISKPGSVRAPQVY 354  
Qy 378 REEMTKNOVSLTCLVKGYFSPDIAVWEESNQEPNNYKTPPVLDSDGSFFLYSKLTV 437

Db. 355 EEEMTKQVLTCTKMTDFPDIYVEVNTNGKTELANTPEPVLDSGSGYFMYSLRVEK 414  
 QY 438 SRWQGVNFCVSMVHEALHNHYTKQSLSPG 469  
 Db 415 KNWERNISYCSVVHEGLNHHHTKSFSTRPG 446

RESULT 9  
 S01321  
 Ig gamma-2b chain precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 23-Jul-1999  
 C:Accession: S01321  
 R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.  
 Eur. J. Biochem. 176, 287-295, 1988  
 A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a  
 A:Reference number: S01320; MUID:88329081  
 A:Accession: S01321  
 A:Molecule type: mRNA  
 A:Residues: 1-475 <DEL>  
 A:Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781  
 A:Note: this sequence was determined from the differentiated gene  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>  
 F:159-223/Domain: immunoglobulin homology <IMM>

Query Match 59.8%; Score 1504.5; DB 2; Length 475;  
 Best Local Similarity 60.8%; Pred. No. 1.4e-78;  
 Matches 290; Conservative 65; Mismatches 113; Indels 9; Gaps 4;

QY 1 MGWSCIILFLVATATGVHSGVQLVQSGAEVKKPGASVKYSCKASGYTFTSYWQWVKQAP 60  
 Db 1 MEWIFLFLSTAGVQSGVQLVQSGAEVKKPGASVKYSCKASGYTFTSYWQWVKQRT 60  
 QY 61 GQLEWMGEIDPSDSTYNQKFKGKATLTVDSTSTAYMELSSLRSEDTAVYICARNRD 120  
 Db 61 GQLEWIGEITPGSGNSYFNEKFKGKATLTVDKSSSTAYVHLSSLTSEDSAVYFCAGPRQ 120  
 QY 121 YSNWTFDVMGQGLTLTVSSASTKGFSPFLAPSSKSTSGGTAALGCLVKDYKPEPTVTS 180  
 Db 121 V-GLLPFGVWGQGLTLTSAAKTTPPSVPLAPCGDITGSSVTGLCLVKGYEPTVTVT 179  
 QY 181 WNSGALTSGVHTPEPAVLQSSGLYSLSVTVPSSTLTQTYICNVNHNKPSNTKVDKRVPE 240  
 Db 180 WNSGSLSSSVHTPEPALQ-SGLTMSSTVTPSSVTPSPQVTCVSAHPASSTVTDKLEP 238  
 QY 241 KSCDKT-HTCPP-----CPAPELLGGPSVFLPPPKDITLMISRTPEVTCVVVDYSHED 293  
 Db 239 SGPTSTINPCCKECHKCAPNLEGPSVFIPPNIKDVLMSLTPEVTCVVVDYSEDD 298  
 QY 294 PEVKFMYVDGVVHNAKTPREQYNSTYRVVSVLTVLDHQLNGKEYCKVSNKALPA 353  
 Db 299 PDQISWFENNVNVELPAQTTHREDYNSTIRVVVSALPIQHDWMSGKEFKCKVNNKDLPA 358  
 QY 354 PIEKTIKAKGQPREQVYTPPPSREEMTKNQVSLTCLVKGYEPPSDIAVEWESNGOPENN 413  
 Db 359 PIERTISKIGIVRAQVILSPPPQLSKVDKSVLTCLAVGSPEDISVWTSNGHTEEN 418  
 QY 414 YKTPPVLDSGSGFFLYSKITVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 470  
 Db 419 YKDTAPVLDSGSGYFIYKLNKMTSKWETDSEFSCNVRHEGLKNYLYKKTISRSPGK 475

RESULT 10  
 S22080  
 Ig heavy chain precursor (B/WT.4A.17.H5.A5) - bovine  
 N:Alternate names: Ig gamma-1 chain C region (clone 8.10)  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999

C:Accession: S22080; S06610; A31303  
 R:Sanders, P.G.  
 submitted to the EMBL Data Library, November 1991  
 A:Reference number: S22080  
 A:Accession: S22080  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-470 <SAN>  
 A:Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440  
 Mol. Immunol. 26, 841-850, 1989  
 A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and g  
 A:Reference number: S06610; MUID:90097956  
 A:Accession: S06610  
 A:Molecule type: DNA  
 A:Residues: 142-470 <SYM>  
 A:Cross-references: EMBL:X16701  
 A:Note: the sequence was determined from the germline gene  
 C:Genetics:  
 A:Gene: Ig CH gamma-1  
 A:Introns: 98/1; 111/1; 221/1  
 A:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein  
 F:161-225/Domain: immunoglobulin homology <IMM>  
 F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 58.6%; Score 1474; DB 2; Length 470;  
 Best Local Similarity 60.2%; Pred. No. 7.8e-77;  
 Matches 284; Conservative 63; Mismatches 115; Indels 10; Gaps 7;

QY 3 WSCIILFLVATATGVHSGVQLVQSGAEVKKPGASVKYSCKASGYTFTSYWQWVKQAPGQ 62  
 Db 5 WT--LLFVLSPAPIGVLSQVQLRESGSLVKPSQTLSTCTVSGFSLSYALTWVRQAPGK 62  
 QY 63 GLEWMEIDPSDSTYNQKFKGKATLTVDSTSTAYMELSSLRSEDTAVYICARNR--D 120  
 Db 63 ALEWVGGI-TSGGTYTYPALKSRLSITKENSQSVLSVSVTPEDTATYICARSTYGE 121  
 QY 121 YSNWTFDVMGQGLTLTVSSASTKGFSPFLAPSSKSTSGGTAALGCLVKDYKPEPTVTS 180  
 Db 122 VGDGATADAGQGLTLTVSSASTAPKVPPLSCCGDKSSSTVTLGCLVSSYMEPTVTVT 181  
 QY 181 WNSGALTSGVHTPEPAVLQSSGLYSLSVTVPSSTLTQTYICNVNHNKPSNTKVDKRVPE 240  
 Db 182 WNSGALKSGVHTPEPAVLQSSGLYSLSMVTPGSTG-QTFTCNVAHPASSTKVDKRAVP 240  
 QY 241 KSCDKTHTCPPCPAPPELLGGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNW 300  
 Db 241 -TC-KPSPDCDCCPPPELPGGPSVFIPPPKDKTLTISGTPETVTCVVVDVGHDDPEVAFSW 298  
 QY 301 YVDGVVHNAKTPREQYNSTYRVVSVLTVLDHQLNGKEYCKVSNKALPAPIEKTIS 360  
 Db 299 FVDDVEVNTATKPREQENSTYRVVSALRIQHDWTGKKEFKCKVHNEGLPAPIVRTIS 358  
 QY 361 KAKGQPREQVYTPPPSREEMTKNQVSLTCLVKGYEPPSDIAVEWESNGQP--ENNYKTPP 418  
 Db 359 RTKGPAPEQVYVLAAPPQBELSKSTVSLTCMTVSFYPDYIAVEWQRNGQPESEDKYGTTP 418  
 QY 419 PVLDSGSGFFLYSKITVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 470  
 Db 419 PQLDADSSYFLYSKLRVDRNSWQEGDITYTCVVMHEALHNHYTKQSKSAGK 470

RESULT 11  
 S31459  
 Ig gamma-1 chain - sheep (fragment)  
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 16-Jul-1999  
 C:Accession: S31459  
 R:Patric, S.; Nau, F.  
 submitted to the EMBL Data Library, December 1992  
 A:Reference number: S31459







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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:23:13 ; Search time 53.64 seconds  
(without alignments)  
339.265 Million cell updates/sec

Title: US-09-499-662-143  
Perfect score: 2517  
Sequence: 1 MGWSCIILFLVATGTVHSQ.....MHEALHNHYTKSLSPGK 470

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1758	69.8	330	1 GCL_HUMAN	P01857 homo sapien
2	1610	64.0	326	1 GC2_HUMAN	P01859 homo sapien
3	1599.5	63.5	327	1 GC4_HUMAN	P01861 homo sapien
4	1231.5	48.9	323	1 GC_RABIT	P01870 oryctolagus
5	1210.5	48.1	329	1 GC2_CAVPO	P01862 cavia porce
6	1162	46.2	290	1 GC3_HUMAN	P01860 homo sapien
7	1155	45.9	326	1 GCL_RAT	P20759 rattus norv
8	1150	45.7	329	1 GC3_MOUSE	P22436 mus musculu
9	1145	45.5	324	1 GCL_MOUSE	P01868 mus musculu
10	1144.5	45.5	333	1 GCB_RAT	P20761 rattus norv
11	1140	45.3	393	1 GCIM_MOUSE	P01869 mus musculu
12	1139	45.3	398	1 GC3M_MOUSE	P03987 mus musculu
13	1129	44.9	330	1 GCAA_MOUSE	P01863 mus musculu
14	1127.5	44.8	329	1 GCC_RAT	P20762 rattus norv
15	1126.5	44.8	335	1 GCAE_MOUSE	P01864 mus musculu
16	1124	44.7	399	1 GCAM_MOUSE	P01865 mus musculu
17	1115	44.3	322	1 GCA_RAT	P20760 rattus norv
18	1085	43.1	336	1 GCB_MOUSE	P01866 mus musculu
19	1080	42.9	405	1 GCBM_MOUSE	P01867 mus musculu
20	562.5	22.3	139	1 HV07_MOUSE	P01751 mus musculu
21	528	21.0	117	1 HV06_MOUSE	P01750 mus musculu
22	524.5	20.8	137	1 HV11_MOUSE	P01755 mus musculu
23	524	20.8	138	1 HV48_MOUSE	P03980 mus musculu
24	516	20.5	117	1 HV05_MOUSE	P01749 mus musculu
25	510	20.3	140	1 HV02_MOUSE	P01746 mus musculu
26	504	20.0	117	1 HV09_MOUSE	P01753 mus musculu
27	491	19.5	117	1 HV04_MOUSE	P01748 mus musculu
28	488	19.4	117	1 HV49_MOUSE	P06328 mus musculu
29	486.5	19.3	429	1 EPC_RAT	P01855 rattus norv
30	486	19.3	428	1 EPC_HUMAN	P01854 homo sapien
31	482	19.1	117	1 HV10_MOUSE	P01754 mus musculu
32	482	19.1	136	1 HV15_MOUSE	P01759 mus musculu
33	477	19.0	117	1 HV1G_HUMAN	P23083 homo sapien

RESULT_1	GCL_HUMAN	STANDARD;	PRT;	330 AA.
AC	P01857;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Ig gamma-1 chain C region.			
GN	IGHG1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
[1]				
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=82274238; PubMed=6287432;			
RA	Ellison J.W., Berson B.J., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene.";			
RL	Nucleic Acids Res. 10:4071-4079(1982).			
[2]				
RN	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RP	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RA	Waxdal M.J., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino			
RL	acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";			
RL	Biochemistry 9:3161-3170(1970).			
[3]				
RN	SEQUENCE OF 136-329 (EU).			
RP	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RA	Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino			
RL	acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";			
RL	Biochemistry 9:3171-3181(1970).			
[4]				
RN	SEQUENCE (MYELOMA PROTEIN NIE).			
RP	MEDLINE=77070269; PubMed=826475;			
RA	Ponstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a			
RT	monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The			
RT	chymotryptic peptides of the H-chain, alignment of the tryptic			
RT	peptides and discussion of the complete structure.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).			
[5]				
RN	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RP	MEDLINE=83289131; PubMed=6884994;			
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RT	"Three-dimensional structure determination of antibodies. Primary			
RT	structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).			
[6]				
RN	DISULFIDE BONDS.			
RP	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X.			

P06336 mus musculu  
P01743 homo sapien  
P01756 mus musculu  
P01757 mus musculu  
P06329 mus musculu  
P01747 mus musculu  
P01744 homo sapien  
P01872 mus musculu  
P01871 homo sapien  
P01745 mus musculu  
P03988 oryctolagus  
P01873 mus musculu

RT Intrachain disulfide bonds.";  
RL Biochemistry 9:3188-3196(1970).  
RN [7]  
RP DISULFIDE BONDS.  
RX MEDLINE-77070267; PubMed-1002129;  
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal  
RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and  
RT characterization of the protein, the L- and H-chains, the  
RT cyanogen bromide cleavage products, and the disulfide bridges.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
RN [8]  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
RX MEDLINE-81208100; PubMed-7236608;  
RA Deisenhofer J.;  
RT "Crystallographic refinement and atomic models of a human Fc fragment  
RT and its complex with fragment B of protein A from Staphylococcus  
RT aureus at 2.9- and 2.8-A resolution.";  
RL Biochemistry 20:2361-2370(1981).  
CC -!- MISCELLANEOUS: NIE HAS THE GLM(17) ALLOTYPIC MARKER, 97-K, & THE  
CC GLM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GLM(3)  
CC MARKER & THE GLM (NON-1) MARKERS.  
CC -!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF  
CC 35.I16,198,269 & 272.  
CC -!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES  
CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES  
CC 268-272.  
CC -!- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF  
CC RESIDUES 198,267&272.  
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CC -----  
DR EMBL; J00228; AAC82527.1; ALT\_INIT.  
DR PIR; A02146; GHU.  
DR PDB; 1FC1; 15-JUL-92.  
DR PDB; 1FC2; 15-JUL-92.  
DR MIM; 147100; -.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003600; Ig\_like.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00410; Ig\_like; 1.  
DR SMART; SM00407; Ig\_c1; 2.  
DR PROSITE; PS00290; Ig\_MHC; 2.  
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
KW 3D-structure.  
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FT HINGE.  
FT DOMAIN 99 110  
FT DOMAIN 111 223  
FT CH2.  
FT DOMAIN 224 330  
FT CH3.  
FT DISULFID 27 83  
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FT DISULFID 109 109  
FT DISULFID 112 112  
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FT INTERCHAIN (WITH HEAVY CHAIN).  
FT INTERCHAIN (WITH HEAVY CHAIN).  
FT DISULFID 144 204  
FT DISULFID 250 308  
FT CARBOHYD 180 180  
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FT VARIANT 239 239  
FT VARIANT 241 241  
FT VARIANT 123 126  
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FT HELIX

FT TURN 136 137  
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FT STRAND 175 178  
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QY 201 GLYSLSVVTVPSSSISGTTQYICNVNHPKSNTKVDKRPKSCDKTHTCCPCPAPPELLGG 260  
Db 61 GLYSLSVVTVPSSSISGTTQYICNVNHPKSNTKVDKRPKSCDKTHTCCPCPAPPELLGG 120  
  
QY 261 PSVFLFPPPKPDKTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320  
Db 121 PSVFLFPPPKPDKTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180  
  
QY 321 STYRVSVLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 380  
Db 181 STYRVSVLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240  
  
QY 381 WTKNOVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 440  
Db 241 LTKNQVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 300  
  
QY 441 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470  
Db 301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330  
  
RESULT 2  
GC2\_HUMAN  
ID GC2\_HUMAN STANDARD; PRT; 326 AA.  
AC P01859;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE IG gamma-2 chain C region.  
GN IGHG2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.



OX NCBI\_TaxID=9606;  
RN [1]  
RN SEQUENCE OF 2-326 FROM N.A.  
RX MEDLINE=82197621; PubMed=6804948;  
RA Ellison J.W., Hood L.E.;  
RT "Linkage and sequence homology of two human immunoglobulin gamma  
TL heavy chain constant region genes";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).  
RN [2]  
RN SEQUENCE OF 88-115 FROM N.A.  
RX TISSUE=Fetal liver;  
RX MEDLINE=83001943; PubMed=6811139;  
RA Takahashi N., Ueda S., Obata M., Nikaide T., Nakai S., Honjo T.;  
RT "Structure of human immunoglobulin gamma genes: Implications for  
TL evolution of a gene family";  
RL Cell 29:671-679(1982).  
RN [3]  
RN SEQUENCE OF 99-177 AND 310-326 FROM N.A.  
RX TISSUE=Fetal liver;  
RX MEDLINE=84235992; PubMed=6329676;  
RA Krawinkel U., Rabbitts T.H.;  
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma  
TL heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass  
RN genes";  
RL EMBO J. 1:403-407(1982).  
RN [4]  
RN SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).  
RX MEDLINE=81007873; PubMed=6774012;  
RA Wang A.-C., Tung E., Fudenberg H.H.;  
RT "The primary structure of a human IgG2 heavy chain: genetic,  
TL evolutionary, and functional implications";  
RL J. Immunol. 125:1048-1054(1980).  
RN [5]  
RN SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).  
RX MEDLINE=80001357; PubMed=113060;  
RA Connell G.E., Parr D.M., Hofmann T.;  
RT "The amino acid sequences of the three heavy chain constant region  
TL domains of a human IgG2 myeloma protein";  
RL Can. J. Biochem. 57:758-767(1979).  
RN [6]  
RN SEQUENCE OF 238-275 (ZIE).  
RX MEDLINE=80114419; PubMed=118920;  
RA Hofmann T., Parr D.M.;  
RT "A note of the amino acid sequence of residues 381-391 of human  
TL immunoglobulins gamma chains";  
RL Mol. Immunol. 16:923-925(1979).  
RN [7]  
RN REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).  
RA Hofmann T., Parr D.M.;  
RL Submitted (MAR-1980) to the PIR data bank.  
RN [8]  
RN SEQUENCE OF 1-121 (DOT).  
RX MEDLINE=95255298; PubMed=7737190;  
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;  
RT "Characterization of the two unique human anti-flavin monoclonal  
TL immunoglobulins";  
RL Eur. J. Biochem. 228:886-893(1995).  
RN [9]  
RN DISULFIDE BONDS.  
RX MEDLINE=72033500; PubMed=4940472;  
RA Milstein C., Frangione B.;  
RT "Disulphide bridges of the heavy chain of human immunoglobulin G2";  
RL Biochem. J. 121:217-225(1971).  
RN [10]  
RN DISULFIDE BONDS.  
RX MEDLINE=69064124; PubMed=5782707;  
RA Frangione B., Milstein C., Pink J.R.L.;  
RT "Structural studies of immunoglobulin G";  
RL Nature 221:145-148(1969).  
RN -----  
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EMBL: J00230; AAB59393.1; -;  
PIR: A02148; G2HU.  
HSSP: P01857; IFC1.  
MIM: 147110; -;  
InterPro: IPR003006; Ig\_MHC.  
InterPro: IPR003597; Ig\_C1.  
InterPro: IPR003600; Ig\_Like.  
Pfam: PF00047; Ig\_3.  
SMART: SM00410; Ig\_Like; 1.  
SMART: SM00407; IGC1; 2.  
PROSITE: PS00290; IG\_MHC; 2.  
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FT NON\_TER 1 98  
FT DOMAIN 1 98 CH1.  
FT DOMAIN 99 110 HINGE.  
FT DOMAIN 111 219 CH2.  
FT DOMAIN 220 326 CH3.  
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).  
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FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).  
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FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
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FT DISULFID 246 304  
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Db 61 GLYSLSVVTVPSNFGTQTYICNVNHNKPSNTKVDKRPKSCDKTHTCPCPAPPELLGG 116  
Qy 261 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320  
Db 117 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 176  
Qy 321 STYRVSVSLTVHQLDNLNGKEYCKKVKSNKALPAPIEKTSKAKGQPREPQVYTLPPSREE 380  
Db 177 STYRVSVSLTVHQLDNLNGKEYCKKVKSNKALPAPIEKTSKAKGQPREPQVYTLPPSREE 236  
Qy 381 MTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 440  
Db 237 MTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 296  
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Db 297 QQGNVFCSCVMHEALHNYTQKSLSPGK 326  
RESULT 3  
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AC P01861; 1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Ig gamma-4 chain C region.  
GN IGHG4.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RX SEQUENCE FROM N.A.  
RP MEDLINE=83157104; PubMed=6299662;  
RA Ellison J.W., Buxbaum J.N., Hood L.E.;  
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";  
RL DNA 1:11-18(1981).  
RN [2]  
RP SEQUENCE OF 1-30 AND 81-326.  
RX MEDLINE=70207560; PubMed=4192699;  
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;  
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the  
RL constant region of a gamma 4 chain.";  
RL Biochem. J. 117:33-47(1970).  
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CC -----  
DR EMBL; K01316; AAB59394.1; ALT\_INIT.  
DR PIR; A02150; G4HU.  
DR HSP; P01842; 7FAB.  
DR MIM; 147130; -.  
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DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003600; Ig-like.  
DR Pfam; PF00047; Ig\_3.  
DR SMART; SM00410; Ig-like; 1.  
DR SMART; SM00407; IGc1; 2.  
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FT NON\_TER 1 1  
FT DOMAIN 1 98  
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FT DOMAIN 111 220  
FT DOMAIN 221 327  
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FT DISULFID 27 83  
FT DISULFID 106 106  
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DB 61 GLYSLSVVTVFSSSLGTQYTCNVNHPKSNPKVDKRVKPSKCDKTHTCPPCPAPELGG 117  
  
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DB 118 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQFN 177  
  
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DB 1 STYRVVSVLTVLDHQLWLNKGEYKCKVSNKGLPSSIEKTIKAKGQPREPOVYTLPPSREE 380

Db 178 STYRVVSVLTVLDHQLWLNKGEYKCKVSNKGLPSSIEKTIKAKGQPREPOVYTLPPSREE 237  
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Db 238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSRW 297  
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AC P01870;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig gamma chain C region.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=84030930; PubMed=6313520;  
RA Bernstein K.E., Alexander C.B., Mage R.G.;  
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant  
RL F-1 haplotype";  
RL Immunogenetics 18:387-397(1983).  
RN [2]  
RP SEQUENCE OF 1-128.  
RX MEDLINE=76135469; PubMed=1243651;  
RA Pratt D.M., Mole L.E.;  
RT "Sequence studies on the constant region of the Fd sections of rabbit  
RL immunoglobulin G of different allotype";  
RL Biochem. J. 151:337-349(1975).  
RN [3]  
RP SEQUENCE OF 88-266 FROM N.A.  
RX MEDLINE=83299917; PubMed=6193512;  
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;  
RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma  
RL heavy chain and identification of two genomic C gamma genes";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).  
RN [4]  
RP SEQUENCE OF 132-161.  
RX MEDLINE=70110015; PubMed=5461106;  
RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;  
RT "Sequence studies of the Fd section of the heavy chain of rabbit  
RL immunoglobulin G";  
RL Biochem. J. 116:249-259(1970).  
RN [5]  
RP SEQUENCE OF 129-131 AND 155-322.  
RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;  
RL (in) Killander J. (eds.);  
RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,  
RL Stockholm (1967).  
CC -!- MISCELLANEOUS; REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,  
CC 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15  
CC MARKERS AND REF.5 THE E15 MARKER.  
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CC -----  
DR EMBL; M16426; AAA31389.1; -.  
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DR HSP; P01857; 1FCL.  
DR InterPro; IPR003006; Ig\_MHC.

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DR SMART: SM00407; IGcl; 2.
DR PROSITE: PS00290; IG_MHC; 1.
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FT CONFLICT 71 71 V -> VPV (IN REF. 2).
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FT CONFLICT 173 173 N -> D (IN REF. 5).
FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 N -> E (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 N -> D (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> D (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).
FT CONFLICT 284 284 N -> S (IN REF. 5).
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Matches 229; Conservative 34; Mismatches 57; Indels 7; Gaps 2;

QY 144 KGPSVFPLAPSSKSTSGTAAALGLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 203
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QY 204 SLSSVWVPSSSSLGTQYICNVNHPKNTKVDKRVKPSKCDKTHCPCPAPELLGSPSV 263
Db 64 SLSSVSVTSSTSS---QPVTGNVAHPAINTKVDKTVASTCSK-----PTCPPPELLGSPSV 116

QY 264 FLPPPKPKDLMISRTPEVTCCVVVDVSHEDPEVKFNKYVDGVVHNHAKTKPREQYNSTY 323
Db 117 FIAPPKPKDLMISRTPEVTCCVVVDVSDQDPEVQFTWYINNEQVARTARPLREQQFNSTI 176

QY 324 RVSVLVTLHQDLWNGKEYKCYKSVNSKALPAPIEKTISKAKGQPREPOVYITLPPSREEMTK 383
Db 177 RVSTLPIHQDLWLRGKEFKCKVHNKALPAPIEKTISKAKGQPLEKPVYITMGPPREELSS 236

QY 384 NOVSLTCLVKGFPYSDIAVEMESNGQPNKYKTPPPVLDSDGSFPLYSKLTVDKSRQQG 443
Db 237 RVSILTCLMNGFPYSDISVEMERKNGAEDNYKTPPAVLDSGYSFLYNKLSVPTSEWQRG 296

QY 444 NVFSCSYMHREALHNYTKLSLSLSPGK 470
Db 297 DVFTCSYMHREALHNYTKLSRSPGK 323

RESULT 5
GC2_CAVPO STANDARD; PRT; 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
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RA Birshtein B.K., Hussain Q.Z., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT half-cystine joining heavy and light chains.";
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT and hinge region cyanogen bromide fragments.";
RL Biochemistry 10:19-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4804-4811(1974).
RN [6]
RP DISULFIDE BONDS
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:26-31(1971).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC 13 INBRED GUINEA PIGS.
DR PIR: A02151; G2GP.
DR HSP; P01772; 2rB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_cl.
DR InterPro: IPR003600; Ig-like.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00410; Ig-like; 1.
DR SMART: SM00407; IGcl; 2.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;
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Query Match 48.1%; Score 1210.5; DB 1; Length 329;
Best Local Similarity 69.8%; Pred. No. 3.9e-76;
Matches 233; Conservative 30; Mismatches 62; Indels 9; Gaps 4;

QY 140 SASTKGPSVFPLAPSSKSTSGGTAALGLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 199
Db 1 SARTTAPSVFPLAASCVDTSGMTLGLVKGYFPEPVTVKWSGALTSGVHTFPAVLQ- 59

QY 200 SGLYSLSVTVPSSSLGTQYICNVNHPKNTKVDKRVKPSKCDKTH--TCPCPAPEL 257
Db 60 SGLYSLTSMVTVPSSQKAT----CNVHPASSTKVDKTVETPIRTZPBPCPTCKPCPPEN 115

QY 258 LGGPSVFLEPPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVVHNHAKTKPRE 317
Db 116 LGGPSVFIFPPKPKDMLMISLTPRVTCVVVDVSDQDEPEVQFTWFDVNDKPVGNATKPRVE 175
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QY 318 QYNSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPIETKTISKAKGQPREPOVYTLPPS 377
Db 176 QYNTTVERVESVLPQIHOQDLWLRGKEFKCKVYNKALPAPIETKTISKAGRMPDVTPLPS 235
QY 378 REEMTKNOVSLCLVKGFPYSDIAVESNGOP--ENNYKTTTPVLDSDGSFELYSLKLV 435
Db 236 RDELSSKSVSVCLLIINFADHVEASNRVPVSEKYKNTPPIDEDAGSYFLYSLKLV 295
QY 436 DKSRWQOGVFCVSCVMHEALHNNHYTKSLSPG 469
Db 296 DKSAWDGIVYTCVSMVHEALHNNHYTKALSRSPG 329
RESULT 6
GC3_HUMAN STANDARD; PRT; 290 AA.
AC P01560.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region (Heavy chain disease protein) (HDC).
GN IGHG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (DISEASE PROTEIN WIS).
RX MEDLINE=81021548; PubMed=6774747;
RA Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
RT "Primary structure of human gamma 3 immunoglobulin deletion mutant:
RL Biochemistry 19:4304-4308(1980).
RN [2]
RP REVISIONS TO 12-97 OF PROTEIN WIS.
RX MEDLINE=77118561; PubMed=402363;
RA Michaelisen T.E., Frangione B., Franklin E.C.;
RT "Primary structure of the 'hinge' region of human IgG3. Probable
RT quadruplication of a 15-amino acid residue basic unit.";
RL J. Biol. Chem. 252:883-889(1977).
RN [3]
RP REVISIONS TO 59-289 OF PROTEIN WIS (DISEASE PROTEIN ZUC).
RX MEDLINE=77021516; PubMed=823945;
RA Wolfstene-Todel C., Frangione B., Prelli F., Franklin E.C.;
RT "The amino acid sequence of 'heavy chain disease' protein ZUC.
RT Structure of the Fc fragment of immunoglobulin G3.";
RL Biochem. Biophys. Res. Commun. 71:907-914(1976).
RN [4]
RP SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
RX MEDLINE=82247835; PubMed=6808505;
RA Alexander A., Steinmetz M., Barritault D., Frangione B.,
RA Franklin E.C., Hood L., Buxbaum J.N.;
RT "Gamma Heavy chain disease in man: cDNA sequence supports partial
RT gene deletion model.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
CC -!- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
CC INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
CC NORMALLY PRESENT IN THE HINGE REGION.
CC -!- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
CC -!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
CC REF. 2.
CC -!- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
CC AND ALL OF THE CH1 REGION.
CC -!- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
CC OF THE CH1 REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
CC GAMMA-3 HEAVY CHAINS.
CC -!- MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
CC OR ANOTHER GAMMA CHAIN SUBCLASS.
CC -!- MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
CC TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
CC IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
CC SEGMENT (12-28).
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DR EMBL: J00231; AAA52805.1; ALT_SEQ.
DR PIR: A02149; G3HUI1.
DR HSSP: P01857; 1FCL.
DR MIM: 147120; -.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_C1.
DR InterPro: IPR003600; Ig_Like.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00410; Ig_Like; 1.
DR SMART: SM00407; IgC1; 1.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat.
FT DOMAIN 12 73
FT HINGE.
FT CH2.
FT CH3.
FT PYRROLIDONE CARBOXYLIC ACID.
FT N-LINKED (GLCNAC...),
FT INTERCHAIN (WITH HEAVY CHAIN DIMER),
FT INTERCHAIN (WITH HEAVY CHAIN DIMER),
FT INTERCHAIN (WITH HEAVY CHAIN DIMER),
FT INTERCHAIN (WITH HEAVY CHAIN DIMER),
FT INTERCHAIN (WITH HEAVY CHAIN DIMER),
FT INTERCHAIN (WITH HEAVY CHAIN DIMER),
FT INTERCHAIN (WITH HEAVY CHAIN DIMER),
FT INTERCHAIN (WITH HEAVY CHAIN DIMER),
FT INTERCHAIN (WITH HEAVY CHAIN DIMER),
FT INTERCHAIN (WITH HEAVY CHAIN DIMER),
FT N-LINKED (GLCNAC...),
FT REMOVED POST-TRANSLATIONALLY.
FT QV -> EB (IN ZUC).
FT /FTID-VAR_003890.
FT P -> L (IN OMM).
FT /FTID-VAR_003891.
FT F -> Y (IN OMM).
FT /FTID-VAR_003892.
FT T -> A (IN OMM).
FT /FTID-VAR_003893.
FT S -> N (IN OMM).
FT /FTID-VAR_003894.
FT MISSING (IN ZUC).
FT /FTID-VAR_003895.
FT F -> Y (IN OMM).
FT /FTID-VAR_003896.
SQ SEQUENCE 290 AA; 32331 MW; E69CBG95705B2F46 CRC64;
Query Match 46.2%; Score 1162; DB 1; Length 290;
Best Local Similarity 91.4%; Pred. No. 7e-73;
Matches 212; Conservative 11; Mismatches 9; Indels 0; Gaps 0;
QY 239 EPKSCDKTHKCPAPPELLGGPSVFLPDKPKDILMISRTPEVTCVVVDVSHEDPEVAF 298
Db 59 EPKSCDTPPPCPAPPELLGGPSVFLPDKPKDILMISRTPEVTCVVVDVSHEDPEVAF 118
QY 299 NMYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKT 358
Db 119 KMYDGVGVHNAKTPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKT 178
QY 359 ISKAGQPREPOVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 418
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Db 179 ISKTGQPREPOVYTLPPSREMTKNQVSLTCLVKGFPSPIADIAVEWESSGQPENNYNTTP 238

QY 419 PVLSDSGSFYLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 470

Db 239 PMLSDSGSFYLYSKLTVDKSRWQGNIFCSCVMHEALHNHYTKQSLSPGK 290

RESULT 7

GC1\_RAT ID GC1\_RAT STANDARD; PRT; 326 AA.

AC P20759;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig gamma-1 chain C region.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89232738; PubMed=3149946;

RA Brueggemann M.;

RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";

RL Gene 74:473-482(1988).

DR PIR; PS0017; PS0017.

DR HSP; P01842; 7FAB.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003597; Ig\_cl.

DR Pfam; PF00047; Ig; 3.

DR SMART; SM00407; IGcl; 2.

DR PROSITE; PS00290; Ig\_MHC; 1.

KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.

FT NON\_TER 1 1

FT DOMAIN 1 97 CHI.

FT DOMAIN 98 112 HINGE.

FT DOMAIN 113 219 CH2.

FT DOMAIN 220 326 CH3.

FT DISULFID 27 82

FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 140 200

FT DISULFID 246 304

FT CARBOHYD 176 176

SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match 45.9%; Score 1155; DB 1; Length 326;

Best Local Similarity 63.4%; Pred. No. 2.4e-72;

Matches 211; Conservative 52; Mismatches 60; Indels 10; Gaps 4;

QY 141 ASTKGPSVFLPAPSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 200

Db 1 AETAPSVYFLAPGALKSNWTLGCLVKGYPPEPTVTVNSGALSSGVHTFPAVLQ-S 59

QY 201 GLXSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKPEKSCDKTHTCP-PCPAPELLG 260

Db 60 GLYTLTSSVTPSPSTWPSQVTCNVAPASSTKVDKKIVPRNCG--GDCRKC-----ICTG 113

QY 261 ---PSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREE 317

Db 114 SEVSSVFIFFPKPKDVLITITPKVTQVNVAPASSTKVDKKIVPRNCG--GDCRKC-----ICTG 113

QY 318 QYNSTYRWVSVLTVLHODWLNKREYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 377

Db 174 QFNSTFRSVELPLTHODWLNKREYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 233

QY 378 REEMTKNQVSLTCLVKGFPSPIADIAVEWESSGQPENNYNTTPPVLSDSGSFYLYSKLVADK 437

Db 234 KEEMTQNEVSIITCWKGYFIPDIIYVEMQMGQPOENYKNTPTMDTDGVSFYLKLVKK 293

QY 438 SRWQGNVFCSCVMHEALHNHYTKQSLSPGK 470

Db 294 EKWQGNFTCTSVLHEGLHNHHTKSLSHSPGK 326

RESULT 8

GC3\_MOUSE ID GC3\_MOUSE STANDARD; PRT; 329 AA.

AC P22436;

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Ig gamma-3 chain C region, secreted form.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=85027161; PubMed=6092053;

RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,

RA Tucker P.W., Blattner F.R.;

RT "Structural analysis of the murine IgG3 constant region gene.";

RL EMBO J. 3:2041-2046(1984).

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CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; J00451; -; NOT\_ANNOTATED\_CDS.

DR PIR; B02156; G3MSC.

DR HSP; P01857; 1FC1.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003597; Ig\_cl.

DR InterPro; IPR003600; Ig\_like.

DR Pfam; PF00047; Ig; 3.

DR SMART; SM00410; IG\_Like; 1.

DR SMART; SM00407; IGcl; 2.

DR PROSITE; PS00290; Ig\_MHC; 1.

KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;

KW Transmembrane; Alternative splicing.

FT NON\_TER 1 1

FT DOMAIN 1 97 CHI.

FT DOMAIN 98 113 HINGE.

FT DOMAIN 114 223 CH2.

FT DOMAIN 224 327 CH3.

SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 45.7%; Score 1150; DB 1; Length 329;

Best Local Similarity 65.0%; Pred. No. 5.5e-72;

Matches 213; Conservative 44; Mismatches 68; Indels 4; Gaps 3;

QY 142 STKGPSVFLPAPSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSG 201

Db 1 TTTAPSVYFLPAPSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQ-SG 59

QY 202 LYSLSVTVTPSSSLGTQTYICNVNHPKNTKVDKPEKSCDKTHTCP--PCPAPELLG 259

Db 60 FYSLSVTVTPSSSLGTQTYICNVNHPKNTKVDKPEKSCDKTHTCP--PCPAPELLG 118

QY 260 GPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQY 319

Db 119 GPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQY 178

QY 320 NSTYRVVSVLTVLHODWLNKREYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRE 379

Db 179 NSTYRVVSVLTVLHODWLNKREYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRE 238



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RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0018; PS0018.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 45.5%; Score 1144.5; DB 1; Length 333;
Best Local Similarity 63.7%; Pred. No. 1.3e-71;
Matches 214; Conservative 45; Mismatches 68; Indels 9; Gaps 3;

QY 141 ASYKGPSVFLPAPSKSTSGTAAGCLVKDYRPPETVSNWNGALTSVGHVTPFAVLQSS 200
Db 1 AQTAPSVYPLAPCGDTTSTVTLGCLVKGYFPETVTVNWSGALSDVHFFAVLIQ-S 59

QY 201 GLXSLSSVTVTPSSLSGTQYICNVNHNKPSNTKVKRVEPKS-----CDKTHTCPPCPA 254
Db 60 GLYTLTSVT--SSTWPSQVTCNVAPASSTKVDKVERRNGGIGHKCPTCTCHKCPV 117

QY 255 PELLGGSVFLPFPKPKDLMISRTPEVTCVVDVSDHEDPEVKFNVDYGVGVNATKTP 314
Db 118 PELLGGSVFIFFPKPKDILLISQNAKVTGVVDVSEEDPVQFSWFNVNVEVHTAQTP 177

QY 315 REEYNSYTRVRSVLTVDHDLWNGKVKCKVSNKALPAPEKTIKSAKGOPREPQVYTL 374
Db 178 REEYNSYTRVRSVLTVDHDLWNGKVKCKVSNKALPAPEKTIKSAKGOPREPQVYTL 374

QY 375 PPSREMTKNQVSLTCLVKGYFSPDIAVWESNGSQPNNTKTPPVLDSDGSFFLYSKLT 434
Db 238 GPPTPEQLTEQVSLTCLTSGLFLPNDIGVWTSNGHIEKNYKNTPEVMDSDGSFFMYSKLN 297

QY 435 VDKSRWQGNVFCSSVWHEALHNNHYTQKSLSPGK 470
Db 298 VERSRWDSRAPVGVSVVHGLNHHVKEKSIRPPGK 333

RESULT 11
GCIM_MOUSE STANDARD; PRT; 393 AA.
AC P01869;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-1 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
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RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 323-393 FROM N.A.
RX MEDLINE=82197626; PubMed=6804950;
RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
RT "mRNA for surface immunoglobulin gamma chains encodes a highly
conserved transmembrane sequence and a 28-residue intracellular
domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
RN [3]
RP SEQUENCE OF 323-366 FROM N.A.
RX MEDLINE=82115295; PubMed=6799207;
RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA Eisenberg D., Wall R.;
RT "Gene segments encoding transmembrane carboxyl termini of
immunoglobulin gamma chains.";
RL Cell 26:19-27(1981).
RN [4]
RP SEQUENCE OF 1-44 FROM N.A.
RX MEDLINE=82222190; PubMed=6283537;
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
immunoglobulin gamma chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
SEGMENT OF MU CHAINS.
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DR EMBL; V00793; CAA24172.1; -
DR EMBL; V00793; CAA24173.1; -
DR EMBL; V00793; CAA24174.1; -
DR PIR; B02159; GINSM.
DR HSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing; Transmembrane.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
FT DISULFID 244 302
FT TRANSMEM 340 357 POTENTIAL.
FT DOMAIN 358 393 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 393 AA; 43386 MW; 4CC88343B7AICE27 CRC64;
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Query Match 45.3%; Score 1140; DB 1; Length 393;  
Best Local Similarity 62.2%; Pred. No. 3.3e-71;  
Matches 206; Conservative 55; Mismatches 60; Indels 10; Gaps 4;

QY 141 ASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200  
 Db 1 AKTTPSVYPLAPGSAQAQNTSMVTLGCLVKGYFPEPVTVTVNSGSLSSGVTTPAVLQSD 60  
 QY 201 GLYSLSVTVPPSSSLGTQYICNVNHNKPSNTKVDKRVKPKSCDKHTCTCP--CPAPELL 258  
 Db 61 -LTLSSVTVPPSSRPSTVTCNVAHPASSTKVDKRIIPVDCG---CKPCICTVPEV- 114  
 QY 259 GGPSVFLFPKPKDMLMISRTPEVTCVVDVSHEDPEVKFNKVDGVGVHNAKTKPREEQ 318  
 Db 115 --SSVFIFFPKPKDVLITLTPKVTGVVDISKDDPEVQFVFWVDVVEHTAQPREEQ 172  
 QY 319 YNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSR 378  
 Db 173 FNSTFRSVSELPIMHQDLNKEFKCRVNSAAPPAPIETKISKGRKRAQVYTIPTPPK 232  
 QY 379 EEMTKNOVSLTCLVKGYFSDIAVESNGQPENNYKTPPVLDSDGSLFLSKLTVDKS 438  
 Db 233 EQMAKDKVSLTCLMIDTFPEPDIIVQWNGQPAENYKNTQPIMTNGSYFVYSKLVQKS 292  
 QY 439 RWOQGVNFCVSMHEALHNHYTKLSLSPG 469  
 Db 293 NWEAGNTFTCSVLHEGLHNHTEKLSHSPG 323  
 RESULT 12  
 GC3M\_MOUSE STANDARD; PRT; 398 AA.  
 AC P03987;  
 DT 23-OCT-1986 (Rel. 02, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig gamma-3 chain C region, membrane-bound form.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85027161; PubMed=6092053;  
 RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,  
 RA Tucker P.W., Blattner F.R.;  
 RT "Structural analysis of the murine IgG3 constant region gene.";  
 RL EMBO J. 3:2041-2046(1984).  
 [2]  
 RP SEQUENCE OF 328-398 FROM N.A.  
 RX MEDLINE=84041483; PubMed=6314258;  
 RA Komarony M., Clayton L., Rogers J., Robertson S., Kettman J.,  
 RA Wall R.;  
 RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene segment.";  
 RL Nucleic Acids Res. 11:6775-6785(1983).  
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 CC -----  
 DR EMBL; J00451; AAB59655.1; -;  
 DR EMBL; V01526; CAA24767.1; ALT\_SEQ.  
 DR PIR; A02155; G3MSM.  
 DR HSSP; P01857; 1FC1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003597; Ig\_cl.  
 DR InterPro; IPR003600; Ig\_like.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00410; Ig-like; 1.  
 DR SMART; SM00407; Igcl; 2.  
 DR PROSITE; PS00290; Ig\_MHC; 1.

KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
 KW Transmembrane; Alternative splicing.  
 FT NON\_TER 1 1 97 CH1.  
 FT DOMAIN 1 97 HINGE.  
 FT DOMAIN 98 113 HINGE.  
 FT DOMAIN 114 223 CH2.  
 FT DOMAIN 224 327 CH3.  
 FT TRANSMEM 346 362 POTENTIAL.  
 FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).  
 FT CONFLICT 333 333 E -> G (IN REF. 2).  
 FT CONFLICT 342 342 E -> Q (IN REF. 2).  
 FT CONFLICT 388 388 P -> F (IN REF. 2).  
 SQ SEQUENCE 398 AA; 43929 MW; CF7E64B50A41B95 CRC64;  
 Query Match 45.3%; Score 1139; DB 1; Length 398;  
 Best Local Similarity 64.7%; Pred. No. 4e-71;  
 Matches 213; Conservative 44; Mismatches 68; Indels 4; Gaps 3;  
 QY 142 STKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 201  
 Db 1 TITAPSVYPLVPGCSDTSGSSVTLGCLVKGYFPEPVTVKWNKYGALSSGVRTSVVLQ-SG 59  
 QY 202 LYSLSVTVPPSSSLGTQYICNVNHNKPSNTKVDKRVKPKSCDKHTCTCP--PCPAPELLG 259  
 Db 60 FYLSLSLTVPPSSVPSQTVICNVAHPASKTELKRIEPR-IPKSTPPGSSCPPGNILG 118  
 QY 260 GPSVFLFPKPKDMLMISRTPEVTCVVDVSHEDPEVKFNKVDGVGVHNAKTKPREEQ 319  
 Db 119 GPSVFIFFPKPKDMLMISLTPTKVTGVVDVSEDDPDVHVSFWFVDNKEVHTAQPREAQY 178  
 QY 320 NSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSR 379  
 Db 179 NSTFRVSVLPIQHODMGRKEFKCKVKNKALPAPIETKISKGRKRAQVYTIPTPPRE 238  
 QY 380 EMTKNOVSLTCLVKGYFSDIAVESNGQPENNYKTPPVLDSDGSLFLSKLTVDKSR 439  
 Db 239 QMSKKKVSITCLVTNFFSEAISVSEWERNGELEQDYKNTPTPILDSGDTYFLYSKLTVDTS 298  
 QY 440 WQGVNFCVSMHEALHNHYTKLSLSP 468  
 Db 299 WLQGEFTCSVHVALHNHHTKQLSRSP 327  
 RESULT 13  
 GCAA\_MOUSE STANDARD; PRT; 330 AA.  
 ID GCAA\_MOUSE  
 AC P01863;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Ig gamma-2A chain C region, A allele.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81076554; PubMed=6777755;  
 RA Sikorav J.-L., Auffray C., Rougeon F.;  
 RT "Structure of the constant and 3' untranslated regions of the murine  
 RT Balb/c gamma 2a heavy chain messenger RNA.";  
 RL Nucleic Acids Res. 8:3143-3155(1980).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81198976; PubMed=6262729;  
 RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;  
 RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene  
 RT and evolution of heavy chain genes: further evidence for intervening  
 RT sequence-mediated domain transfer.";  
 RL Nucleic Acids Res. 9:1365-1381(1981).  
 RN [3]  
 RP SEQUENCE FROM N.A.



RX MEDLINE=81223894; PubMed=6787604;  
 RA Olio R., Auffray C., Morchamps C., Rougeon F.;  
 RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes  
 RT suggests that exons can be exchanged between genes in a multigenic  
 RT family.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).  
 RN [4]  
 RP MYELOMA PROTEIN MOPC 173.  
 RX MEDLINE=74175517; PubMed=4831970;  
 RA Bourgois A., Fougereau M., Rocca-Serra J.;  
 RT "Determination of the primary structure of a mouse IgG2a  
 RT immunoglobulin:amino-acid sequence of the Fc fragment. Implications  
 RT for the evolution of immunoglobulin structure and function.";  
 RL Eur. J. Biochem. 43:423-435(1974).  
 RN [5]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=73056887; PubMed=4565406;  
 RA de Preval C., Fougereau M.;  
 RT "Determination of the primary structure of a mouse gamma G2a  
 RT immunoglobulin. Identification of the disulfide bridges.";  
 RL Eur. J. Biochem. 30:452-462(1972).  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; V00798; CAA24178.1; -;  
 DR PIR; A02152; G2MSA.  
 DR HSSP; P01842; 7FAB.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003600; Ig-like.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00410; IG-like; 1.  
 DR SMART; SM00407; IGcl; 2.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 DR Immunoglobulin domain; Immunoglobulin C region.  
 KW NON\_TER 1  
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 27 82  
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 144 204  
 FT DISULFID 250 308  
 FT MOD\_RES 330 330 REMOVED POST-TRANSLATIONALLY.  
 SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;  
  
 Query Match 44.98; Score 1129; DB 1; Length 330;  
 Best Local Similarity 63.98; Pred. No. 1.5e-70;  
 Matches 212; Conservative 43; Mismatches 73; Indels 4; Gaps 3;  
  
 QY 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 200  
 Db 1 AKTTAPSVYPLAPVCGDTGSSVTLGCLVKGYFPEPTVLTWNSGSLSSGVHTFPAVLQSD 60  
  
 QY 201 GLYSLSSVTVPPSSSLGQTQYICNVNHPKPSNTKDKRVEPKSCDKTHTCPP--CPAPEL 258  
 Db 61 -LYTLSSSVTVTSSTWPSQSTICNVNHPKPSNTKDKRVEPKSCDKTHTCPP--CPAPEL 118  
  
 QY 259 GGPSVFLPPPKPKDTLMISRPETVCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 318  
 Db 119 GGPSVFIIPPKPKDKVTLISPIVTVVDVSEDPPQVSIWFNVNNEVHTAQVTHRED 178  
  
 QY 319 YNSTYRVSVLTVLHDLNLSKCKVSKNALKAPAPTEKTIISKAKGPPEPQVYTLPPSR 378  
 Db 179 YNSTLRVVVSALPIQHQQDWMSKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPE 238

QY 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDK 438  
 Db 239 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDK 298  
  
 QY 439 RWOOGNPFVSCSVNHEALNHYTKOKSLSLSPGK 470  
 Db 299 NWVERNSYSCSVNHEGLNHHHTTKFSRTPGK 330  
  
 RESULT 14  
 GCC\_RAT  
 ID GCC\_RAT STANDARD; PRT; 329 AA.  
 AC P20762;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig gamma-2C chain C region.  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88166903; PubMed=3127222;  
 RA Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;  
 RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant  
 RT region cDNA: extensive homology to mouse gamma 3.";  
 RL Eur. J. Immunol. 18:317-319(1988).  
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 CC -----  
 DR EMBL; X07189; CAA30169.1; -;  
 DR PIR; S00847; S00847.  
 DR HSSP; P01857; 1FC1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003600; Ig-like.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00410; IG-like; 1.  
 DR SMART; SM00407; IGcl; 2.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 DR Immunoglobulin domain; Immunoglobulin C region.  
 KW NON\_TER 1  
 FT DOMAIN 1 97 CH1.  
 FT DOMAIN 98 113 HINGE.  
 FT DOMAIN 114 222 CH2.  
 FT DOMAIN 223 329 CH3.  
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 27 82  
 FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 143 203  
 FT DISULFID 249 307  
 SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;  
  
 Query Match 44.8%; Score 1127.5; DB 1; Length 329;  
 Best Local Similarity 62.8%; Pred. No. 1.9e-70;  
 Matches 209; Conservative 51; Mismatches 66; Indels 7; Gaps 3;  
  
 QY 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 200  
 Db 1 ARTTAPSVYPLVPVCGSTSGSLVTLGCLVKGYFPEPTVTKNSGALSSGVHTFPAVLQ-S 59  
  
 QY 201 GLYSLSSVTVPPSSSLGQTQYICNVNHPKPSNTKDKRVEPKSCDKTHTCPP--CPAPEL 257  
 Db 60 GLYTLSSSVTVPPSSWSSTQVTCVAHPATKSNLIKRIEPR---RPKRPPTPTDICSDDN 116

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QY 258 LGSPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREE 317
  |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
Db 117 LGRPSVFIFPPPKDILMITLPKVTCCVVVDVSEEDPDQFSWFVNVRFVTAQTQPHHE 176
QY 318 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 377
  |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
Db 177 QLNGTRFVVSTLHQIQDWMSGKEFKCKVNNKDLPSPIEKTISKPRGKARTPOVYTIPPP 236
QY 378 REEMTKNOVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 437
  |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
Db 237 REQMSKNKVSILTCMTVTSFTPASISVSWERNGELEDYKNTLPVLDSDSEYFELYSKLSDVT 296
QY 438 SRMQQGNVFSVCSVMHEALHNHYTKQSLSLSPGK 470
  |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
Db 297 DSMRGRDIIVTCVSVVHEALHNHHTQKNLSRSPGK 329

RESULT 15
GCAB_MOUSE STANDARD; PRT; 335 AA.
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2A chain C region, B allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
RT IgG2a and IgG2b alleles of the mouse.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN [2]
RP SEQUENCE.
RX MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwereys M., Strosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
RT chain Fc regions of Ig1a and Ig1b allotypic forms.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -!- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
CC FROM BALB/C MICE, AT 15% OF THE POSITIONS.
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CC -----
DR EMBL; J00479; ; NOT_ANNOTATED_CDS.
DR PIR; A02153; G2MSAB.
DR HSP; P01857; 1FC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
SQ SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;
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Query Match 44.8%; Score 1126.5; DB 1; Length 335;  
Best Local Similarity 61.6%; Pred. No. 2.3e-70;



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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:22:15 ; Search time 187.61 Seconds  
(without alignments)  
433.386 Million cell updates/sec

Title: US-09-499-662-143

Perfect score: 2517

Sequence: 1 MGWSCIIILFLVATATGVHSQ.....MHEALHNHYTKSLSPCK 470

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mmc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1639.5	65.1	473	11 Q9D8L4	Q9d8l4 mus musculus
2	1628.5	64.7	463	11 Q99LC4	Q99lc4 mus musculus
3	1598.5	63.1	473	11 Q99L25	Q99l25 mus musculus
4	1562	62.1	468	11 Q99L31	Q99l31 mus musculus
5	1433.5	57.0	437	11 Q99L14	Q99l14 mus musculus
6	1420.5	56.4	473	11 Q91205	Q91205 mus musculus
7	1263.5	50.2	337	6 Q95M34	Q95m34 equus caball
8	1257	49.9	701	4 Q96P08	Q96pc8 homo sapien
9	986	39.2	278	11 Q921K1	Q921k1 mus musculus
10	927.5	36.8	614	4 Q96GA6	Q96ga6 homo sapien
11	890.5	35.4	481	11 Q91WT3	Q91wt3 mus musculus
12	859	34.1	500	4 Q9BRV0	Q9brv0 homo sapien
13	836.5	33.2	481	11 Q91WT1	Q91wt1 mus musculus
14	820	32.6	488	11 Q91WR1	Q91wr1 mus musculus
15	812.5	32.3	597	4 Q96BB9	Q96bb9 homo sapien
16	804	31.9	496	4 Q96DK0	Q96dk0 homo sapien

17	762.5	30.3	597	4 Q9BU10	Q9bu10 homo sapien
18	758.5	30.1	597	4 Q9BQB8	Q9bqb8 homo sapien
19	758	30.1	484	11 Q99LA6	Q99la6 mus musculus
20	752.5	29.9	618	4 Q96AA6	Q96aa6 homo sapien
21	734	29.2	494	4 Q96K68	Q96k68 homo sapien
22	732	29.1	613	4 Q96EX0	Q96ey0 homo sapien
23	724.5	28.8	487	11 Q99KA4	Q99ka4 mus musculus
24	718.5	28.5	479	11 Q91WP5	Q91wp5 mus musculus
25	700	27.8	486	11 Q91Z07	Q91z07 mus musculus
26	689.5	27.4	480	11 Q91XE1	Q91xe1 mus musculus
27	656	26.1	482	11 Q91X92	Q91x92 mus musculus
28	652	25.9	479	11 Q99M22	Q99m22 mus musculus
29	641	25.5	496	4 Q96KX8	Q96kx8 homo sapien
30	605	24.0	426	11 Q9DCD9	Q9dcd9 mus musculus
31	580.5	23.1	416	4 Q9NPP6	Q9np66 homo sapien
32	542.5	21.6	143	11 Q91V67	Q91v67 mus musculus
33	530.5	21.1	143	11 Q92AP9	Q92ap9 mus musculus
34	525	20.9	150	4 Q9Y298	Q9y298 homo sapien
35	517	20.5	142	11 Q92AQ2	Q92aq2 mus musculus
36	513.5	20.4	145	11 Q92AR3	Q92ar3 mus musculus
37	508	20.2	157	4 Q95978	Q95978 homo sapien
38	498.5	19.8	143	11 Q92AQ5	Q92aq5 mus musculus
39	497	19.7	146	11 Q92AR8	Q92ar8 mus musculus
40	496.5	19.7	159	4 Q96Q50	Q96q50 homo sapien
41	496	19.7	144	11 Q92AP5	Q92ap5 mus musculus
42	495.5	19.7	145	11 Q92AQ7	Q92aq7 mus musculus
43	491.5	19.5	145	11 Q92AR4	Q92ar4 mus musculus
44	489.5	19.4	143	11 Q92AQ0	Q92aq0 mus musculus
45	489	19.4	140	11 Q92AP8	Q92ap8 mus musculus

## ALIGNMENTS

RESULT 1

ID	Q9D8L4	PRELIMINARY;	PRT;	473 AA.
AC	Q9D8L4;			
DT	01-JUN-2001 (TrEMBLrel. 17, Created)			
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)			
DE	1810060009RIK PROTEIN.			
GN	IGH-1 OR 1810060009RIK.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=PANCREAS;			
RX	MEDLINE=21085660; PubMed=11217851;			
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,			
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,			
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,			
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,			
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,			
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,			
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,			
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,			
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,			
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,			
RA	Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,			
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,			
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,			
RT	Hayashizaki Y.			
RT	"Functional annotation of a full-length mouse cDNA collection."			
EL	Nature 409:685-690(2001).			
DR	EMBL; AK007918; BAB25349.1; -.			
DR	HSSP; P01842; 7FAB.			

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DR MGD; MGI:96443; Igh-1.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003600; Ig_like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IGc1; 3.
DR SMART: SM00406; IGv; 1.
DR SMART: SM00410; IG_Like; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match      65.1%; Score 1639.5; DB 11; Length 473;
Best Local Similarity 63.9%; Pred. No. 8.2e-129;
Matches 304; Conservative 69; Mismatches 94; Indels 9; Gaps 4;

QY 1 MGWSCILFLVATATGVSQVLQVSGAEVKKPGASVKYKSCASGYTFTSYMHWVKQAP 60
DB 1 MEWSWVFLFLSVTAGVHCQVLQKQSGAELVKPGASVKISCRASGYTFTDYIYNWVKQP 60

QY 61 GQGLEWMEIDPSDSTNTNQKFGKATLTVDSTSTAYMELSSLRSEDTAVYYCARNRD 120
DB 61 GQGLEWIGIGPGSGSTYNEKFKGKATLTADKSSSTAYMQLSLTSSESAVYFCARS-G 119

QY 121 YSNNWYFDVWGQGLTVTVSSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVS 180
DB 120 YDYDW-FATWGQGLTVVSAAKTATPSVPLAPVCGGTGSSVTLGCLVKGYFPEPTVT 178

QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVSPSSSLGTQTYICNVNHPKNTKVDKRVPP 240
DB 179 WNSGSLSSGVHTFPAVLQ-SGLYTLSSVTVSTNTWPSQTITCNVAHPASSIKVDKKIEP 237

QY 241 K-----SCDKTHCTCPCPAPPELLGGPSVFLPDKPKDITLMISRTPEVTCVVVDVSHEDP 294
DB 238 RVPITQNPCCPLKECPCCAAPDLGGPSVFIFPPKIKDVLMISSLSPMVTQVVDVSEDDP 297

QY 295 EVKFNMYDGVVHNNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 354
DB 298 DQVISFVNVEVHTAQTQTHREDYNSTLRVYSALPIQHDWMSGKEFKCKVNNRALPSP 357

QY 355 IEKTSKAGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 414
DB 358 IEKTSIKRGPVRAPQGVYVLPAPAEEMTKKEFSLTTCMITGFLPAETAVDWTSGNRTEQNY 417

QY 415 KTTPPVLDSDGSFFLYSKLTVDKSRHQQGNVFCSCVYHMEALHNHYTQKSLSLSPGK 470
DB 418 KNTATVLDSDGSFYMYSKLRVOKSTWERSGLFACSVYHGLNHLTKTISRSLGK 473

RESULT 2
Q99LC4 PRELIMINARY; PRT; 463 AA.
AC Q99LC4;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003600; Ig_Like.

QY 1 MGWSCILFLVATATGVSQVLQVSGAEVKKPGASVKYKSCASGYTFTSYMHWVKQAP 60
DB 1 MEWIFLFLISGTAGVHSQVLQKQSGAELRPGASVRLSCKASGYTFTGYGVSWVKQRT 60

QY 61 GQGLEWMEIDPSDSTNTNQKFGKATLTVDSTSTAYMELSSLRSEDTAVYYCARNRD 120
DB 61 GQGLEWVGEIYFGSGNTYYSEKFKGATLTDDKSSSTAYMHLSSLTSEDSAVYFCARSS 120

QY 121 YSNNWYFDVWGQGLTVTVSSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVS 180
DB 121 YSYD-LFAYWGQGLTVVSAAKTTPPSVPLAPGSAAQTNMSWVTLGCLVKGYFPEPTVT 179

QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVSPSSSLGTQTYICNVNHPKNTKVDKRVPP 240
DB 180 WNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVSPSTWPSSETVTCNVAHPASSIKVDKKIIV 238

QY 241 KSKDKTHCTCP--CPAPELLGGPSVFLPDKPKDITLMISRTPEVTCVVVDVSHEDPEVKF 298
DB 239 RDCG-----CKPCICTYPEV---SSVFIFPPKPKDVLITLTPKVTQVVDVSKDDPEVQF 291

QY 299 NMYDGVGVHNNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 358
DB 292 SWFVDVVEVHTAQTQPREQFNSTFRSVSELPITMHQDWLNGKEFKCRVNSAAPPAPIEKT 351

QY 359 ISKAGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 418
DB 352 ISKTKGRPKAPQVYITPPPEQMAKDKVSLTTCMITDFFEDITVEWQWNGQPAENYKNTQ 411

QY 419 PVLDSDGSFFLYSKLTVDKSRHQQGNVFCSCVYHMEALHNHYTQKSLSLSPGK 470
DB 412 PIMDTDGSFYIYKLVNQSNEAGNFTCTSVLHGLHNHHTKSLSHSPGK 463

RESULT 3
Q99L25 PRELIMINARY; PRT; 473 AA.
AC Q99L25;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AAH03888.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
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DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IGc1; 2.
DR SMART: SM00406; IGv; 1.
DR SMART: SM00410; IG_Like; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Query Match      64.7%; Score 1628.5; DB 11; Length 463;
Best Local Similarity 63.8%; Pred. No. 6.6e-128;
Matches 301; Conservative 71; Mismatches 89; Indels 11; Gaps 5;

QY 1 MGWSCILFLVATATGVSQVLQVSGAEVKKPGASVKYKSCASGYTFTSYMHWVKQAP 60
DB 1 MEWIFLFLISGTAGVHSQVLQKQSGAELRPGASVRLSCKASGYTFTGYGVSWVKQRT 60

QY 61 GQGLEWMEIDPSDSTNTNQKFGKATLTVDSTSTAYMELSSLRSEDTAVYYCARNRD 120
DB 61 GQGLEWVGEIYFGSGNTYYSEKFKGATLTDDKSSSTAYMHLSSLTSEDSAVYFCARSS 120

QY 121 YSNNWYFDVWGQGLTVTVSSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVS 180
DB 121 YSYD-LFAYWGQGLTVVSAAKTTPPSVPLAPGSAAQTNMSWVTLGCLVKGYFPEPTVT 179

QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVSPSSSLGTQTYICNVNHPKNTKVDKRVPP 240
DB 180 WNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVSPSTWPSSETVTCNVAHPASSIKVDKKIIV 238

QY 241 KSKDKTHCTCP--CPAPELLGGPSVFLPDKPKDITLMISRTPEVTCVVVDVSHEDPEVKF 298
DB 239 RDCG-----CKPCICTYPEV---SSVFIFPPKPKDVLITLTPKVTQVVDVSKDDPEVQF 291

QY 299 NMYDGVGVHNNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 358
DB 292 SWFVDVVEVHTAQTQPREQFNSTFRSVSELPITMHQDWLNGKEFKCRVNSAAPPAPIEKT 351

QY 359 ISKAGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 418
DB 352 ISKTKGRPKAPQVYITPPPEQMAKDKVSLTTCMITDFFEDITVEWQWNGQPAENYKNTQ 411

QY 419 PVLDSDGSFFLYSKLTVDKSRHQQGNVFCSCVYHMEALHNHYTQKSLSLSPGK 470
DB 412 PIMDTDGSFYIYKLVNQSNEAGNFTCTSVLHGLHNHHTKSLSHSPGK 463

RESULT 3
Q99L25 PRELIMINARY; PRT; 473 AA.
AC Q99L25;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AAH03888.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
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DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match
Best Local Similarity 63.1%; Score 1588.5; DB 11; Length 473;
Matches 302; Conservative 60; Mismatches 106; Indels 7; Gaps 5;

QY 1 MGWSCIIILFVATATGVHSGAELVQSGAEVKKPGASVKVSCKASGYSYFTTSYMMQVVKQAP 60
DQ 1 MEWSWVLEFFLVSTVGVHSGVQLQDAGELVQSGAEVKKPGASVKVSCKASGYSYFTTTHHWKQRP 60
QY 61 GQLEWNGEIDPDSYNYNQKPKGKATLTVDTSSTAYMELSLRSSTEDTAIYVCARNRD 120
DQ 61 EQLEWNGEIDPDSYNYNQKPKGKATLTVDTSSTAYMELSLRSSTEDTAIYVCARNRD 120
QY 121 YSNWYEDVWGQGLVTVSSASTKGPSVFPLAPSKSTSGGTAALGCLVKGYFPEPV 177
DQ 121 YSNWYEDVWGQGLVTVSSASTKGPSVFPLAPSKSTSGGTAALGCLVKGYFPEPV 177
QY 121 IYGYGLYFYDWGOGTITVSSAKTAPSVYPLAPVCGDTTGSSTLGLCLVKGYFPEPV 180
DQ 121 IYGYGLYFYDWGOGTITVSSAKTAPSVYPLAPVCGDTTGSSTLGLCLVKGYFPEPV 180
QY 178 TVSNWNGALTSVGTFFPAVLQSSGLYSLSVTVTPSSSLGQTQYICNVNHNKPSNTKVDKR 237
DQ 178 TVSNWNGALTSVGTFFPAVLQSSGLYSLSVTVTPSSSLGQTQYICNVNHNKPSNTKVDKR 237
QY 181 TLTWNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVTSSTWPSQSTCNVAHPASSTKVDKK 239
DQ 181 TLTWNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVTSSTWPSQSTCNVAHPASSTKVDKK 239
QY 238 VEPKSCDKTHTCPP--CPAPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDYSHEDPE 295
DQ 238 VEPKSCDKTHTCPP--CPAPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDYSHEDPE 295
QY 240 IEPRG-PTIKPCPKCPAPNLLGGPSVFIIPPKIKDVLMLSLSPMYTCVVVDYSEDDPD 298
DQ 240 IEPRG-PTIKPCPKCPAPNLLGGPSVFIIPPKIKDVLMLSLSPMYTCVVVDYSEDDPD 298
QY 296 VKFWYVDGVEVHNNAKTPREEQNSYRVVSVLTVLHQDWLNGKEYCKCKVSNKALPAPI 355
DQ 296 VKFWYVDGVEVHNNAKTPREEQNSYRVVSVLTVLHQDWLNGKEYCKCKVSNKALPAPI 355
QY 299 VQISWFVNNVEVLTAQTQTHREDYNSTLRVVSALPIQHDWMSCKEFCCKVNNKALPAPI 358
DQ 299 VQISWFVNNVEVLTAQTQTHREDYNSTLRVVSALPIQHDWMSCKEFCCKVNNKALPAPI 358
QY 356 EKTISKAKGQPREQVYTLPPSREEMTKNQVSLTCLVKGYFSPDIAVEWESNGOPENNYK 415
DQ 356 EKTISKAKGQPREQVYTLPPSREEMTKNQVSLTCLVKGYFSPDIAVEWESNGOPENNYK 415
QY 359 ERTISKKPGSVRAQVYVLPPEPEEMTKKQVTLTCMTVDFMPEDIVYEWNTNGKTELNYK 418
DQ 359 ERTISKKPGSVRAQVYVLPPEPEEMTKKQVTLTCMTVDFMPEDIVYEWNTNGKTELNYK 418
QY 416 TTPVLDSDGSFFLYSKLTVDKSRWQQGNFSCSVHMEALHNHYTOKSLSLSPGK 470
DQ 416 TTPVLDSDGSFFLYSKLTVDKSRWQQGNFSCSVHMEALHNHYTOKSLSLSPGK 470
QY 419 NTEPVLSDSGSYFYMSKLRVEKNKNNVRSYSCSVVHEGLHNHHTTKSFSRTPGK 473
DQ 419 NTEPVLSDSGSYFYMSKLRVEKNKNNVRSYSCSVVHEGLHNHHTTKSFSRTPGK 473

RESULT 4
Q99L31 PRELIMINARY; PRT; 468 AA.
ID Q99L31
AC Q99L31
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DE 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060C09 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AA003878.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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SQ SEQUENCE 468 AA; 51661 MW; 96352328B332ADB CRC64;

Query Match
Best Local Similarity 62.1%; Score 1562; DB 11; Length 468;
Matches 297; Conservative 61; Mismatches 108; Indels 6; Gaps 4;

QY 1 MGWSCIIILFVATATGVHSGAELVQSGAEVKKPGASVKVSCKASGYSYFTTSYMMQVVKQAP 60
DQ 1 MEWSWVLEFFLVSTVGVHSGVQLQDAGELVQSGAEVKKPGASVKVSCKASGYSYFTTTHHWKQRP 60
QY 61 GQLEWNGEIDPDSYNYNQKPKGKATLTVDTSSTAYMELSLRSSTEDTAIYVCARNRD 120
DQ 61 EQLEWNGEIDPDSYNYNQKPKGKATLTVDTSSTAYMELSLRSSTEDTAIYVCARNRD 120
QY 121 YSNWYEDVWGQGLVTVSSASTKGPSVFPLAPSKSTSGGTAALGCLVKGYFPEPV 178
DQ 121 YSNWYEDVWGQGLVTVSSASTKGPSVFPLAPSKSTSGGTAALGCLVKGYFPEPV 178
QY 181 WNSGALTSVGTFFPAVLQSSGLYSLSVTVTPSSSLGQTQYICNVNHNKPSNTKVDKREP 240
DQ 181 WNSGALTSVGTFFPAVLQSSGLYSLSVTVTPSSSLGQTQYICNVNHNKPSNTKVDKREP 240
QY 179 WNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVTSSTWPSQSTCNVAHPASSTKVDKKIEP 237
DQ 179 WNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVTSSTWPSQSTCNVAHPASSTKVDKKIEP 237
QY 241 KSCDKTHTCPP--CPAPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDYSHEDPEVK 298
DQ 241 KSCDKTHTCPP--CPAPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDYSHEDPEVK 298
QY 238 RG-PTIKPCPKCPAPNLLGGPSVFIIPPKIKDVLMLSLSPMYTCVVVDYSEDDPDVQI 296
DQ 238 RG-PTIKPCPKCPAPNLLGGPSVFIIPPKIKDVLMLSLSPMYTCVVVDYSEDDPDVQI 296
QY 299 NWYVDGVEVHNNAKTPREEQNSYRVVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKT 358
DQ 299 NWYVDGVEVHNNAKTPREEQNSYRVVSVLTVLHQDWLNGKEYCKCKVSNKALPAPIEKT 358
QY 297 SWFYNNVEVLTAQTQTHREDYNSTLRVVSALPIQHDWMSCKEFCCKVNNKALPAPIERT 356
DQ 297 SWFYNNVEVLTAQTQTHREDYNSTLRVVSALPIQHDWMSCKEFCCKVNNKALPAPIERT 356
QY 359 ISKAKGQPREQVYTLPPSREEMTKNQVSLTCLVKGYFSPDIAVEWESNGOPENNYKTP 418
DQ 359 ISKAKGQPREQVYTLPPSREEMTKNQVSLTCLVKGYFSPDIAVEWESNGOPENNYKTP 418
QY 357 ISKPKGSVRAQVYVLPPEPEEMTKKQVTLTCMTVDFMPEDIVYEWNTNGKTELNYKTE 416
DQ 357 ISKPKGSVRAQVYVLPPEPEEMTKKQVTLTCMTVDFMPEDIVYEWNTNGKTELNYKTE 416
QY 419 PVLSDSGSFFLYSKLTVDKSRWQQGNFSCSVHMEALHNHYTOKSLSLSPGK 470
DQ 419 PVLSDSGSFFLYSKLTVDKSRWQQGNFSCSVHMEALHNHYTOKSLSLSPGK 470
QY 417 PVLSDSGSYFYMSKLRVEKNKNNVRSYSCSVVHEGLHNHHTTKSFSRTPGK 468
DQ 417 PVLSDSGSYFYMSKLRVEKNKNNVRSYSCSVVHEGLHNHHTTKSFSRTPGK 468

RESULT 5
Q99L14 PRELIMINARY; PRT; 437 AA.
ID Q99L14
AC Q99L14
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GAMMA1 HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AA040243.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00410; IG_like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;
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Query Match          57.0%; Score 1433.5; DB 11; Length 437;
Best Local Similarity 59.1%; Pred. No. 1.3e-111;
Matches 267; Conservative 72; Mismatches 96; Indels 17; Gaps 7;

QY 21 VQLVQSGAEVKKPCASVKVSKRAGTFTSYWQWVKQAPGGQLEWGEIDPSDSTNN 80
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 VQLQESGGGLVKGGLSKLCAASGTFSSYAMSWYRQTPKRLWVASFS-SGGIYYT 59
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 81 QKFKGKATLVDTSTAYMELSSLSRSEDYAVYICARNRDYSNNWYFDVWGGTGLTVSS 140
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60 DSVKGRFTIYKDKDRNLSLQWSSLSRSEDYAMYYCARG-DYS-----ATWGPGLTVSA 113
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 141 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPVQLQSS 200
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 114 AKTTPSVVPLAPGSAQTSMVTLGCLVKGYPPEPTVTWNSGSLSSGVHTFPVQLQSD 173
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 201 GLYSLSSVTVPSSSLGCTQYICNVNHPKSNKYDKRVEPKSCDKTHTCPP--CPAPELL 258
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 174 -LYTSSSVTVPSSTWSPSETVTCNVAHPASSTKVDRKKIIPRDCG----CKPCICTVPEV- 227
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 259 GGPSVFLPPKPKDMLMISRTPEVTCVVDVSHEDPEVAFNFWVDGVEVHNNAKTKPREQ 318
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 228 --SSVFIPPPKDVLTILTPKVTGVVDVDSKDDPEVQFSWFVDVVEVHTAQTPREQ 285
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 319 YNSTYRVSVLTVLHQDLWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 286 FNSTFRSVSELPIMHQDLWLNKGEYKCKVSNAAFPAPIEKTISKGRKPAQVYTIPTPPK 345
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 379 EEMTKNOVSLTCLVKGFFYSDIAVENESGQPNENYKTTTPVLDSGDSFFLYSKLTVDKS 438
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 346 EQAKDKVSLTCMITDFFPEDITVEWQWQGAENYKNTQPIMDTDGDSFYVYSKLVNQKS 405
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 439 RWOQGNVFCSCVMHEALHNHYTKQSLSPGK 470
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 406 NWEAGNTFTCSVLHGLNHNHHEKNSHSPGK 437
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
Q91Z05 PRELIMINARY; PRT; 473 AA.
AC Q91Z05;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DE HYPOTHETICAL 51.9 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAH0327.1; -.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match          56.4%; Score 1420.5; DB 11; Length 473;
Best Local Similarity 56.9%; Pred. No. 1.7e-110;
Matches 269; Conservative 75; Mismatches 114; Indels 15; Gaps 5;

QY 7 ILFLVATATGVHSQVLQVSGAEVKKPGASVKVSKRAGTFTSYWQWVKQAPGGQLEW 66
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7 LVFLVLILKGVQCEVLQVSGGLVKGGRKLSLCAASGTFSDYGMHWVRQAPKEGLEW 66
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 67 MGEIDPSDSTYNNQKFKGKATLVDTSTAYMELSSLSRSEDYAVYICARNRDYSNNY 126
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 67 VAYINSGSTIYVADYTVKGRFTISRDNKNTLFLQMTSLRSEDYAMYYCAREL-----WL 121
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 127 --FDVWGGQGLTVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSG 184
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 122 RIDYWGQGTITTVSSAKTTPSVYPLAPGCGDTTGLGCLVKGYPESVTVTNWSS 181
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 185 ALTSGVHTFPVQLQSSGLYSLSVTVPSSSLGCTQYICNVNHPKSNKYDKRVEPKSCD 244
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 182 SLSSSVHTFPALLO-SGLYTMSSSVTPSWTPSQVTCVAHPASSTTVDDKLESGPI 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 245 KT-HTCPSV-----CPAPELLGGPSVFLPPKPKDMLMISRTPEVTCVVDVSHEDPEVK 297
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 STINPCPPCKECHKCAPNLEGGPSVFIIPNKLMLISLTLPKVTCTVVVDVSEDDPDVQ 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 298 FHWYVDGVEVHNNAKTKPREEQYNSTYRVSVLTVLHQDLWLNKGEYKCKVSNKALPAPIEK 357
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 ISMFVNNVVEHTAQTHREDYNSITRVVSALPIQHDWMSGKEFKCKVNNKDLPSPIER 360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 358 TTSKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFFYPSDIAVENESGQPNENYKTT 417
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 TTSKIKGLVRAQVYTLPPPAEQLSRKDYSLTCLVGFNPGDISVEMTNGHTEENYKDT 420
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 418 PPVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 470
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 APVLDSGDSFYISKLDIKTSKWEKTDSPSCNVRHEGLKNYILKTKTSRSPGK 473
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
Q95M34 PRELIMINARY; PRT; 337 AA.
ID Q95M34;
AC Q95M34;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE IMMUNOGLOBULIN GAMMA 1 HEAVY CHAIN CONSTANT REGION
GN (FRAGMENT).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Wagner B.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98383416; Pubmed=9717671;
RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
RA Leibold W., Radbruch A.;
RT "Organization of the equine immunoglobulin heavy chain constant region
RT genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL Immunobiology 199;105-119(1998).
DR EMBL; AJ300675; CAC44624.1; -.
FT NON_TER 1
SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;

Query Match          50.2%; Score 1263.5; DB 6; Length 337;
Best Local Similarity 68.9%; Pred. No. 1.4e-97;
Matches 233; Conservative 44; Mismatches 52; Indels 9; Gaps 3;

QY 141 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPVQLQSS 200
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 ASTTAPKVFALAPGCCGTTSDSTVALGCLVSGYFPEPEPKVYKSWNSGSLTSVHTFPVQLQSS 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 201 GLYSLSSVTVPSSSLGCTQYICNVNHPKSNKYDKRVEP-----KSCDKTHTCPPCPA 254
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 GFYSLSSVTVPASTWTSETYICNVVHAASNFVKDRRIEPIPDNHQKQCDMS-KCPKCPA 119
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 255 PELLGGPSVFLPPKPKDMLMISRTPEVTCVVDVSHEDPEVKNWYVDGVEVHNNAKTKP 314
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 120 PELLGGPSVFIIPNKKPDTLMTIRTPETVTCVVDVDSQENPDVKNWYMDGVEVHTATRP 179
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 315 REEQYNSTYRVSVLTVLHQDLWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 374
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 180 KEQQFNSTYRVSVLRIHQDLWLSGKEFKCKVNNQALPQPIERTITTKGRSQEPQVYVL 239
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 375 PPSREEMTKNOVSLTCLVKGFPSPDIAVEWESNGQP--ENNYKTTTPPVLDSDGSFFLYSK 432
Db 240 APHDELUSKSVSTCLVKDFPPEINIEWQSNQOPELETKYSTTQAQQSDGSFYLYSK 299

QY 433 LTVDKSRWQGNVFPSCSMHEALHNHYTQKSLSPGK 470
Db 300 LSVDRNRWQGTTCGVMHEALHNHYTQKNVKNPKG 337

RESULT 8
Q96PQ8 ID Q96P08 PRELIMINARY; PRT; 701 AA.
AC Q96P08:
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE FACTOR VII ACTIVE SITE MUTANT IMMUNOCOJUGATE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.;
RT "targeting tissue factor on tumor vascular endothelial cells and tumor
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
DR EMBL; AF272774; AAK58686.1; -.
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;

Query Match 49.9%; Score 1257; DB 4; Length 701;
Best Local Similarity 99.1%; Pred. No. 1.4e-96;
Matches 230; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 239 EPKSCDTHTCPPCPAPPELLGGPSVFLFPPKPKDITLMSRTPEVTCVVVDVSHEDPEVKF 298
Db 470 EPKSCDTHTCPPCPAPPELLGGPSVFLFPPKPKDITLMSRTPEVTCVVVDVSHEDPEVKF 529

QY 299 NWYVDGVEVHNAKTKPREQYNSRYRVSVLTVLHODWLNKKEYCKVSNKALPAPTEKT 358
Db 530 NWYVDGVEVHNAKTKPREQYNSRYRVSVLTVLHODWLNKKEYCKVSNKALPAPTEKT 589

QY 359 ISKAKGQPREPQVYVTLPPPSREEMTKNOVSLTCLVKGFPSPDIAVEWESNGQPENNYKTTP 418
Db 590 ISKAKGQPREPQVYVTLPPSRDELTKNOVSLTCLVKGFPSPDIAVEWESNGQPENNYKTTP 649

QY 419 PVLDSGSGFFLYSKLTVDKSRWQGNVFPSCSMHEALHNHYTQKSLSPGK 470
Db 650 PVLDSGSGFFLYSKLTVDKSRWQGNVFPSCSMHEALHNHYTQKSLSPGK 701

RESULT 9
Q921K1 ID Q921K1 PRELIMINARY; PRT; 278 AA.
AC Q921K1:
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE UNKNOWN (PROTEIN FOR MGC:18977).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012207; AAH12207.1; -.
SQ SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;

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Query Match 39.2%; Score 986; DB 11; Length 278;
Best Local Similarity 67.5%; Pred. No. 1.8e-74;
Matches 187; Conservative 32; Mismatches 50; Indels 8; Gaps 3;

QY 1 MGWSCIILFLVATATGVHSGAEVKKPGASVKVSKCKASGYTFTSYMMQWVKQAP 60
Db 1 MGWSCIILFLVATATGVHSGAEVKKPGASVKVSKCKASGYTFTSYMMQWVKQAP 60

QY 61 GGLEWMEIDPDSYTNYNOKFKGKATLTVDSTSTAYMELSSLRSDTAYVYCARNRD 120
Db 61 GGLEWMEIDPDSYTNYNOKFKGKATLTVDSTSTAYMELSSLRSDTAYVYCARNRD 120

QY 121 YSNWYFDVWQGTTLVTVSSASTKGPSVFLPAPLAPSKSTSGTAAALGCLVKDYFPEPVTVS 180
Db 121 Y-DDVYFDVWQGTTLVTVSSASTKGPSVFLPAPLAPSKSTSGTAAALGCLVKDYFPEPVTVS 180

QY 181 WNSGALTSQVHTFPVAVLQSSGLYSLSSVTVTPSSSLGTTQYICNVNHNKPSNTKVDKRVPE 240
Db 180 WNSGALTSQVHTFPVAVLQSSGLYSLSSVTVTPSSSLGTTQYICNVNHNKPSNTKVDKRVPE 240

QY 241 K-----SCDKTHTCPPCPAPPELLGGPSVFLFPPKPK 271
Db 239 RVPITQNPCLPKCEPCCAAPDLGLGSPVFIFPPRSR 275

RESULT 10
Q96GA6 ID Q96GA6 PRELIMINARY; PRT; 614 AA.
AC Q96GA6:
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE UNKNOWN (PROTEIN FOR MGC:15420).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009851; AAH09851.1; -.
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match 36.8%; Score 927.5; DB 4; Length 614;
Best Local Similarity 36.6%; Pred. No. 4.3e-63;
Matches 211; Conservative 85; Mismatches 166; Indels 115; Gaps 17;

QY 1 MGWSCIILFLVATATGVHSGAEVKKPGASVKVSKCKASGYTFTSYMMQWVKQAP 60
Db 1 MDWTWRIILFLVAATDAYSQMLVQSGAEVKKTKGSSVKVSKCKASGYTFTSYLHVVRQAP 60

QY 61 GGLEWMEIDPDSYTNYNOKFKGKATLTVDSTSTAYMELSSLRSDTAYVYCARNRD 120
Db 61 GQALEWGWITPFGNTNTYAKQFQDRVTITRDRSMNTAYMELSSLRSDTAYVYCARC-- 118

QY 121 YSNW--YFDVWQGTTLVTVSSASTKGPSVFLPAPLAPSKSTSG-GTAAALGCLVKDYFPEPV 177
Db 119 YSSWDDAFDIWGGTWTMTVSSGSASAPTLFPLVSCNSPSTSSVAVGCLAQFLPDISI 178

QY 178 TVSW--NSGALTSQVHTFPVAVLQSSGLYSLSSVTVTPSSSL--GTQTY-ICNVNHNKPSN- 231
Db 179 TFSWKYKNNSDISSTRGFPVSLR-GGKYAATSQVLLPSKDVQMGCTDEHVVCVKQHPGNK 237

QY 232 -----TKVDKRVPEPKS-----CDKTHTCP----- 250
Db 238 EKNVPLPVIAELPPKVSFVFPDRGFCGNPRKSLKICQATGFSRQIQVSWLREGKQVGS 297

QY 251 -----PCPAPPELLGSPS----- 262
Db 298 GVTTDQVOAEAKESGPTTYKVTSTLTIKESDWLSQSMTFCRDVHRGLTFTQONASSMCMCPD 357

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 15:15:37 ; Search time 230.21 seconds  
(without alignments)  
226.770 Million cell updates/sec

Title: US-09-499-662-145

Perfect score: 2517

Sequence: 1 MWGSCILFLVATATGVHSQ.....MHEALHNYTQKSLSPCK 470

Scoring table:

BLOSUM62DX

Gapop 10.0 , Gapext 0.5.

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_032802.\*  
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2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.\*  
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6: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.\*  
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12: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.\*  
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22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2517	100.0	470	21	AAW90934 Humanised anti-Fas
2	2515	99.9	470	21	AAW90933 Humanised anti-Fas
3	2512	99.8	470	19	AAW83037 Anti-Fas humanised
4	2512	99.8	470	21	AAW14779 Humanised anti-Fas
5	2512	99.8	470	21	AAW90929 Humanised HFE7A de
6	2512	99.8	470	21	AAW90935 Humanised anti-Fas
7	2499	99.3	470	19	AAW83036 Anti-Fas humanised
8	2499	99.3	470	21	AAW14776 Humanised anti-Fas
9	2499	99.3	470	21	AAW90926 Humanised HFE7A de
10	2497	99.2	470	21	AAW90936 Humanised HFE7A de
11	2348.5	93.3	731	22	AAW52156 Humanised HMFV-1 h

12	2348.5	93.3	741	22	AAW52159 Humanised HMFV-1 h
13	2343.5	93.1	729	22	AAW52158 Humanised HMFV-1 h
14	2343.5	93.1	739	22	AAW52161 Humanised HMFV-1 h
15	2337.5	92.9	730	22	AAW52157 Humanised HMFV-1 h
16	2337.5	92.9	740	22	AAW52160 Humanised HMFV-1 h
17	2303	91.5	652	19	AAW48650 Heavy chain of hma
18	2290.5	91.0	465	22	AAW72228 Humanised 323/A3 (
19	2285.5	90.8	464	22	AAW72232 Humanised 323/A3 (
20	2285	90.8	470	21	AAW808026 A dimeric anti-CD2
21	2284	90.7	466	22	AAW03755 Chimeric 2403 IgG
22	2254	89.6	476	20	AAW98464 Monoclonal antibody
23	2253.5	89.5	481	13	AAW44442 Sequence of antibody
24	2246	89.2	472	20	AAW50166 Human reshaped Flg
25	2232	88.7	476	14	AAW31023 Antibody D heavy c
26	2231.5	88.7	583	22	AAW83156 Ganglioside GM2 an
27	2230	88.6	449	14	AAW43339 Completely humanis
28	2230	88.6	449	19	AAW49816 Amino acid sequenc
29	2200.5	87.4	467	22	AAW36210 Human immune syste
30	2198.5	87.3	452	20	AAW29458 Recombinant immuno
31	2198.5	87.3	452	21	AAW30322 Humanised anti-IL-
32	2198.5	87.3	452	21	AAW77766 Humanised anti-IL-
33	2198	87.3	472	20	AAW50157 Chimeric mouse/hum
34	2191	87.0	592	22	AAW83838 Amino acid sequenc
35	2189.5	87.0	452	19	AAW93316 Anti-IL-8 humanise
36	2188	86.9	474	22	AAW14177 Human novel protei
37	2188	86.9	595	20	AAW86003 Anti-5T4 single ch
38	2186.5	86.9	473	22	AAW64475 Human type antihum
39	2183.5	86.8	473	22	AAW64471 Human type antihum
40	2183.5	86.8	475	22	AAW63640 Amino acid sequenc
41	2178.5	86.6	473	22	AAW64469 Human type antihum
42	2177	86.5	468	20	AAW5689 D9D10 heavy chain
43	2177	86.5	711	20	AAW85692 MoTabII fusion pro
44	2171.5	86.3	473	22	AAW64473 Human type antihum
45	2161	85.9	470	13	AAW22757 Reshaped CAMPATH-1

ALIGNMENTS

RESULT 1

AAW90934

ID AAW90934 standard; Protein; 470 AA.

AC AAW90934;

DT 08-AUG-2000 (first entry)

DE Humanised anti-Fas designed heavy chain Heu 2 protein.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
XX anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;  
XX dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
XX nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;  
XX hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
XX Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
XX Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
XX Goodpasture syndrome; Crohn's disease; thrombopenia purpura; allergy;  
XX multiple sclerosis; Basedow's disease; arteriosclerosis; myocarditis;  
XX insulin dependent diabetes mellitus; hepatitis; transplant rejection.  
XX cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

OS Synthetic.

XX EP990663-A2.

PN 05-APR-2000.

XX 29-SEP-1999; 99EP-0307711.

XX 30-SEP-1998; 98JP-0276881.

XX 30-SEP-1998; 98JP-0276882.

XX (SANY ) SANKYO CO LTD.

PA

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 PI WPI: 2000-258930/23.  
 XX N-PSDB; AAA11645.  
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems -  
 XX Claim 2 : Page 174-176; 263pp; English.  
 XX This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antiartherosclerotic, cardiatic and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody heavy chain construct designated Heu 2  
 CC which is described in the method of the invention.  
 XX Sequence 470 AA:  
 SQ

Query Match 100.0%; Score 2517; DB 21; Length 470;  
 Best Local Similarity 100.0%; Pred. NO. 4.4e-143;  
 Matches 470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVATATGVHSGVQLVQSGAEVKKPGASVKVKSCASGVTFTSYMQWVKQAP 60  
 DB 1 mgwscililflvatatgvhsgvqlvqsgaevkpgasvkvsckasgytftsywmqwkqap 60  
 QY 61 GCGLEWMEIDPSDSTNTNOKFKGKATITVDTSTSTAYMEISSLSEDTAVYVCARNRD 120  
 DB 61 gggilewmeidpsdstyntnqkfkgkatitvdtststaymeisslrse dtavyvcarn-d 120  
 QY 121 YSNWNVDFYWGQGLTVTSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDFPPEPTVTS 180  
 DB 121 ysnwnyfdvwgqgltvtsastkgpsvfplapskstsggtaalgclvkdyfppeptvts 180  
 QY 181 WNSGALTSVGHVFPVQLQSGSLYSLSVTVSPSSSLGQTQTYICNVNWKPSNTKVDKRVVP 240  
 DB 181 wnsгалtsvghvfpvqlqsgslsylvstvpssslgtqtyicnvnhkpsn tkvdkrvvp 240  
 QY 241 KSCDKHTCCPCPAPPELLGGPSVFLFPPPKDITLMTSRPEVTCVVVDVSHEDPEVKENW 300  
 DB 241 kscdkhtccpcpapellggpsvflfppkpditlmsrtpevtcvvvdvshedepevkfw 300  
 QY 301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTIS 360  
 DB 301 yvdgvevhnaktkpreeqynstyrvvsvltvlhqlngkeykckvsnkalpapi ektis 360  
 QY 361 KAKGQPREPQVYTLPPSREMTKNQVSLTCLVKGFPSDIAVWESNGQPENNYKTTTPV 420  
 DB 361 kkgqprepqvtytlppsreemtknqvsltclvkgfypsdiavwesngqpennykttppv 420

Db 361 kkgqprepqvtytlppsreemtknqvsltclvkgfypsdiavwesngqpennykttppv 420  
 QY 421 LDSGGSFFLYSKLTVDKSRWQGNVPSCSVMHEALHNHYTKQKLSLSPGK 470  
 DB 421 ldsdgsfflyskltvdksrwqgnvfscsvmhealhnhytcqkslsispgk 470  
 RESULT 2  
 AAW90933  
 ID AAW90933 standard; Protein; 470 AA.  
 XX  
 AC AAW90933;  
 XX  
 DT 08-AUG-2000 (first entry)  
 XX  
 DE Humanised anti-Fas designed heavy chain Heu 1 protein.  
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiatic;  
 KW dermatological; immunosuppressive; thyromimetic; antiartherosclerotic;  
 KW nephrotropic; antinfertility; neuroprotective; antiartherosclerotic;  
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KW Goodpasture syndrome; Crohn's disease; myasthenia gravis;  
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
 XX Synthetic.  
 OS  
 XX EP990663-A2.  
 PN  
 XX 05-APR-2000.  
 PD  
 XX 29-SEP-1999; 99EP-0307711.  
 PF  
 XX 30-SEP-1998; 98JP-0276881.  
 PR  
 XX 30-SEP-1998; 98JP-0276882.  
 XX  
 PA (SANY ) SANKYO CO LTD.  
 XX  
 PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 XX  
 DR WPI: 2000-258930/23.  
 DR N-PSDB; AAA11644.  
 XX  
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems -  
 XX  
 PS Claim 2; Page 169-170; 263pp; English.  
 XX This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antiartherosclerotic, cardiatic and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively

CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
CC cells. They bind to both human and murine Fas, so can be evaluated in  
CC murine disease models. (1) act on the active site of Fas, i.e. they mimic  
CC the native ligand, do not induce liver disease, and have reduced risk of  
CC inducing a human anti-murine antibody response. This sequence represents  
CC a humanised anti-Fas antibody heavy chain construct designated Heu 1  
CC which is described in the method of the invention.

XX SQ Sequence 470 AA;

Query Match 99.98; Score 2515; DB 21; Length 470;  
Best Local Similarity 99.88; Pred. No. 5.8e-143;  
Matches 469; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWQWVKQAP 60  
Db 1 mgwscilflvatatgvhsqvlvqsgaeavkpgasvkvsckasgytftsywqwkqap 60  
QY 61 GQLEWNGEIDPSQSYNYNOKFKGKATITVDTSTSTAYMELSLRSEDVAVYICARNRD 120  
Db 61 gqglewngeidpsdsytnyngdkfgkatitvdtststaymelslrseadvavyicarnrd 120  
QY 121 YSNWYFDVWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKKDYFEPPTVTS 180  
Db 121 ysnwyfdvwwgqglvtvssastkgpsvfplapssksts gtaalgclvkkdyfepptvts 180  
QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGQTQYICNVNHPKSNTKVDKRVPE 240  
Db 181 wnsгалtsgvhtfpavlgssglyslssvstvtpssslgqtqyicnvnhpkpsntkvdkrvpe 240  
QY 241 KSCDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300  
Db 241 kscdkthctcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw 300  
QY 301 YVDGVEVHNATKPREQYNSTYRVVSVLTVLHDWLGNGKEYCKVSNKALPAPIEKTIS 360  
Db 301 yvdgvevhnatkpreqynstyrvvsvltvldwlngkeyckvsnkalpapiektis 360  
QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 420  
Db 361 kakgqprepqvtytlppsreemtknqvs ltc lkv gfy psdiavewesngqpennykttppv 420  
QY 421 LDSGSEFLYSLKLVDRKRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470  
Db 421 ldsdgsfflysklvtvdkrsrwqgnvfscsvmh ealhnhytqkslsispgk 470

RESULT 3

ID AAW83037 standard; Protein; 470 AA.

XX AC AAW83037;

XX DT 15-MAR-1999 (first entry)

XX DE Anti-Fas humanised antibody HFE7A heavy chain.

KW HFE7A: monoclonal antibody; mouse; Fas; humanised antibody;  
KW apoptosis; HFE7A: autoimmune disease; Hashimoto's disease;  
KW systemic lupus erythematosus; graft versus host disease;  
KW Sjogren syndrome; pernicious anaemia; Addison's disease;  
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
KW rheumatoid arthritis; autoimmune haemolytic anaemia;  
KW myasthenia gravis; multiple sclerosis; Basedow's disease;  
KW thrombopenia purpura; insulin-dependent diabetes; allergy;  
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
KW transplant rejection; therapy.

OS Homo sapiens.

OS Synthetic.

XX

Query Match 99.8%; Score 2512; DB 19; Length 470;  
Best Local Similarity 99.6%; Pred. No. 8.8e-143;

SQ Sequence 470 AA;

FH Key Location/Qualifiers  
FT Peptide 1..19  
FT Protein /label= Sig\_peptide  
FT 20..470  
FT /label= Mat\_protein  
FT Region 20..140  
FT /label= Variable  
FT Region 141..464  
FT /label= Constant  
FT Region 50..54  
FT /label= CDR\_H1  
FT /note= "Claim 9"  
FT Region 69..84  
FT /label= CDR\_H2  
FT /note= "claim 9"  
FT Region 118..129  
FT /label= CDR\_H3  
FT /note= "claim 9"

XX AU9859701-A.

XX 08-OCT-1998.

XX 30-MAR-1998; 98AU-0059701.

XX 08-OCT-1997; 97JP-0276064.

XX 01-APR-1997; 97JP-0082953.

XX 25-JUN-1997; 97JP-0169088.

XX (SANY ) SANKYO CO LTD.

XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;

XX Masahiko O, Nobufusa S, Shin Y, Tohru T;

XX WPI; 1998-543440/47.

XX N-PSDB; AAV70080.

DR New antibodies and proteins bind conserved epitope of Fas antigen -  
XX used to evaluate drugs in animal models and to treat Fas-associated  
XX diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
XX myocarditis, hepatitis and AIDS

PS Claim 22; Page 225-227; 292pp; English.

XX This is the amino acid sequence of the HV type humanised heavy  
CC chain of murine anti-human Fas monoclonal antibody HFE7A. It  
CC includes humanising R44G and A76T amino acid substitutions that are  
CC conserved in the human IgG heavy chain. Host Escherichia coli  
CC pgHPDHV3 SANK 70298 harbors plasmid pgHPDHV3 carrying a fusion  
CC fragment of the humanised HV type HFE7A heavy chain and DNA  
CC as FERM gp-6273 (Claimed). The invention provides methods for  
CC producing humanised antibodies by culturing host cells. Humanised  
CC versions of HFE7A (see AAW83031-37), like native HFE7A, are capable  
CC of inducing apoptosis in abnormal cells expressing Fas, and of  
CC inhibiting Fas-induced apoptosis in normal cells. The humanised  
CC antibodies are used to evaluate, in animal models, treatments of  
CC diseases that involve Fas/Fas ligand interactions, and also to  
CC treat such diseases, including autoimmune disease (e.g. systemic  
CC lupus erythematosus, Hashimoto's disease, graft versus host disease,  
CC Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,  
CC Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,  
CC autoimmune haemolytic anaemia, sterility, myasthenia gravis,  
CC multiple scleritis, Basedow's disease, thrombopenia purpura and  
CC insulin-dependent diabetes), allergies, atopy, arteriosclerosis,  
CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic  
CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).

Matches 468; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVATATGVSQVQLVQSGAEVKKPGASVKVCKASGAGTFTSYWQWVKQAP 60  
Db 1 mgwsciilflvatatgvsqvlvqsgaevkkpgasvkvckasgytftsywmqwkqap 60

QY 61 GQGLEWNGEITDPSDSTYNNQKFKGKATITVDSTSTAYMELSSLRSEDFAVYYCARNRD 120  
Db 61 gqglewngeltdpsdsytnynqkfkgtatltvdtststaymelslsrsedcavyyccarnrd 120

QY 121 YSNWNYFDVWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGTAAALCLVLDYFPEPTVS 180  
Db 121 ysnwnyfdvwgqgltvvtssastkgpsvflpapskstsrgtaalclvldyfpptvs 180

QY 181 WNSGALTSVHTTTPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKRVPE 240  
Db 181 wnsгалtsvhttpavllqssglyslssvtpvssslgtqtyicnvnhkpsntkvdkrvpe 240

QY 241 KSCDKHTCPCPAPPELLGGPSVFLPAPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300  
Db 241 kscdkhtcpcpapellggpsvflpapkdtlmisrtpevtcvvvdvshedpevkfnw 300

QY 301 YVDGVEVHNKTKPREQYNSTYRVVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTIS 360  
Db 301 yvdgvevhnaktpreeqynstyrvvsvltvlhqdnlngkeyckvsnkalpapiektis 360

QY 361 KAKGQPREQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420  
Db 361 kagqpreqvtytlppsreemtknqvslltclvkgyfypsdiavewesngqpennnykttppv 420

QY 421 LDSGSEFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKLSLSPGK 470  
Db 421 ldsdgsfflyskltvdksrwqgnvfscsvmhcalhnhytqklsispgk 470

RESULT 4  
AAB14779 standard; Protein; 470 AA.

XX AAB14779;  
XX 24-NOV-2000 (first entry)  
XX Humanised anti-Fas antibody heavy chain, SEQ ID NO:117.

XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;  
KW murine; humanised antibody; complementarity determining region; CDR;  
KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;  
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;  
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;  
KW hepatitis; AIDS; graft rejection; heavy chain.

XX Chimeric - Mus musculus.  
OS Chimeric - Homo sapiens.  
XX JP2000169393-A.  
XX 20-JUN-2000.  
XX 30-SEP-1999; 99JP-0278301.  
XX 30-SEP-1999; 98JP-0276883.  
XX (SANY ) SANKYO CO LTD.  
XX WPI: 2000-485645/43.  
DR N-PSDB; AAB72184.  
XX Preventive or treating agent for the diseases caused by an abnormality  
PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains  
PT anti-Fas antibody -  
XX Claim 21; Page 108-109; 139pp; Japanese.

XX The invention relates to compositions for the prevention or treatment  
CC of diseases caused by an abnormality in the Fas/Fas ligand system  
CC containing an anti-Fas antibody as the active component. The anti-Fas  
CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,  
CC or a humanised version of HFE7A containing identical CDRs  
CC (complementarity determining regions) to antibody HFE7A. Via its  
CC interaction with Fas, the antibody of the invention acts as a modulator  
CC of apoptosis. The composition of the invention may therefore be used in  
CC the treatment or prevention of conditions such as autoimmune diseases,  
CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,  
CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS  
CC and organ graft rejection. Sequences AAB14775-B14776 and AAB14779  
CC represent the heavy chains (or fragments thereof) of various humanised  
CC HFE7A-derived anti-Fas antibodies.

XX Sequence 470 AA;  
SQ

Query Match 99.8%; Score 2512; DB 21; Length 470;  
Best Local Similarity 99.6%; Pred. No. 8.8e-143;  
Matches 468; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVATATGVSQVQLVQSGAEVKKPGASVKVCKASGAGTFTSYWQWVKQAP 60  
Db 1 mgwsciilflvatatgvsqvlvqsgaevkkpgasvkvckasgytftsywmqwkqap 60

QY 61 GQGLEWNGEITDPSDSTYNNQKFKGKATITVDSTSTAYMELSSLRSEDFAVYYCARNRD 120  
Db 61 gqglewngeltdpsdsytnynqkfkgtatltvdtststaymelslsrsedcavyyccarnrd 120

QY 121 YSNWNYFDVWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGTAAALCLVLDYFPEPTVS 180  
Db 121 ysnwnyfdvwgqgltvvtssastkgpsvflpapskstsrgtaalclvldyfpptvs 180

QY 181 WNSGALTSVHTTTPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKRVPE 240  
Db 181 wnsгалtsvhttpavllqssglyslssvtpvssslgtqtyicnvnhkpsntkvdkrvpe 240

QY 241 KSCDKHTCPCPAPPELLGGPSVFLPAPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300  
Db 241 kscdkhtcpcpapellggpsvflpapkdtlmisrtpevtcvvvdvshedpevkfnw 300

QY 301 YVDGVEVHNKTKPREQYNSTYRVVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTIS 360  
Db 301 yvdgvevhnaktpreeqynstyrvvsvltvlhqdnlngkeyckvsnkalpapiektis 360

QY 361 KAKGQPREQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420  
Db 361 kagqpreqvtytlppsreemtknqvslltclvkgyfypsdiavewesngqpennnykttppv 420

QY 421 LDSGSEFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKLSLSPGK 470  
Db 421 ldsdgsfflyskltvdksrwqgnvfscsvmhcalhnhytqklsispgk 470

RESULT 5  
AAW90929 standard; Protein; 470 AA.

XX AAW90929;  
XX 08-AUG-2000 (first entry)  
XX Humanised HFE7A designed heavy chain protein #2.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;  
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
KW nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;  
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;





CC apoptosis in cells with a normal system, by inhibiting binding between  
CC Fas and its ligand. The products of the invention have anti-inflammatory,  
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,  
CC antiarteriosclerotic, cardiant and hepatotropic activity. (I) induce  
CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
CC inhibition of ligand binding. (II) are used to treat and/or prevent  
CC diseases associated with the Fas/Fas ligand system, especially systemic  
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
CC cells. They bind to both human and murine Fas, so can be evaluated in  
CC murine disease models. (II) act on the active site of Fas, i.e. they mimic  
CC the native ligand, do not induce liver disease, and have reduced risk of  
CC inducing a human anti-murine antibody response. This sequence represents  
CC a humanised anti-Fas antibody heavy chain construct designated Heu 3  
CC which is described in the method of the invention.

XX Sequence 470 AA;

Query Match 99.8%; Score 2512; DB 21; Length 470;  
Best Local Similarity 99.6%; Pred. No. 8.8e-143;  
Matches 468; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCIILFVATGCVHQSQVLQSGAEVKKPGASVKYSCKASGYFTFSYMWQWYKQAP 60  
DB 1 mgwsciilflvatgcvhqsqvlqsgaevkkgpgasvkysckasgyftfswmwwvrrqp 60  
QY 61 GQGLEWMEIDPSDSTNTNQKFKGKATITVDSTSTAYMELSSLRSEDATVYICARNRD 120  
DB 61 gqglewmeidpsdstyntnqkfkgkatitvdststaymelsslrsestavyvycarnrd 120  
QY 121 YSNWYFDVWGQGLTVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVYS 180  
DB 121 ysnwyfdvwgqglvtvssastkgpsvflapsskstsggtaalgclvkdypfepvptvs 180  
QY 181 WNSGALTSQVHTFPAPVLOSGLYSLSVVTVFPSSSLGTQTYICNVNHPKSNTKVDKRVEP 240  
DB 181 wnsгалtsqvhtfpavlosgylsylvstvfpssslgtqtyicnvnhpkpntkvdkrvep 240  
QY 241 KSCDKTHTCPCPAPPELLGSPSVFLFPPKPKDTLMISRTPEVTCVVYVDSHEDPEVKFNW 300  
DB 241 kscdkthtccpccpapellgspsvflfppkpkdtlmisrtpevtcvvyvdsheedpevkfnw 300  
QY 301 YVDGVEVHNAKTKPREQYNSTRYVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 360  
DB 301 yvdgvevhnaaktpreeqynstryvsvltvlhqdwlngkeyckvsnkalpapiektis 360  
QY 361 KAKGQPREPVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 420  
DB 361 kagqprepvtytlppsreemtkngvsltclvkgfypsdiavewesngqpennyyktppv 420  
QY 421 LQSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTKQSLSPGK 470  
DB 421 lqsdgsfflyskltvdksrwqqgnvfscvsmhealhnytkqslslspgk 470

RESULT 7

ID AAWB3036 standard; Protein; 470 AA.

XX AAWB3036;

XX 15-MAR-1999 (first entry)

XX

DE Anti-Fas humanised antibody HFE7A heavy chain.  
XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;  
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;  
KW systemic lupus erythematosus; graft versus host disease;  
KW Sjogren syndrome; pernicious anaemia; Addison's disease;  
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
KW rheumatoid arthritis; autoimmune haemolytic anaemia;  
KW myasthenia gravis; multiple sclerosis; Basedow's disease;  
KW thrombopenia purpura; insulin-dependent diabetes; allergy;  
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy; AIDS;  
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
KW transplant rejection; therapy.  
OS Homo sapiens.  
OS Synthetic.  
Key Location/Qualifiers  
FT Peptide 1..19 /label= sig\_peptide  
FT Protein 20..470 /label= Mat\_protein  
FT Region 20..140 /label= Variable  
FT Region 141..464 /label= Constant  
FT Region 50..54 /label= CDR\_H1  
FT Region 69..84 /label= CDR\_H2  
FT Region 118..129 /label= CDR\_H3  
FT Region 118..129 /note= "claim 9"  
FT Region 118..129 /label= CDR\_H3  
FT Region 118..129 /note= "claim 9"  
XX AU9859701-A.  
XX 08-OCT-1998.  
XX 30-MAR-1998; 98AU-0059701.  
XX 08-OCT-1997; 97JP-0276064.  
XX 01-APR-1997; 97JP-0082953.  
XX 25-JUN-1997; 97JP-0169088.  
XX (SANY ) SANKYO CO LTD.  
XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;  
XX Masahiko O, Nobufusa S, Shin Y, Tohru T;  
XX WPI; 1998-543440/47.  
XX N-PSDB; AAV70079.  
XX New antibodies and proteins bind conserved epitope of Fas antigen -  
XX used to evaluate drugs in animal models and to treat Fas-associated  
XX diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
XX myocarditis, hepatitis and AIDS  
PS Claim 22; Page 212-213; 292pp; English.  
XX This is the amino acid sequence of the VD type humanised heavy  
XX chain of murine anti-human Fas monoclonal antibody HFE7A. E. coli  
XX pgHSL7A62 SANK 73397 harbors plasmid pgHSL7A62 carrying a fusion  
XX fragment of the humanised VD type HFE7A heavy chain and DNA  
XX encoding human IgG1 constant region (see AAV70079), and is deposited  
XX as FERM BP-6074 (claimed). The invention provides methods for  
XX producing humanised antibodies by culturing host cells. Humanised  
XX versions of HFE7A (see AAW83031-37), like native HFE7A, are capable  
XX of inducing apoptosis in abnormal cells expressing Fas, and of  
XX inhibiting Fas-induced apoptosis in normal cells. The humanised  
XX antibodies are used to evaluate, in animal models, treatments of  
XX diseases that involve Fas/Fas ligand interactions, and also to

CC treat such diseases, including autoimmune disease (e.g. systemic  
CC lupus erythematosus, Hashimoto's disease, graft versus host disease,  
CC Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,  
CC Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,  
CC autoimmune haemolytic anaemia, sterility, myasthenia gravis,  
CC multiple sclerosis, Basedow's disease, thrombopenia purpura and  
CC insulin-dependent diabetes), allergies, atopy, arteriosclerosis,  
CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic  
CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).  
XX  
SQ Sequence 470 AA;

Query Match 99.3%; Score 2499; DB 19; Length 470;  
Best Local Similarity 99.1%; Pred. No. 5.3e-142;  
Matches 466; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 MGWSCIIILFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCKASGYFTSTYMWQVVKQAP 60  
Db 1 mgwsciiilflvatatgvhsqvlvqsgaevkpgasvkvsckasgyftstymwqvkqap 60  
Qy 61 GQGLEWMGEIDPSDSTNYNOKFKGKATITVDTSTAYMELSLRSEDATVYYCARNRD 120  
Db 61 gqglewmgeidpsdstnyngkfkgkatltvdtstastaymelslrseadtavyyccarnrd 120  
Qy 121 YSNNNWYFDVWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180  
Db 121 ysnnnwyfdvweglvtvssastkgpsvfplapsskstsggtaalgclvdyfpeptvts 180  
Qy 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVEP 240  
Db 181 wnsгалtsгvhtfpavllqssglyslssvtpvssslgtqtyicnvnhnkpsntkvdkrvеп 240  
Qy 241 KSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300  
Db 241 kscdkthtccpсpаpеllggpsvflfppkpkdtlmisrtpevtcvvdshedpevkfnw 300  
Qy 301 YVDGVEVHNATKPREQYNSTYRVVSVLTVLHODWLNKGKEYCKVSNKALPAPIETKIS 360  
Db 301 yvdgvevhnatkpreqynstyrvvsvlvtlhdwlngkeyckvsnkalpapietkis 360  
Qy 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNKTTPPV 420  
Db 361 kkgqprepqvtytlppsreemtknqvsltcclvkgyfypsdiavewesngopennykttppv 420  
Qy 421 LDSGGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470  
Db 421 ldsdgsfflyskltvdksrwqgnvfscsvmhеalhnhytqkslspsgk 470

RESULT 8  
AAB14776  
ID AAB14776 standard; Protein: 470 AA.  
AC AAB14776;  
XX  
XX 24-NOV-2000 (first entry)  
XX  
XX Humanised anti-Fas antibody heavy chain, SEQ ID NO:89.  
XX  
KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;  
KW murine; humanised antibody; complementarity determining region; CDR;  
KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;  
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;  
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;  
KW hepatitis; AIDS; graft rejection; heavy chain.  
XX  
OS Chimeric - Mus musculus.  
OS Chimeric - Homo sapiens.  
XX  
XX JP2000169393-A.  
XX  
XX 20-JUN-2000.

XX 30-SEP-1999; 99JP-0278301.  
XX 30-SEP-1998; 98JP-0276883.  
XX (SANY ) SANKYO CO LTD.  
XX WPI; 2000-485645/43.  
XX N-PSDB; AAA72159.  
XX  
XX Preventive or treating agent for the diseases caused by an abnormality  
XX in the Fas/Fas ligand system e.g. autoimmune diseases, contains  
XX anti-Fas antibody -  
XX  
XX Claim 21; Page 95-96; 139pp; Japanese.  
XX  
XX The invention relates to compositions for the prevention or treatment  
XX or diseases caused by an abnormality in the Fas/Fas ligand system  
XX containing an anti-Fas antibody as the active component. The anti-Fas  
XX antibody is either the murine anti-human Fas monoclonal antibody HFE7A,  
XX or a humanised version of HFE7A containing identical CDRs  
XX (complementarity determining regions) to antibody HFE7A. Via its  
XX interaction with Fas, the antibody of the invention acts as a modulator  
XX of apoptosis. The compositions of the invention may therefore be used in  
XX the treatment or prevention of conditions such as autoimmune diseases,  
XX allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,  
XX glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS  
XX and organ graft rejection. Sequences AAB14775-B14776 and AAB14779  
XX represent the heavy chains (or fragments thereof) of various humanised  
XX HFE7A-derived anti-Fas antibodies.  
XX  
SQ Sequence 470 AA;

Query Match 99.3%; Score 2499; DB 21; Length 470;  
Best Local Similarity 99.1%; Pred. No. 5.3e-142;  
Matches 466; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 MGWSCIIILFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCKASGYFTSTYMWQVVKQAP 60  
Db 1 mgwsciiilflvatatgvhsqvlvqsgaevkpgasvkvsckasgyftstymwqvkqap 60  
Qy 61 GQGLEWMGEIDPSDSTNYNOKFKGKATITVDTSTAYMELSLRSEDATVYYCARNRD 120  
Db 61 gqglewmgeidpsdstnyngkfkgkatltvdtstastaymelslrseadtavyyccarnrd 120  
Qy 121 YSNNNWYFDVWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180  
Db 121 ysnnnwyfdvweglvtvssastkgpsvfplapsskstsggtaalgclvdyfpeptvts 180  
Qy 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVEP 240  
Db 181 wnsгалtsгvhtfpavllqssglyslssvtpvssslgtqtyicnvnhnkpsntkvdkrvеп 240  
Qy 241 KSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300  
Db 241 kscdkthtccpсpаpеllggpsvflfppkpkdtlmisrtpevtcvvdshedpevkfnw 300  
Qy 301 YVDGVEVHNATKPREQYNSTYRVVSVLTVLHODWLNKGKEYCKVSNKALPAPIETKIS 360  
Db 301 yvdgvevhnatkpreqynstyrvvsvlvtlhdwlngkeyckvsnkalpapietkis 360  
Qy 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNKTTPPV 420  
Db 361 kkgqprepqvtytlppsreemtknqvsltcclvkgyfypsdiavewesngopennykttppv 420  
Qy 421 LDSGGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470  
Db 421 ldsdgsfflyskltvdksrwqgnvfscsvmhеalhnhytqkslspsgk 470

RESULT 9  
AAW90926

AAW90926 standard; Protein; 470 AA.

AAW90926;

08-AUG-2000 (first entry)

Humanised HFE7A designed heavy chain protein.

Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

Synthetic.

EP990663-A2.

05-APR-2000.

29-SEP-1999; 99EP-0307711.

30-SEP-1998; 98JP-0276881.

30-SEP-1998; 98JP-0276882.

(SANY ) SANKYO CO LTD.

Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T; WPI: 2000-258930/23.

N-PSDB; AA11597.

New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems -

Example reference 15; Page 134-136; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antiinfertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody HFE7A designed heavy chain which is used in the method described in the invention.

Sequence 470 AA;

Query Match 99.3%; Score 2499; DB 21; Length 470;  
Best Local Similarity 99.1%; Pred. No. 5.3e-142;  
Matches 466; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGWSCIIILFLVATATGVHSQVLVQSGAEVKKPGCASVKVSKASGYTFTSYWMQVVKQAP 60  
Db 1 mgwsciiilflvatatgvhsqvlvqsgaevkkpgcasvkvsckasgytftsywmqvwkqap 60  
QY 61 GCGLEWNGETDPSDSYTNYNQKPKGKATINVDISTPAYMELSLRSEDPAVYVCARNRD 120  
Db 61 gqrlwmgeltdpsdsytnynqkfkxkatlvtvdsastaymelslrsecdavyyccarnrd 120  
QY 121 YSNWTFDVMGQCTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180  
Db 121 ysnwtfdvwmgqctlvtvssastkgpsvfplapssksts gtaalgclvkdypcptvts 180  
QY 181 WNSGALTSGVHTTTPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVKDKRVEP 240  
Db 181 wnsгалtsгvhttfpavlqssglyslssvstvtpssslgtqtyicnvnhpkntkvdkrvеp 240  
QY 241 KSCDKHTCTPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300  
Db 241 kscdkhtctpcpapel lggpsvflppkpkdtlmisrtpеvtcvvvdvshеdpevkfnw 300  
QY 301 YVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDMLNNGKEYCKVSNKALPAPIEKTIS 360  
Db 301 yvdgvevhnaaktprееqynstyrvvsvltvlhqdwlngkeyckvksnkalpapiеktis 360  
QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGOPENYKKTTPPV 420  
Db 361 kakgqprepqvylppsreemtknqvsltclvkgfypsdiavewesngopenykttppv 420  
QY 421 LQSDGSFFLYSKLTVDKSRWQQGNVSCFVSVMHEALHNHYTQKSLSLSPGK 470  
Db 421 ldsdgsfflyskltvdksrwqqgnvfscvsmhealhnhytqkslsispgk 470

RESULT 10  
AAW90936  
ID AAW90936 standard; Protein; 470 AA.  
XX AC AAW90936;  
XX DT 08-AUG-2000 (first entry)  
XX DE Humanised HFE7A designed heavy chain HHH type protein.  
XX KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus; KW Hashimoto disease; rheumatoid arthritis; graft versus host disease; KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
XX OS Synthetic.  
XX PN EP990663-A2.  
XX PD 05-APR-2000.  
XX PF 29-SEP-1999; 99EP-0307711.  
XX PR 30-SEP-1998; 98JP-0276881.  
XX PR 30-SEP-1998; 98JP-0276882.  
XX PA (SANY ) SANKYO CO LTD.

Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 WPI: 2000-258930/23.  
 N-PSDB; ARA11655.  
 New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems -  
 Claim 2; Page 188-189; 263pp; English.  
 This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antifertility, neuroprotective, antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody HFE/A heavy chain construct HHH type which is described in the method of the invention.  
 Sequence 470 AA;  
 Query Match 99.2%; Score 2497; DB 21; Length 470;  
 Best Local Similarity 98.9%; Pred. No. 7e-142;  
 Matches 465; Conservative 3; Mismatches 2; Indels 0; Gaps 0  
 QY 1 MGWSCIIILFLVATATGVHSOVQLVQSGAEVKKPGASVKSCASGYTFTSYMQWVKQAP 60  
 Db 1 mgwsciiilflvatatgvhsqvlvgsgaevkkgpgasvkscasgytftsymwvqrqp 60  
 QY 61 GQGLEWMEIDPPSDSYTNYNKFCKGKATITVDTSSTAYMEISSLRSEDATVYVCARNRD 120  
 Db 61 gqglewmeidpsdsytynykfgrvltitrdtsstaymeisslrsedatvyyccarnrd 120  
 QY 121 YSNMNYFDVWGGTILTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDFPPEPTVYS 180  
 Db 121 ysnmnyfdwgegtlvtssastkgpsvfplapsskstsggtaalgclvdfpепtvys 180  
 QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYTCINNVNHHKSNYTKDKRREP 240  
 Db 181 wnsгалtsгvhtfpavlgssglyssvvtvpssslgtqtytcinnvnhkspntkvdkrrep 240  
 QY 241 KSCDKTHPCCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300  
 Db 241 kscdkthcpcpapel1ggpsvflfppkpkdtlmsrtpevtcvvvdvshedpevkfnw 300  
 QY 301 YVDGEVHNATKPREEQYNSTYRVVSVLTVLIHQDLNGKEYCKYKSNKALPAPIEKTIS 360  
 Db 301 yvdgevhnatkpreeqynstyrvvsvltvlihqdlngkeykckvsnkalpapiеktis 360  
 QY 361 KAKGQPREPQVYTLPPSRREMTKNQVSLTCLVKGPYPSPIAWEVESNGOPENNYKTPPV 420  
 Db 361 kakgqprepqvtytlppsrremtknvsltclvkgpyppspiawevesngopennyktppv 420



CC having specificity for polymorphic epithelial mucin (PEM) or its antigen  
CC binding fragment and a cytotoxic portion having endonucleolytic activity,  
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The  
CC compound has cytostatic activity useful for treating cancer and acting as  
CC a potential inducer of apoptosis.  
XX  
SQ Sequence 729 AA;

Query Match 93.1%; Score 2343.5; DB 22; Length 729;  
Best Local Similarity 93.0%; Pred. No. 1.7e-132;  
Matches 436; Conservative 20; Mismatches 10; Indels 3; Gaps 1;  
Qy 1 MGWSCIIILFLVATATGVSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQVWKOAP 60  
Db 1 mgwsciiilflvatatgvsqvlvqsgaevkpgasvkvsckasgytftsyawiewvraq 60  
Qy 61 GQGLEWGEIDPDSYNYNOKFKGKATITVDSTSTAYMELSLRSDETAIVYICARNRD 120  
Db 61 gqglewgeidpdsyynyokfkgrvtvtrdtstncaymelslrsedtaviycarsyd 120  
Qy 121 YSNWNYEDVMGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180  
Db 121 fa---wfaywgggtlvtvssastkgpsvfplapsskstsggtaalgclvkdypfepvtvs 177  
Qy 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVIVPSSSLGTQYICNVNHNKPSNTKVDKRVPE 240  
Db 178 wnsгалtsгvhtfpavllqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvpe 237  
Qy 241 KSCDKTHTCCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300  
Db 238 kscdkthtcpcpapellggpsvflfppkpkdtlmisrtpevtcvvvdshedpevkfnw 297  
Qy 301 YVDGVEVHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 360  
Db 298 yvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeyckvsnkalpapiektis 357  
Qy 361 KAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420  
Db 358 kagqprepqvytllppsrdeitknqvsitclvkgfypsdiavewesngqpennykttppv 417  
Qy 421 LDSGSEFLYSLKLTVDKSRWQGNVFCVSMHEALHNHYTQKSLSLSPG 469  
Db 418 ldsdgsfflyskltvdksrwqgnvfscvsmhealhnhytdqkslsispg 466

RESULT 14  
AAM52161  
ID AAM52161 standard; Protein; 739 AA.  
XX  
AC AAM52161;  
XX  
XX  
DT 05-FEB-2002 (first entry)  
XX  
DE Humanised HMFG-1 heavy chain/DNase I fusion protein 6.  
XX  
XX Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;  
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX WO200174905-A1.  
PN  
XX  
XX 11-OCT-2001.  
PD  
XX  
XX 26-MAR-2001; 2001WO-GB01324.  
PF  
XX  
XX 03-APR-2000; 2000GB-0008049.  
PR  
XX 02-OCT-2000; 2000US-237159P.  
PR  
XX (ANTI-) ANTISOMA RES LTD.  
PA  
XX

PI Young RJ;  
XX  
DR WPI; 2001-662969/76.  
XX  
XX Novel compound used to treat cancer has target cell-specific portion  
PT comprising humanised monoclonal antibody having specificity for  
PT polymorphic epithelial mucin, and cytotoxic portion having  
PT endonucleolytic activity -  
XX  
PS Claim 20; Figure 12; 176pp; English.  
XX  
CC The invention relates to a compound which comprises a target  
CC cell-specific portion, comprising an humanised monoclonal antibody,  
CC having specificity for polymorphic epithelial mucin (PEM) or its antigen  
CC binding fragment and a cytotoxic portion having endonucleolytic activity,  
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The  
CC compound has cytostatic activity useful for treating cancer and acting as  
CC a potential inducer of apoptosis.  
XX  
SQ Sequence 739 AA;  
Query Match 93.1%; Score 2343.5; DB 22; Length 739;  
Best Local Similarity 93.0%; Pred. No. 1.8e-132;  
Matches 436; Conservative 20; Mismatches 10; Indels 3; Gaps 1;  
Qy 1 MGWSCIIILFLVATATGVSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQVWKOAP 60  
Db 1 mgwsciiilflvatatgvsqvlvqsgaevkpgasvkvsckasgytftsayiewvraq 60  
Qy 61 GQGLEWGEIDPDSYNYNOKFKGKATITVDSTSTAYMELSLRSDETAIVYICARNRD 120  
Db 61 gqglewgeidpdsyynyokfkgrvtvtrdtstncaymelslrsedtaviycarsyd 120  
Qy 121 YSNWNYEDVMGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180  
Db 121 fa---wfaywgggtlvtvssastkgpsvfplapsskstsggtaalgclvkdypfepvtvs 177  
Qy 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVIVPSSSLGTQYICNVNHNKPSNTKVDKRVPE 240  
Db 178 wnsгалtsгvhtfpavllqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkkvpe 237  
Qy 241 KSCDKTHTCCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300  
Db 238 kscdkthtcpcpapellggpsvflfppkpkdtlmisrtpevtcvvvdshedpevkfnw 297  
Qy 301 YVDGVEVHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 360  
Db 298 yvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeyckvsnkalpapiektis 357  
Qy 361 KAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420  
Db 358 kagqprepqvytllppsrdeitknqvsitclvkgfypsdiavewesngqpennykttppv 417  
Qy 421 LDSGSEFLYSLKLTVDKSRWQGNVFCVSMHEALHNHYTQKSLSLSPG 469  
Db 418 ldsdgsfflyskltvdksrwqgnvfscvsmhealhnhytdqkslsispg 466

RESULT 15  
AAM52157  
ID AAM52157 standard; Protein; 730 AA.  
XX  
AC AAM52157;  
XX  
XX  
DT 05-FEB-2002 (first entry)  
XX  
DE Humanised HMFG-1 heavy chain/DNase I fusion protein 2.  
XX  
XX Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;  
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.  
XX  
OS Homo sapiens.







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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:17:05 ; Search time 82.88 Seconds  
(without alignments)  
138.514 Million cell updates/sec

Title: US-09-499-662-145  
Perfect score: 2517  
Sequence: 1 MGWSCIIILFLVATATGVHSQ.....MHEALHNYTOKSLSLSPCK 470

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2232	88.7	476	2	US-08-378-939-10
2	2230	88.6	449	1	US-08-458-516-13
3	2200.5	87.4	467	4	US-09-049-672A-8
4	2198.5	87.3	452	3	US-09-027-449-71
5	2198.5	87.3	452	4	US-09-026-985-71
6	2177	86.5	468	4	US-09-485-737B-67
7	2177	86.5	711	4	US-09-485-737B-90
8	2159.5	85.8	454	2	US-07-934-373C-22
9	2159.5	85.8	454	3	US-08-437-642B-22
10	2159.5	85.8	454	5	PCT-US93-07832-22
11	2146	85.3	472	4	US-08-793-450-8
12	2126	84.5	451	2	US-08-887-352B-14
13	2126	84.5	451	2	US-08-887-352B-16
14	2126	84.5	451	3	US-08-466-151-65
15	2126	84.5	451	4	US-09-109-207C-14
16	2126	84.5	451	4	US-09-109-207C-16
17	2126	84.5	451	4	US-09-296-005-14
18	2126	84.5	451	4	US-09-296-005-16
19	2123	84.3	478	3	US-08-487-550-8
20	2118	84.1	451	2	US-08-887-352B-18
21	2118	84.1	451	4	US-09-109-207C-18
22	2118	84.1	451	4	US-09-282-505-2
23	2118	84.1	451	4	US-09-054-255-2
24	2118	84.1	451	4	US-09-296-005-18
25	2107	83.7	453	3	US-08-466-151-8
26	2107	83.7	453	4	US-08-466-163B-8
27	2105.5	83.7	467	2	US-07-916-098A-45

Sequence 2, Appli  
Sequence 23, Appli  
Sequence 23, Appli  
Sequence 23, Appli  
Sequence 3, Appli  
Sequence 7, Appli  
Sequence 81, Appli  
Sequence 4, Appli  
Sequence 17, Appli  
Sequence 7, Appli  
Sequence 12, Appli  
Sequence 9, Appli  
Sequence 4, Appli  
Sequence 5, Appli  
Sequence 12, Appli  
Sequence 2, Appli  
Sequence 2, Appli

28 2104.5 83.6 449 4 US-09-679-397-2  
29 2101.5 83.5 552 5 PCT-US93-07832-23  
30 2098.5 83.4 469 3 US-07-934-373C-23  
31 2098.5 83.4 469 3 US-08-437-642B-23  
32 2096 83.3 451 4 US-09-247-352-3  
33 2092.5 83.1 459 1 US-08-157-101A-7  
34 2074.5 82.4 467 1 US-08-704-744-81  
35 2072.5 82.3 473 4 US-09-049-672A-4  
36 2062.5 81.9 445 4 US-08-341-560B-17  
37 2056.5 81.7 446 3 US-08-397-411-7  
38 2056 81.7 476 3 US-08-487-550-12  
39 2024 80.4 442 5 PCT-US96-10043-9  
40 2024 80.4 476 3 US-08-487-550-4  
41 2012 79.9 442 1 US-08-461-968A-5  
42 2012 79.9 442 2 US-08-462-571-5  
43 1997.5 79.4 450 2 US-08-788-800-12  
44 1988 79.0 442 1 US-08-480-036-2  
45 1988 79.0 442 1 US-08-461-968A-2

ALIGNMENTS

RESULT 1  
US-08-378-939-10  
; Sequence 10, Application US/08378939  
; Patent No. 5876961  
; GENERAL INFORMATION:  
; APPLICANT: CROWE, JAMES SCOTT  
; APPLICANT: LEWIS, ALAN PETER  
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ  
; STREET: 555 THIRTEENTH ST. N.W.  
; CITY: WASHINGTON  
; STATE: D. C.  
; COUNTRY: U.S.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/378,939  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/952640  
; FILING DATE: 01-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ERNST, BARBARA G  
; REGISTRATION NUMBER: 30,377  
; REFERENCE/DOCKET NUMBER: 1808-118  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 783-6040  
; TELEFAX: (202) 783-6031  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 476 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-378-939-10

Query Match 88.7%; Score 2232; DB 2; Length 476;  
Best Local Similarity 88.7%; Pred. No. 5.2e-159;  
Matches 422; Conservative 20; Mismatches 28; Indels 6; Gaps 1;  
QY 1 MGWSCIIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQVKAP 60  
| | : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| : |||

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Db 1 MDWTRFLFVAAATGVOSQVQSGAEVKKPGSSVTVSCKASGGTFSNVAISWRQAP 60
QY 61 GQLEWMEIDPDSSTNYNOKFKGKATITVDTSTAYMELSSLRSEDFAVYICARNR- 119
Db 61 GQLEWGGIIPFGTPTYSQNFQGRVTITADKSTSTAHMELTSLRSEDFAVYICATDRY 120
QY 120 -----DYSNNWYFDVWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVXDYFP 174
Db 121 ROANFRARVGFDPWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVXDYFP 180
QY 175 EPTVSWNSGALTSVHTTPAVLQSSGLYSLSSVTVVPSSSLGTQYICNVNHPKSNTKV 234
Db 181 EPTVSWNSGALTSVHTTPAVLQSSGLYSLSSVTVVPSSSLGTQYICNVNHPKSNTKV 240
QY 235 DKRVEPKSCDKTHTCCPAPELLGSPSVFLFPKPKDMLMISRTPEVTCVVVDVSHEDP 294
Db 241 DKRVEPKSCDKTHTCCPAPELLGSPSVFLFPKPKDMLMISRTPEVTCVVVDVSHEDP 300
QY 295 EVKFNWYDGVVHNAKTPREQYNSTYRVSVLTVLHQQDWLNGKEYCKKVSNNKALPAP 354
Db 301 EVKFNWYDGVVHNAKTPREQYNSTYRVSVLTVLHQQDWLNGKEYCKKVSNNKALPAP 360
QY 355 IEKTIKAKGQPREPOVYITLPPSRREEMTKNOVSLTCLVKGFPSPDIAVEWESNGQPENNY 414
Db 361 IEKTIKAKGQPREPOVYITLPPSRDELTKNQVSLTCLVKGFPSPDIAVEWESNGQPENNY 420
QY 415 KTTTPVLDSDGSPFLYSKLTVDKSRQOQGNVFCSCVMHEALHNYTKQSLSLSPGK 470
Db 421 KTTTPVLDSDGSPFLYSKLTVDKSRQOQGNVFCSCVMHEALHNYTKQSLSLSPGK 476

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RESULT 2

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US-08-458-516-13
; Sequence 13, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co. Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
US-08-458-516-13

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Query Match 88.6%; Score 2230; DB 1; Length 449;

Best Local Similarity 92.9%; Pred. No. 6.8e-159;

Matches 419; Conservative 15; Mismatches 15; Indels 2; Gaps 2;

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QY 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAPGQGLEWMGIDPDSSTNYN 79
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYAFTNYLIEVNRQAPGQGLEWIGVYIYPSGGTNY 60
QY 80 NQKFKGKATITVDTSTAYMELSSLRSEDFAVYICARNRDYNNWYFDVWGQGLTVTVS 139
Db 61 NEKFKGRVTLTVDESTNTAYMELSSLRSEDFAVYFCAR-RDGNYGW-FAYWGQGLTVTVS 118
QY 140 SASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSVHTTFAVLQ 199
Db 119 SASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSVHTTFAVLQ 178
QY 200 SGLYSLSSVTVVPSSSLGTQYICNVNHPKSNTKVDKRVPEKSCDKTHTCCPAPELLG 259
Db 179 SGLYSLSSVTVVPSSSLGTQYICNVNHPKSNTKVDKRVPEKSCDKTHTCCPAPELLG 238
QY 260 GPSVFLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 319
Db 239 GPSVFLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 298
QY 320 NSTYRVSVLTVLHQQDWLNGKEYCKKVSNNKALPAPIEKTISKAKGQPREPOVYITLPPSR 379
Db 299 NSTYRVSVLTVLHQQDWLNGKEYCKKVSNNKALPAPIEKTISKAKGQPREPOVYITLPPSR 358
QY 380 EMTKNQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSR 439
Db 359 ELTKNQVSLTCLVKGFPSPDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVDKSR 418
QY 440 WQGNVFCSCVMHEALHNYTKQSLSLSPGK 470
Db 419 WQGNVFCSCVMHEALHNYTKQSLSLSPGK 449

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RESULT 3

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US-09-049-672A-8
; Sequence 8, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ceirone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGTU11
; CLONE: 2747531
; US-09-049-672A-8

Query Match      87.4%  Score 2200.5;  DB 4;  Length 467;
Best Local Similarity 89.0%;  Pred. No. 1.1e-156;
Matches 413;  Conservative 20;  Mismatches 28;  Indels 3;  Gaps 1;

Qy  7  ILFLVATATGVHVSQVLQVSGAELKPGASVKSCASGYTFTSYMMQWVQKAPQCGLEW 66
Db  7  ILFLVAAATGTHAQVLQVSGAELKPGASVQVCTVSGFTLSDLSLVHVVQAPQCGLEW 66

Qy  67  MGEIDPSDSYNNQKFGKATITVDSTSTAYMELSLRSEDATVYYCARNRDNYSNWY 126
Db  67  MGGLAPENGEAVYAKQFLGRULTSDDTSADTAYMFLNGLSGEDSAIYYCARQH---YDFF 123

Qy  127  FDVWGQGLTVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYRPEPTVTSNNSGAL 186
Db  124  FDFWGQGLTVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYRPEPTVTSNNSGAL 183

Qy  187  TSGVHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKYDKRVEPKSCDKT 246
Db  184  TSGVHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKT 243

Qy  247  HTCPCPAPELLGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFNNYVDGVE 306
Db  244  HTCPCPAPELLGSPVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFNNYVDGVE 303

Qy  307  VHNATKPREQYNTSYRVSVLVTLVHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQP 366
Db  304  VHNATKPREQYNTSYRVSVLVTLVHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQP 363

Qy  367  REPQVYTLPPSREMTKNQVSLTCLVKGFPYSDIAVWESNGQPENNYKTTTPPVLDSDGS 426
Db  364  REPQVYTLPPSREMTKNQVSLTCLVKGFPYSDIAVWESNGQPENNYKTTTPPVLDSDGS 423

Qy  427  FFLYSKLTVDKSRQOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
Db  424  FFLYSKLTVDKSRQOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 467

RESULT 4
US-09-027-449-71
; Sequence 71, Application US/09027449
; Patent No. 6025158
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
```

```

; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,449
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074,330
; FILING DATE: 22-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,664
; FILING DATE: 21-Feb-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-027-449-71

Query Match      87.3%  Score 2198.5;  DB 3;  Length 452;
Best Local Similarity 89.8%;  Pred. No. 1.5e-156;
Matches 406;  Conservative 28;  Mismatches 17;  Indels 1;  Gaps 1;

Qy  20  QVQLVQSGAEYKKPGASVKSCASGYTFTSYMMQWVQKAPQGLEWMEIDPSDSYNY 79
Db  1  EVQLVQSGGLVQPGGSLRLSCAASGYSFSSHYMHWRQAPGKGLIEWGYIDPSNGETTY 60

Qy  80  NQKFKGKATITVDSTSTAYMELSLRSEDATVYYCAR- NRDYSNNWYFDVWGQGLTVTV 138
Db  61  NQKFKGRTLSRDNSKNTAYLQMNLSRAEDTAVYYCARGDYRYNGDWFDFVWGQGLTVTV 120

Qy  139  SSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYRPEPTVTSNNSGALTSGVHTFPVAVLQ 198
Db  121  SSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYRPEPTVTSNNSGALTSGVHTFPVAVLQ 180

Qy  199  SSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKYDKRVEPKSCDKTHTCCPPAPELL 258
Db  181  SSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTCCPPAPELL 240

Qy  259  GGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFNNYVDGVEVHNATKPREEQ 318
Db  241  GGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFNNYVDGVEVHNATKPREEQ 300

Qy  319  YNSTYRVYVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 378
Db  301  YNSTYRVYVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 360

Qy  379  EEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKS 438
Db  361  EEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKS 420

Qy  439  RWQOQNVFCSCVMHEALHNHYTQKSLSLSPGK 470
Db  421  RWQOQNVFCSCVMHEALHNHYTQKSLSLSPGK 452

RESULT 5
US-09-026-985-71
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Patent No. 6350860  
GENERAL INFORMATION:  
APPLICANT: Buysse, Marie-Ange  
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,  
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS  
FILE REFERENCE: INNS:015  
CURRENT APPLICATION NUMBER: US/09/485,737B  
CURRENT FILING DATE: 2000-02-14  
PRIOR APPLICATION NUMBER: PCT/EP 98/05165  
PRIOR FILING DATE: 1998-08-14  
PRIOR APPLICATION NUMBER: EPO 98870139.7  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: EPO 97870122.5  
PRIOR FILING DATE: 1997-08-18  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 90  
LENGTH: 711  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: SYNTHETIC  
US-09-485-737B-90

Query Match 86.5%; Score 2177; DB 4; Length 711;  
Best Local Similarity 88.2%; Pred. No. 1.1e-154;  
Matches 410; Conservative 20; Mismatches 31; Indels 4; Gaps 1;

Qy 6 ILFLVATATGVHSQVLVQSQAEEVKPGASVKYCKASGTFSTYMWQWVQKAPGQGLE 65  
Db 7 IFSELLISASVLSQVLVQSSELKPGASVKISCKASGYTFDYGNWVQKAPGQGLK 66  
Qy 66 WMGEIDPDSYTNKQKFKGATITVDSTSTAYMELSLRSEDATVYICARNRDYSNNW 125  
Db 67 WMGLINTYTGESTYVDYDFKGRFVSLDTSVSAALQISSLKAEDATYFCARRGFYA--- 123  
Qy 126 YFDVWQGTLYTVSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGA 185  
Db 124 -MDYWGQGTTVTVSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGA 182  
Qy 186 LTSGVHTPEAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHHKPSNTKVKRVEPKSCDK 245  
Db 183 LTSGVHTPEAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHHKPSNTKVKRVEPKSCDK 242  
Qy 246 THTCPPEAPPELLGSPSVFLPPPKDPLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 305  
Db 243 THTCPPEAPPELLGSPSVFLPPPKDPLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 302  
Qy 306 EVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQ 365  
Db 303 EVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQ 362  
Qy 366 PREPOVYTLPPSREEMTNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 425  
Db 363 PREPOVYTLPPSREEMTNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 422  
Qy 426 SFELYSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 470  
Db 423 SFELYSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 467

RESULT 8  
US-07-934-373C-22  
Sequence 22, Application US/07934373C  
Patent No. 5821337  
GENERAL INFORMATION:  
APPLICANT: Paul J. Carter  
APPLICANT: Leonard G. Presta  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/934,373C  
FILING DATE: 21-Aug-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05126  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/715272  
FILING DATE: 14-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 40,378  
REFERENCE/DOCKET NUMBER: P0709P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-1994  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 454 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-07-934-373C-22

Query Match 85.8%; Score 2159.5; DB 2; Length 454;  
Best Local Similarity 89.2%; Pred. No. 1.3e-153;  
Matches 405; Conservative 18; Mismatches 28; Indels 3; Gaps 1;  
Qy 20 QVOLVQSGAEVKKPGASVKYCKASGYTFSTYMWQWVQKAPGQGLEWMEIDPDSYTN 79  
Db 1 QVOLVQSGPELVKPGASVKISCKTSGYTFETYMHWKQSHGKSLWIGGFPNKGSSH 60  
Qy 80 NQKFKGATITVDSTSTAYMELSLRSEDATVYICARNRDYSNNW---YFDVWQGTLY 136  
Db 61 NQREMDKATLAVDKSTSTAYMELSLTSEDSGIYYCARWGLNYGFDVRYEDWVGAGTV 120  
Qy 137 TVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFP 196  
Db 121 TVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFP 180  
Qy 197 LOSGLYSLSSVTVVPSSSLGTQTYICNVNHHKPSNTKVKRVEPKSCDKTHTCPCPAPE 256  
Db 181 LOSGLYSLSSVTVVPSSSLGTQTYICNVNHHKPSNTKVKRVEPKSCDKTHTCPCPAPE 240  
Qy 257 LLGGPSVFLPPPKDPLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVEVHNATKPRE 316  
Db 241 LLGGPSVFLPPPKDPLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVEVHNATKPRE 300  
Qy 317 EYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGPREPVYTLPP 376  
Db 301 EYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGPREPVYTLPP 360  
Qy 377 SREEMTNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVD 436  
Db 361 SREEMTNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVD 420  
Qy 437 KSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 470  
Db 421 KSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 454





Db 61 NQRFMDKATLAVDKSTSTAYMELSLTSEDSGIYYCARWGLNTGFDVRYFDVWGAGTIV 120  
Qy 137 TVSSASTKGPSVFFPLAPSSKSTSGGTAALGCLVRDYFPEPTVTVSWNSGALTSGVHTFPAP 196  
Db 121 TVSSASTKGPSVFFPLAPSSKSTSGGTAALGCLVRDYFPEPTVTVSWNSGALTSGVHTFPAP 180  
Qy 197 LQSSGLYSLSVTVVPSSLSGTQYICNVNHPKNTKVDKRVKPKSCDKTHCTCPCPAPE 256  
Db 181 LQSSGLYSLSVTVVPSSLSGTQYICNVNHPKNTKVDKRVKPKSCDKTHCTCPCPAPE 240  
Qy 257 LGGPSVFLRPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKPRE 316  
Db 241 LGGPSVFLRPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTKPRE 300  
Qy 317 EYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPP 376  
Db 301 EYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPP 360  
Qy 377 SREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVD 436  
Db 361 SREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVD 420  
Qy 437 KSRWQGNVFSCSVHMEALHNHYTQKSLSLSPGK 470  
Db 421 KSRWQGNVFSCSVHMEALHNHYTQKSLSLSPGK 454

RESULT 11  
US-08-793-450-8  
; Sequence 8, Application US/08793450  
; Patent No. 6312690  
; GENERAL INFORMATION:  
; APPLICANT: EDELMAN, LENA  
; APPLICANT: MARGARITTE, CHRISTEL  
; APPLICANT: KACZOREK, MICHEL  
; APPLICANT: CHABABIHI, HASSAN  
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D  
; TITLE OF INVENTION:  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/793,450  
; FILING DATE: 03-MAR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94/10566  
; FILING DATE: 02-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 472 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-793-450-8

Query Match 85.3%; Score 2146; DB 4; Length 472;  
Best Local Similarity 85.1%; Pred. No. 1.4e-152;  
Matches 404; Conservative 26; Mismatches 37; Indels 8; Gaps 3;  
Qy 1 MGWSCILFLVATATGVHSGVOLVOSGAENVKPGASVKVSKCKASGYTFTSYWQWVQKAP 60  
Db 1 MGWSCILFLVATATGVHSGVOLVOSGAENVKPGASVKVSKCKASGYTFTSYWQWVQKAP 60  
Qy 61 GQGLEWMEIDPSDSTYNNOKFKGKATITVDITSTSTAYMELSSLSRSEDATVYYICARND 120  
Db 61 GQGLEWMEIDPSDSTYNNOKFKGKATITVDITSTSTAYMELSSLSRSEDATVYYICARND 119  
Qy 121 YSNWN-----YFDVWGQGLTVTVSSASTKGPSVFFPLAPSSKSTSGGTAALGCLVRDYFPE 175  
Db 120 Y--KWKYHGDFDPWGQGTITTVSSASTKGPSVFFPLAPSSKSTSGGTAALGCLVRDYFPE 177  
Qy 176 PVTYSWNSGALTSGVHTFPAPVLQSSGLYSLSVTVVPSSLSGTQYICNVNHPKNTKVD 235  
Db 178 PVTYSWNSGALTSGVHTFPAPVLQSSGLYSLSVTVVPSSLSGTQYICNVNHPKNTKVD 237  
Qy 236 KRVEPKSCDKTHCTCPCPAPELGGPSVFLRPKPKDPTLMISRTPEVTCVVVDVSHEDPE 295  
Db 238 KKAEPKSCDKTQTCTCPCPAPELGGPSVFLRPKPKDPTLMISRTPEVTCVVVDVSHEDPE 297  
Qy 296 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVYVSLTVLHQDWLNGKEYKCKVSNKALPAPI 355  
Db 298 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVYVSLTVLHQDWLNGKEYKCKVSNKALPAPI 357  
Qy 356 EKTISKAKGQPREPOVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYK 415  
Db 358 EKTISKAKGQPREPOVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYK 417  
Qy 416 TTPPVLDSDGSEFFLYSKLTVDKSRWQGNVFSCSVHMEALHNHYTQKSLSLSPGK 470  
Db 418 TTPPVLDSDGSEFFLYSKLTVDKSRWQGNVFSCSVHMEALHNHYTQKSLSLSPGK 472  
RESULT 12  
US-08-887-352B-14  
; Sequence 14, Application US/08887352B  
; Patent No. 5994511  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
; TITLE OF INVENTION: Improving Polypeptides  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,352B  
; FILING DATE: 03-Jul-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P1123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 14:

```
;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 451 amino acids
;   TYPE: Amino Acid
;   TOPOLOGY: Linear
US-08-887-352B-14

Query Match      84.5%; Score 2126; DB 2; Length 451;
Best Local Similarity 87.8%; Pred. No. 4e-151;
Matches 397; Conservative 23; Mismatches 30; Indels 2; Gaps 2;

QY 20 QVQLVSGAEVKKPGASVKVSCKASGYTFTS-YVMQWVQAQPGQGLEWMGEIDPDSYTN 78
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNWIRQAQPGKGLEWVASI-TYDGSN 59

QY 79 YNOKFKGKATITVDSTSTAYMELSLRSDEDTAVYYCARNRDYSNWYFDVWGQGLTVV 138
Db 60 YNPVKGRITISRDOSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVV 119

QY 139 SSASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 198
Db 120 SSASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 179

QY 199 SSGLYSLSSVTVVPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKTHTCPPCPAPELL 258
Db 180 SSGLYSLSSVTVVPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKTHTCPPCPAPELL 239

QY 259 GGPVSFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQ 318
Db 240 GGPVSFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQ 299

QY 319 YNSTYRVVSVLTVLHODWLNGLKEIKYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
Db 300 YNSTYRVVSVLTVLHODWLNGLKEIKYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359

QY 379 EEMTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKS 438
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEHESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKS 419

QY 439 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
Db 420 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 14
US-08-887-352B-16
; Sequence 16, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-466-151-65

Query Match 84.5%; Score 2126; DB 3; Length 451;
Best Local Similarity 87.8%; Pred. No. 4e-151;
Matches 397; Conservative 23; Mismatches 30; Indels 2; Gaps 2;

QY 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YMQMWVKQAPGOGLEWMGEIDPSDSTN 78
Db 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSWNWIRQAPGKLEWVASI-TYDGS 59

QY 79 YNOKFKGKATITVDITSTAYMELSSLRSEDYAVYYCARNRDYSNNYFDVWGQGLTV 138
Db 60 YNPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWFHFAVWGQGLTV 119

QY 139 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 198
Db 120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 179

QY 199 SSGLYSLSSVVTVPSSSLGQTQYICNVNHPKSNTKVDKRVKPKSCDKTHTCPCPAPELL 258
Db 180 SSGLYSLSSVVTVPSSSLGQTQYICNVNHPKSNTKVDKRVKPKSCDKTHTCPCPAPELL 239

QY 259 GGPSVFLFPPPKPKDTLMISRTPEVTCVVVDYSHEDPEVKFNWYVDGVEVHNKATKPREE 318
Db 240 GGPSVFLFPPPKPKDTLMISRTPEVTCVVVDYSHEDPEVKFNWYVDGVEVHNKATKPREE 299

QY 319 YNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
Db 300 YNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359

QY 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKS 438
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKS 419

QY 439 RWQOGNVFSCSMHEALHNHYTQKSLSLSPGK 470
Db 420 RWQOGNVFSCSMHEALHNHYTQKSLSLSPGK 451

RESULT 15

US-09-109-207C-14
; Sequence 14, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-1ge Antibodies and Method of Improving Polypeptide

; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
; US-09-109-207C-14

Query Match 84.5%; Score 2126; DB 4; Length 451;
Best Local Similarity 87.8%; Pred. No. 4e-151;
Matches 397; Conservative 23; Mismatches 30; Indels 2; Gaps 2;

QY 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YMQMWVKQAPGOGLEWMGEIDPSDSTN 78
Db 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSWNWIRQAPGKLEWVASI-TYDGS 59

QY 79 YNOKFKGKATITVDITSTAYMELSSLRSEDYAVYYCARNRDYSNNYFDVWGQGLTV 138
Db 60 YNPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWFHFAVWGQGLTV 119

QY 139 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 198
Db 120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 179

QY 199 SSGLYSLSSVVTVPSSSLGQTQYICNVNHPKSNTKVDKRVKPKSCDKTHTCPCPAPELL 258
Db 180 SSGLYSLSSVVTVPSSSLGQTQYICNVNHPKSNTKVDKRVKPKSCDKTHTCPCPAPELL 239

QY 259 GGPSVFLFPPPKPKDTLMISRTPEVTCVVVDYSHEDPEVKFNWYVDGVEVHNKATKPREE 318
Db 240 GGPSVFLFPPPKPKDTLMISRTPEVTCVVVDYSHEDPEVKFNWYVDGVEVHNKATKPREE 299

QY 319 YNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
Db 300 YNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359

QY 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKS 438
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKS 419

QY 439 RWQOGNVFSCSMHEALHNHYTQKSLSLSPGK 470
Db 420 RWQOGNVFSCSMHEALHNHYTQKSLSLSPGK 451

Search completed: August 14, 2002, 15:17:06
Job time: 689 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 15:19:00 ; Search time 108.64 Seconds  
(without alignments)  
415.703 Million cell updates/sec

Title: US-09-499-662-145  
Perfect score: 2517  
Sequence: 1 MGWSCIILFLVATGVHSQ.....MHEALHNHYTQKSLSLSPGK 470

Scoring table:  
BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR.71.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1758	69.8	330	1 GHU	Ig gamma-1 chain C
2	1639.5	65.1	377	2 A23511	Ig gamma-3 chain C
3	1637.5	65.1	377	2 A60764	Ig gamma-3 chain C
4	1611.5	64.0	469	2 S37483	Ig gamma-2a chain C
5	1610	64.0	326	1 G2HU	Ig gamma-2 chain C
6	1599.5	63.5	327	1 G4HU	Ig gamma-4 chain C
7	1547	61.5	474	1 G2MS11	Ig gamma-2b chain C
8	1545	61.4	446	2 S40295	Ig gamma-2a chain C
9	1502.5	59.7	475	2 S01321	Ig gamma-2b chain C
10	1476	58.6	470	2 S22080	Ig heavy chain pre
11	1469	58.4	472	2 S31459	Ig gamma-1 chain - r
12	1434	57.0	374	2 S69339	Ig heavy chain v r
13	1428.5	56.8	444	2 PC4436	monoclonal antibody
14	1267	50.3	328	2 I47159	Ig gamma 2a chain
15	1261	50.1	328	2 I47160	Ig gamma 2b chain
16	1253	49.8	255	4 S31866	Ig gamma-1 chain C
17	1245	49.5	234	2 PT0207	Ig gamma chain C r
18	1235	49.1	328	2 I47158	Ig gamma 1 chain c
19	1231.5	48.9	323	1 GHRB	Ig gamma chain C r
20	1231	48.9	328	2 I47161	Ig gamma 3 chain c
21	1210.5	48.1	329	1 G2GP	Ig gamma-2 chain C
22	1165.5	46.3	308	2 C30554	Ig heavy chain C r
23	1157	46.0	289	1 G3HUW1	Ig gamma-3 heavy c
24	1155	45.9	326	2 PS0017	Ig gamma-1 chain C
25	1150	45.7	329	1 G3MSC	Ig gamma-3 chain C
26	1145	45.5	324	1 G1MS	Ig gamma-1 chain C
27	1144.5	45.5	333	2 PS0018	Ig gamma-2b chain C
28	1140	45.3	393	1 G1MSM	Ig gamma-1 chain C
29	1139	45.3	398	1 G3MSM	Ig gamma-3 chain C

Ig gamma-2a chain  
Ig gamma-2c chain  
Ig gamma-2a chain  
Ig gamma-2a chain  
Ig gamma-2a chain  
Ig gamma-2 chain C  
Ig gamma-2b chain  
Ig gamma 4 chain c  
Ig epsilon chain C  
Ig mu chain precu  
Ig heavy chain pre  
Ig heavy chain (DO  
Ig gamma chain - m  
Ig gamma chain - m  
Ig gamma-1 heavy c  
Ig heavy chain VHI  
Ig Y heavy chain (

## ALIGNMENTS

RESULT 1

GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence\_revision 18-Aug-1982 #text\_change 16-Jul-1999  
C:Accession: A93433; S33887; B90563; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.  
Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <ELL>

A:Cross-references: EMBL:Z17370

A:Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) marker

A:Note: Lys-330 is removed after translation

R:Harris, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of

A:Reference number: S33887; MUID:83001943

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113;235-330 <TAK>

A:Cross-references: EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq

A:Reference number: A90563; MUID:71064024

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96,'R',98-135 <CUN>

A:Note: this sequence has the Glm(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se

A:Reference number: A90564; MUID:71064025

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',2

A:Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met

R:Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein NI

## igen Primaerstruktur.

A:Reference number: A91668; MUID:77070269  
A:Contents: myeloma protein Nie  
A:Accession: B91668  
A:Molecule type: protein  
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27  
A:Note: this sequence has the Gln(17) and Gln(1) markers  
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
A:Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL  
A:Reference number: A91723; MUID:83289131  
A:Contents: myeloma protein KOL; disulfide bonds  
A:Accession: A91723  
A:Molecule type: protein  
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH  
A:Note: this sequence has the Gln(3) and Gln(non-1) markers  
R:Call, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid  
A:Reference number: A90565; MUID:71064027  
A:Contents: annotation; disulfide bonds  
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976  
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob  
enbromide cleavage products, and the disulfide bridges.  
A:Reference number: A91667; MUID:77070267  
A:Contents: annotation; disulfide bonds  
C:Genetics:  
A:Gene: GDB:IGHG1

A:Cross-references: GDB:120085; OMIM:147100  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1; 114/1; 224/1  
C:Comment: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:137-206/Domain: immunoglobulin homology <IM1>  
F:243-310/Domain: immunoglobulin homology <IM2>  
F:27-83,144-204,250-308/Disulfide bonds: #status experimental  
F:103/Disulfide bonds: interchain (to light chain) #status experimental  
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 69.8%; Score 1758; DB 1; Length 330;  
Best Local Similarity 99.1%; Pred. No. 4.5e-93;  
Matches 327; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 141 ASTKGSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPAVLQSS 200  
|||||  
Db 1 ASTKGSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPAVLQSS 60  
QY 201 GLYSLSSVTVPSSSSLGTQTYICNVNPKSNTKVDKRVKSKDTHTPCPAPPELLGG 260  
|||||  
Db 61 GLYSLSSVTVPSSSSLGTQTYICNVNPKSNTKVDKRVKSKDTHTPCPAPPELLGG 120  
QY 261 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320  
|||||  
Db 121 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180  
QY 321 STYRVSVLTQLHQLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 380  
|||||  
Db 181 STYRVSVLTQLHQLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 240  
QY 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRW 440  
|||||  
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRW 300  
QY 441 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 470  
|||||  
Db 301 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 330

## RESULT 2

A23511

Ig gamma-3 chain C region (allotype G3m(b)) - human

C:Species: Homo sapiens (man)

C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 23-Jul-1999

C:Accession: A23511

R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.

Nucleic Acids Res. 14, 1779-1789, 1986

A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene:

A:Reference number: A23511; MUID:86148507

A:Accession: A23511

A:Molecule type: DNA

A:Residues: 1-377 &lt;HUC&gt;

A:Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056

C:Genetics:

A:Gene: GDB:IGHG3

A:Cross-references: GDB:119339; OMIM:147120

A:Map position: 14q32.33-14q32.33

A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin

F:20-85/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 65.1%; Score 1639.5; DB 2; Length 377;

Best Local Similarity 82.8%; Pred. No. 2.8e-86;

Matches 312; Conservative 7; Mismatches 11; Indels 47; Gaps 1;

QY 141 ASTKGSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPAVLQSS 200

|||||

Db 1 ASTKGSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPAVLQSS 60

QY 201 GLYSLSSVTVPSSSSLGTQTYICNVNPKSNTKVDKRVKSKDTHTPCPAPPELLGG 238

|||||

Db 61 GLYSLSSVTVPSSSSLGTQTYICNVNPKSNTKVDKRVKSKDTHTPCPAPPELLGG 120

QY 239 -----EPKSCDKTHTPCPAPPELLGGPSVFLFPPPKPKDT 273

|||||

Db 121 DTPPC 180

QY 274 LMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLH 333

|||||

Db 181 LMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLH 240

QY 334 QDWLNKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNOVSLTCLVK 393

|||||

Db 241 QDWLNKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNOVSLTCLVK 300

QY 394 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRWQOGNIFSCSYMHE 453

|||||

Db 301 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRWQOGNIFSCSYMHE 360

QY 454 ALHNHYTQKSLSLSPGK 470

|||||

Db 361 ALHNHYTQKSLSLSPGK 377

## RESULT 3

A60764

Ig gamma-3 chain C region, form LAT - human

C:Species: Homo sapiens (man)

C:Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 16-Jul-1999

C:Accession: A60764

R:Huck, S.; Lefranc, G.; Lefranc, M.P.

Immunogenetics 30, 250-257, 1989

A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 conv

A:Reference number: A60764; MUID:90007613

A:Accession: A60764

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-377 &lt;HUC&gt;

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 65.1%; Score 1637.5; DB 2; Length 377;  
Best Local Similarity 82.8%; Pred. No. 3.7e-86;  
Matches 312; Conservative 7; Mismatches 11; Indels 47; Gaps 1;

QY 141 ASTKGPSVFLAPSSKSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 200  
Db 1 ASTKGPSVFLAPCSRSTSGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
QY 201 GLYSLSWTVVPSLSLTQYICNVNHPKNTKVKRY----- 238  
Db 61 GLYSLSWTVVPSLSLTQYICNVNHPKNTKVKRY----- 238  
QY 239 -----EPKSCDKHTPCPCPAPELLGPGSPVFLFPKPKDT 273  
Db 121 DTPPCPCPEPKSCDTPPCPCPEPKSCDTPPCPCPAPELLGPGSPVFLFPKPKDT 180  
QY 274 LMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNNAKTKPREQYNSTYRVVSVLTVLH 333  
Db 181 LMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNNAKTKPREQYNSTYRVVSVLTVLH 240  
QY 334 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSREEMTKNQVSLTCLVK 393  
Db 241 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSREEMTKNQVSLTCLVK 300  
QY 394 GFYPDSIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVWHE 453  
Db 301 GFYPDSIAVWESSGQPNENYNTTPVLDSDGSFFLYSLRLTVDKSRWQEGNVFCSCVWHE 360  
QY 454 ALHNHYTQKSLSLSPGK 470  
Db 361 ALHNRETQKSLSLSPGK 377

RESULT 4  
S37483  
Ig gamma-2a chain - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C;Accession: S37483  
R;Ducancel, F.F.D.  
submitted to the EMBL Data Library, February 1993  
A;Reference number: S37483  
A;Accession: S37483  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-469 <DUC>  
A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;276-345/Domain: immunoglobulin homology <IMM>

Query Match 64.0%; Score 1611.5; DB 2; Length 469;  
Best Local Similarity 64.4%; Pred. No. 1.4e-84;  
Matches 304; Conservative 60; Mismatches 103; Indels 5; Gaps 4;

QY 1 MGWSCIILFLVATATGVHSQVLVQSGAEVKKPGASVKVSCKASGYFTFTSYWQWVVKQAP 60  
Db 1 MGWSWIFLLSGTAGVHCQIQLOQQSGPELVKPGASVKISCKASGYFTFTDYIYNWVKQP 60  
QY 61 GQGLEWMEIDPDSYNYNOKPKGKATITVDSTSTAYMELSLRSDDTAVYYCARNRD 120  
Db 61 GQGLUKWIGWIYASGNTRYENFKGKATLVDTSSSTAYMQLSLTSDDTAVYYFCARAMG 120  
QY 121 YNNWYFDVWGQGLTVTVSSASTKGPSVFLPASPCKSTSGTAAALGCLVKDYFPEPTVTS 180  
Db 121 -ATATLLDYGQGLTVTVSSAKTAPSVYPLAPVCGDTTSSVTLGCLVKGYPPEPTVLT 179  
QY 181 WNSGALTSGVHTFPAPVLQSSGLYSLSSVTVTPSSSLGTQTQYICNVNHPKNTKVKRVEP 240

Db 180 WNSGSLSSGVHTFPAPVLQSD-LYTLSSSVTVTSTWFSQSITCNVAHPASSTKVDKKTIEP 238  
QY 241 KSCDKTHTCPP-CPAPELGGPSVFLPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKF 298  
Db 239 RG-PTIKPCPCPKCAPNLLGSPSVFPPPKIKDVLMLSLSPITCVTVVVDVSEDDPDVQI 297  
QY 299 NWYVDGVEVHNNAKTKPREQYNSTYRVVSVLTVLHQDMLNGKEYKCKVSNKALPAPIEKT 358  
Db 298 SWFVNNVEVHTAQQTHTREDYNSTLRVVSALPIQHDNMSGEKFKCKVNNKDLPAPIERT 357  
QY 359 ISKAKGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 418  
Db 358 ISKPKGSVRAPQVTVLPPPEEETKKQVTLCTMVTDFEPDIYVEWTNGKTELNKNTE 417  
QY 419 PVLDSDGSFFLYSLTVDKSRWQQGNVFCSCVMHEALNNHYTQKSLSLSPGK 470  
Db 418 PVLDSDGSFYFMYSKLRVEKKNNVERNVSVCVVHGLEHNNHHTTKSFSTRTPCK 469  
RESULT 5  
G2HU  
Ig gamma-2 chain C region - human  
C;Species: Homo sapiens (man)  
C;Date: 30-Apr-1981 #sequence\_revision 13-Jun-1983 #text\_change 21-Jul-2000  
C;Accession: A93906; A92809; A90752; A93132; A02148  
R;Ellison, J.; Hood, L.  
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982  
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain  
A;Reference number: A93906; MUID:82197621  
A;Accession: A93906  
A;Molecule type: DNA  
A;Residues: 1-326 <ELL>  
A;Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056  
A;Note: Lys-326 is probably removed posttranslationally  
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.  
J. Immunol. 125, 1048-1054, 1980  
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and  
A;Reference number: A92809; MUID:81007873  
A;Contents: myeloma protein T11  
A;Accession: A92809  
A;Molecule type: protein  
A;Residues: 1-19,'Q',21-57,'2',59,'A',61-193,'D',195-325 <WAN>  
A;Note: Trp-156 is at or near the complement-binding site  
R;Connell, G.E.; Parr, D.M.; Hofmann, T.  
Can. J. Biochem. 57, 758-767, 1979  
A;Title: The amino acid sequences of the three heavy chain constant region domains of  
A;Reference number: A90752; MUID:80001357  
A;Contents: myeloma protein Zie  
A;Accession: A90752  
A;Molecule type: protein  
A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',1  
A;Note: this sequence has since been revised  
R;Hofmann, T.; Parr, D.M.  
Mol. Immunol. 16, 923-925, 1979  
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin  
A;Reference number: A93132; MUID:80114419  
A;Contents: Zie  
A;Accession: A93132  
A;Molecule type: protein  
A;Residues: 238-275 <HOF>  
R;Hofmann, T.; Parr, D.M.  
submitted to the Atlas, March 1980  
A;Reference number: A94591  
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268  
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amid  
ned  
R;Milstein, C.; Frangione, B.  
Biochem. J. 121, 217-225, 1971  
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.  
A;Reference number: A90253; MUID:72033500  
A;Contents: annotation; myeloma protein Sa, disulfide bonds  
R;Frangione, B.; Milstein, C.; Pink, J.R.L.

Nature 221, 145-148, 1969  
 A:Title: Structural studies of immunoglobulin G.  
 A:Reference number: A93157; MUID:69064124  
 A:Contents: annotation; Sa, disulfide bonds  
 C:Genetics:  
 A:Gene: GDB:IGHC2

A:Cross-references: GDB:119338; OMIM:147110  
 A:Map position: 14q32.33-14q32.33  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
 F:20-85/Domain: immunoglobulin homology <IM1>  
 F:133-202/Domain: immunoglobulin homology <IM2>  
 F:239-306/Domain: immunoglobulin homology <IM3>  
 F:14/Disulfide bonds: interchain (to light chain) #status experimental  
 F:27-83,140-200,246-304/Disulfide bonds: #status experimental  
 F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
 F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 64.0%; Score 1610; DB 1; Length 326;  
 Best Local Similarity 91.8%; Pred. No. 1.1e-84;  
 Matches 303; Conservative 10; Mismatches 13; Indels 4; Gaps 2;

QY 141 ASTKGPSVPEPLAPSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSVHTFPVAVLQSS 200  
 |||||  
 Db 1 ASTKGPSVPEPLAPSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSVHTFPVAVLQSS 60  
 QY 201 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNTRKVDKRPVKSCDKTHCTCPAPPELLGG 260  
 |||||  
 Db 61 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNTRKVDKRPVKSCDKTHCTCPAPPELLGG 116  
 QY 261 PSVFLEPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNAKTKPREEQYN 320  
 |||||  
 Db 117 PSVFLEPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNAKTKPREEQYN 176  
 QY 321 STYRVVSVLTUHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 380  
 |||||  
 Db 177 STYRVVSVLTUHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 236  
 QY 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 440  
 |||||  
 Db 237 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 296  
 QY 441 QGQNFVSCVMHEALHNHYTQKSLSLSPGK 470  
 |||||  
 Db 297 QGQNFVSCVMHEALHNHYTQKSLSLSPGK 326

RESULT 6  
 G4HU  
 Ig gamma-4 chain C region - human  
 C:Species: Homo sapiens (man)  
 C:Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 16-Jul-1999  
 C:Accession: A90933; A90249; A02150  
 R:Ellison, J.; Buxbaum, J.; Hood, L.  
 DNA 1, 11-18, 1981  
 A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.  
 A:Reference number: A90933; MUID:83157104  
 A:Accession: A90933  
 A:Molecule type: DNA  
 A:Residues: 1-327 <ELL>  
 A>Note: the sequence was determined from the germline gene  
 R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.  
 Biochem. J. 117, 33-47, 1970  
 A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant region of the gamma4 chain.  
 A:Reference number: A90249; MUID:70207560  
 A:Accession: A90249  
 A:Molecule type: protein  
 A:Residues: 1-30;81-326 <PIN>  
 C:Genetics:  
 A:Gene: GDB:IGHG4

A:Cross-references: GDB:119340; OMIM:147130  
 A:Map position: 14q32.33-14q32.33  
 A:Introns: 99/1; 111/1; 221/1  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
 F:20-85/Domain: immunoglobulin homology <IM1>  
 F:99-110/Region: hinge  
 F:134-203/Domain: immunoglobulin homology <IM2>  
 F:240-307/Domain: immunoglobulin homology <IM3>  
 F:14/Disulfide bonds: interchain (to light chain) #status experimental  
 F:27-83,141-201,247-305/Disulfide bonds: #status predicted  
 F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
 F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 63.5%; Score 1599.5; DB 1; Length 327;  
 Best Local Similarity 91.8%; Pred. No. 4.5e-84;  
 Matches 303; Conservative 9; Mismatches 15; Indels 3; Gaps 1;

QY 141 ASTKGPSVPEPLAPSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSVHTFPVAVLQSS 200  
 |||||  
 Db 1 ASTKGPSVPEPLAPSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSVHTFPVAVLQSS 60  
 QY 201 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNTRKVDKRPVKSCDKTHCTCPAPPELLGG 260  
 |||||  
 Db 61 GLYSLSSVVTVPSSSLGTQTYICNVNHPKSNTRKVDKRPVKSCDKTHCTCPAPPELLGG 117  
 QY 261 PSVFLEPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNAKTKPREEQYN 320  
 |||||  
 Db 118 PSVFLEPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNAKTKPREEQYN 177  
 QY 321 STYRVVSVLTUHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 380  
 |||||  
 Db 178 STYRVVSVLTUHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 237  
 QY 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 440  
 |||||  
 Db 238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 297  
 QY 441 QGQNFVSCVMHEALHNHYTQKSLSLSPGK 470  
 |||||  
 Db 298 QGQNFVSCVMHEALHNHYTQKSLSLSPGK 327

RESULT 7  
 G2MS11  
 Ig gamma-2b chain - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 31-Mar-1980 #sequence\_revision 01-Dec-2000 #text\_change 01-Dec-2000  
 C:Accession: S25057; A02157; A26235; A26233; A26233; A53598  
 R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.  
 submitted to the EMBL Data Library, July 1992  
 A:Description: Production of a tobacco mosaic virus (TMV) inactivating neotop specific  
 A:Reference number: S25057  
 A:Accession: S25057  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-474 <FIS>  
 A:Cross-references: EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827  
 R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.  
 Nature 283, 786-789, 1980  
 A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from  
 A:Reference number: A02157; MUID:80120716  
 A:Contents: a allele  
 A:Accession: A02157  
 A:Molecule type: DNA  
 A:Residues: 138-161, '1', '163-189, 'FP', '193-474 <YAN>  
 A:Cross-references: GB:J00461  
 A>Note: the sequence was determined from the germline gene  
 R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.  
 Science 206, 1299-1303, 1979



A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b heavy chain  
A:Reference number: A26235; MUID:80081501  
A:Contents: MPC 11  
A:Accession: A26235  
A:Molecule type: mRNA  
A:Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TU1>  
A:Note: Lys-474 is probably removed posttranslationally  
R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.  
Science 206, 1303-1306, 1979  
A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglobulin heavy chain  
A:Reference number: A26232; MUID:80081502  
A:Accession: A26232  
A:Molecule type: DNA  
A:Residues: 138-172,'P',174-189,'FP',193-376,'T',378-474 <TU2>  
R:Ollio, R.; Rougeon, F.  
Nature 296, 761-763, 1982  
A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma2b heavy chain  
A:Reference number: A26233; MUID:82173203  
A:Contents: b allele  
A:Accession: A26233  
A:Molecule type: DNA  
A:Residues: 138-161,'L',163-189,'FP',193-300,'R',302-331,'A',333-437,'DI',440-474 <OLL>  
A:Cross-references: GB:J00461  
R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi, J.  
J. Biol. Chem. 269, 12345-12350, 1994  
A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.  
A:Reference number: A53598; MUID:94216359  
A:Accession: A53598  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 234-251 <KIM>  
C:Comment: The a allele sequence is shown.  
C:Genetics:  
A:Introns: 138/1; 236/1; 258/1; 368/1  
A:Complex: An immunoglobulin heterotrimer consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:157-222/Domain: alternative splicing; duplication; glycoprotein; heterotrimer; immunoglobulin homology  
F:236-257/Region: hinge  
F:281-350/Domain: immunoglobulin homology <IM2>  
F:387-454/Domain: immunoglobulin homology <IM3>  
F:152/Disulfide bonds: interchain (to light chain) #status predicted  
F:164-220,288-348,394-452/Disulfide bonds: #status predicted  
F:247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted  
F:324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 61.58; Score 1547; DB 1; Length 474;  
Best Local Similarity 61.28; Pred. No. 6.7e-81;  
Matches 292; Conservative 67; Mismatches 108; Indels 10; Gaps 3;

Qy 1 MGWSCIIFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVQKAP 60  
Db 1 MENSWIFLFLSGTAGVHSEVQLQSGPELVNPGASVKMSCKASGYTFTITVHWWVKQK 60

Qy 61 GQLEWMGEIDPSDYTNYNQKFGKATITVDSTSTAYMELSLRSDEDTAVYYCARNRD 120  
Db 61 GQGLEWIGYINPNKDGTKFNEKEKFKATLTSDKSNTAYMELSLTSDESAVYYCARDYD 120

Qy 121 YSNWYFDVWQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGLVKKYDFPEPTVS 180  
Db 121 YD---WFAYWQGGFLTVTSAKTTTPPSYIPLAPGCGDTTGGSSVTSGCLVKGYPFESVT 177

Qy 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTPSSSLGTQTYICNVNHPKSNKTKDKRVEP 240  
Db 181 WNSGSLSSVHTLSQLQSGLYTHSSSVTPSSITWFSQTVCSVAHPASSTTVDKKLEP 237

Qy 241 KSCDKT-HTCPP-----CPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHED 293  
Db 238 SGPISTINPCPCKECHKCPAPNLEGGPSVFIFFPNPKDVLMSITLTKVTCVVDVSEDD 297

Qy 294 PEVKFNWYDGVVEVHNNAKTRPEEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALP 353

Db 298 PDVQISWFMVNNVEVHTAQTQTHREDYNTIRVSTPLQHQDMGSGKEFKCKVNNKNDLPS 357  
Qy 354 PIEKTISKAKQPREPQVYITLPPSGREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 413  
Db 358 PIERTISKIKGLVRAPQVYILPPAEQLSRKDVSLTCLVGFNPGDISVEWTSNGTTEEN 417  
Qy 414 YKTTTPVLDSGSPFLYSKLVTDKSRWQGNVFCSSVMHEALHNYHTOKSLSLSPGK 470  
Db 418 YKDTAPVLDSGSIYFKLNMKTSKWEKTSFSCNVRHEGLKNYLLKTKTISRSPGK 474

RESULT 8  
Ig gamma-2a chain (mAb735) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 16-Jul-1999  
C:Accession: S40295  
R:Kiebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; submitted to the EMBL Data Library, January 1993  
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 again  
A:Reference number: S40295  
A:Accession: S40295  
A:Molecule type: protein  
A:Residues: 1-446 <KLE>  
C:Genetics:  
A:Map position: 12  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid  
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>  
F:1-117/Domain: V-D-J region <VDJ>  
F:118-446/Domain: C region <CHR>  
F:118-214/Domain: C1 region <CH1>  
F:215-230/Region: hinge  
F:231-340/Domain: C2 region <CH2>  
F:341-446/Domain: C3 region <CH3>  
F:360-427/Domain: immunoglobulin homology <IMM>  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted  
F:132/Disulfide bonds: interchain (to light chain) #status predicted  
F:224,227,229/Disulfide bonds: interchain #status predicted  
F:237/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 61.48; Score 1545; DB 2; Length 446;  
Best Local Similarity 64.48; Pred. No. 8.1e-81;  
Matches 291; Conservative 59; Mismatches 94; Indels 8; Gaps 4;

Qy 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVQKAPQGLEWMGEIDPSDSYNY 79  
Db 1 QIQLQSGPELVNPGASVKISCKASGYTFTDYIHWVKQRPGEGLWIGWYPGSGNTKY 60

Qy 80 NQKFKGKATITVDSTSTAYMELSLRSDEDTAVYYCARNRDYNNWYFDVWQGLTVTVS 139  
Db 61 NEKFKGKATITVDSSSTAYMQLSLSLTSDEDSAVYFCARGGFA----MDYWGQGTSTVTS 116

Qy 140 SASTKGPSVFPLAPSSKSTSGGTAAALGLVKKYDFPEPTVSVMNSGALTSGVHTFPAVLQ 199  
Db 117 SAKTTAPSVYPLAPVCGDTTGGSSVTGLCVKGYPEPTVLTWNSSGSLSSGVTFAVLQ 176

Qy 200 SGLYSLSVTVTPSSSLGTQTYICNVNHPKSNKTKDKRVEPKSCDKTHTCPP--CPAP 257  
Db 177 D-LYTLSSSVTVTSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPCPKCPAPNL 234

Qy 258 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVEVHNNAKTRPEE 317  
Db 235 LGGPSVFLFPPKPKIDVLMISLSPWTCVVDVSEDDPDVQISWFNNVEVLTQQTTHRE 294

Qy 318 QYNSTRYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQRPPEVYTLPPS 377  
Db 295 DYNSTRYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIERTISPKGSRAPQVYVLP 354

Qy 378 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSLKTV 437





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QY 196 VLQSSGLYSLSSVVVPSSSLGTQTYICNVNHNKPSNTKVDKRVKPSCKDKTHTCPP--CP 253
Db 176 VLQSD-LYTLSSSVTVFSSSTSETVTCNVAHPASSTKVDKVIKVRDCG----CKPCICT 230
QY 254 APPELLGGSPVLEFPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 313
Db 231 VPEV---SSVFIAPPKPKDGLITLTPKVTCCVVVDLSKDDPEVQFSWFVDDVEVHTAQTQ 287
QY 314 PREEQYNSTYRVVSVLTVLDQWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 373
Db 288 PREEQNSTFRSVELPIHMDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPOVYT 347
QY 374 LPSPREEMTKNQVSLTCLVKGYGSPDSIAVEWESNGOPENNPKTPPVLDSDGSFFLYSKL 433
Db 348 IPPPKQNAKDKVSLTCMITDFPEDITVEQWNGQPAENYKNTQPIMDTDSYFYYSKL 407
QY 434 TVDKSRWQOGNVFSCSVMEALHNNHYTKQSLSLSPGK 470
Db 408 NVQKSNWEAGNTFTCSVLHEGLHHNHTKSLSRSPGK 444

RESULT 14
I47159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47159; MUID:95015845
A:Accession: I47159
A>Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C:Gene: IgG2a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMX>

Query Match 50.3%; Score 1267; DB 2; Length 328;
Best Local Similarity 69.9%; Pred. No. 3.6e-65;
Matches 232; Conservative 42; Mismatches 52; Indels 6; Gaps 2;

QY 141 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSS 200
Db 1 APTAPSVYPLAPCSRDTSGPNVALGCLASSYPPEPTVTWNSGALTSGVHTFPSPVLQPS 60
QY 201 GLYSLSSVVTVPSLSLGTQTYICNVNHNKPSNTKVDKRVKPSCKDKTHTCPPCPAPPELLGG 260
Db 61 GLYSLSSMTVTPASSLSKSYTCNVNHPATTTKVDKRVGTKTKPPCPCIPACESP----G 116
QY 261 PSVFLFPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320
Db 117 PSVFIFPPKPKDGLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHTAQTTRKPEEQFN 176
QY 321 STYRVSVLTVLHMDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 380
Db 177 STYRVSVLPIQHMDWLNGKEFKCKVNNKDLPAITRIISKAKGQTRPEQVYTLPPHAE 236
QY 381 MTKNOVSLTCLVKGYFSPDSIAVEWESNGQ--PENNYKTTTPPVLDSDGSFFLYSKLTVDKS 438
Db 237 STYRVSVLPIQHMDWLNGKEFKCKVNNKDLPAITRIISKAKGQTRPEQVYTLPPHAE 236
QY 439 RWOQGNVFCVSMHEALHNNHYTKQSLSLSPGK 470
Db 297 SNQGGGIFOCVAVMEALHNNHYTKQSLSKTPGK 328

Search completed: August 14, 2002, 15:19:01
Job time: 689 sec
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RESULT 15

I47160



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GenCore version 4.5

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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:23:14 ; Search time 53.64 Seconds  
(without alignments)  
339.265 Million cell updates/sec

Title: US-09-499-662-145

Perfect score: 2517

Sequence: 1 MGWSCIIILFLVATAGVHSQ.....MHEALHHYTKSLSPQK 470

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1758	69.8	330	1	GCL_HUMAN	P01857 homo sapien
2	1610	64.0	326	1	GC2_HUMAN	P01859 homo sapien
3	1599.5	63.5	327	1	GC4_HUMAN	P01861 homo sapien
4	1231.5	48.9	323	1	GC_RABIT	P01870 oryctolagus
5	1210.5	48.1	329	1	GC2_CAVPO	P01862 cavia porce
6	1162	46.2	290	1	GC3_HUMAN	P01860 homo sapien
7	1155	45.9	326	1	GC1_RAT	P20759 rattus norv
8	1150	45.7	329	1	GC3_MOUSE	P22436 mus musculu
9	1145	45.5	324	1	GC1_MOUSE	P01868 mus musculu
10	1144.5	45.5	333	1	GC8_RAT	P20761 rattus norv
11	1140	45.3	393	1	GC1M_MOUSE	P01869 mus musculu
12	1139	45.3	398	1	GC3M_MOUSE	P03987 mus musculu
13	1129	44.9	330	1	GCAA_MOUSE	P01863 mus musculu
14	1127.5	44.8	329	1	GCC_RAT	P20762 rattus norv
15	1126.5	44.8	335	1	GCAE_MOUSE	P01864 mus musculu
16	1124	44.7	399	1	GCAE_MOUSE	P01865 mus musculu
17	1115	44.3	322	1	GCA_RAT	P20760 rattus norv
18	1085	43.1	336	1	GCB_MOUSE	P01866 mus musculu
19	1080	42.9	405	1	GCB_MOUSE	P01867 mus musculu
20	560.5	22.3	139	1	HV07_MOUSE	P01751 mus musculu
21	526	20.9	117	1	HV06_MOUSE	P01750 mus musculu
22	522.5	20.8	137	1	HV11_MOUSE	P01755 mus musculu
23	522	20.7	138	1	HV48_MOUSE	P03980 mus musculu
24	514	20.4	117	1	HV05_MOUSE	P01749 mus musculu
25	508	20.2	140	1	HV02_MOUSE	P01746 mus musculu
26	502	19.9	117	1	HV09_MOUSE	P01753 mus musculu
27	489	19.4	117	1	HV04_MOUSE	P01748 mus musculu
28	486.5	19.3	429	1	EPC_RAT	P01855 rattus norv
29	486	19.3	117	1	HV49_MOUSE	P06328 mus musculu
30	486	19.3	428	1	EPC_HUMAN	P01854 homo sapien
31	481	19.1	136	1	HV15_MOUSE	P01759 mus musculu
32	480	19.1	117	1	HV10_MOUSE	P01754 mus musculu
33	477	19.0	117	1	HV1G_HUMAN	P23083 homo sapien

## ALIGNMENTS

## RESULT 1

ID	GCL_HUMAN	STANDARD;	PRT;	330 AA.
AC	P01857;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Ig gamma-1 chain C region.			
GN	IGHG1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82274238; PubMed=6287432;			
RA	Ellison J.W., Berson B.J., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene."			
RL	Nucleic Acids Res. 10:4071-4079(1982).			
RN	[2]			
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RA	Waxdal M.J., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino			
RL	acid sequence of heavy-chain cyanogen bromide fragments H1-H4."			
RL	Biochemistry 9:3161-3170(1970).			
RN	[3]			
RP	SEQUENCE OF 136-329 (EU).			
RX	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RA	Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino			
RL	acid sequence of heavy-chain cyanogen bromide fragments H5-H7."			
RL	Biochemistry 9:3171-3181(1970).			
RN	[4]			
RP	SEQUENCE (MYELOMA PROTEIN NIE).			
RX	MEDLINE=77070269; PubMed=826475;			
RA	Ponstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a			
RL	monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The			
RT	chymotryptic peptides of the H-chain, alignment of the tryptic			
RL	peptides and discussion of the complete structure."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).			
RN	[5]			
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RX	MEDLINE=83289131; PubMed=6884994;			
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RT	"Three-dimensional structure determination of antibodies. Primary			
RL	structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).			
RN	[6]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X.			

P06336 mus musculu  
P01743 homo sapien  
P01756 mus musculu  
P01757 mus musculu  
P06329 mus musculu  
P01747 mus musculu  
P01744 homo sapien  
P01872 mus musculu  
P01871 homo sapien  
P01745 mus musculu  
P03988 oryctolagus  
P01873 mus musculu

RT Intrachain disulfide bonds.";  
RL Biochemistry 9:3188-3196(1970).  
RN [7]  
RP DISULFIDE BONDS.  
RX MEDLINE-77070267; PubMed-1002129;  
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal  
RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and  
RT characterization of the protein, the L- and H-chains, the  
RT cyanogen bromide cleavage products, and the disulfide bridges.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
RN [8]  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
RX MEDLINE-81208100; PubMed-7236608;  
RA Deisenhofer J.;  
RT "Crystallographic refinement and atomic models of a human Fc fragment  
RT and its complex with fragment B of protein A from Staphylococcus  
RT aureus at 2.9- and 2.8-A resolution.";  
RL Biochemistry 20:2361-2370(1981).  
CC -!- MISCELLANEOUS: NIE HAS THE GLM(17) ALLOTYPIC MARKER, 97-K, & THE  
CC GLM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GLM(3)  
CC MARKER & THE GLM (NON-1) MARKERS.  
CC -!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF  
CC 35,116,198,269 & 272.  
CC -!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES  
CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES  
CC 268-272.  
CC -!- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF  
CC RESIDUES 198,267&272.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; J00228; AAC82527.1; ALT\_INIT.  
DR PIR; A02146; GHU.  
DR PDB; 1FC1; 15-JUL-92.  
DR PDB; 1FC2; 15-JUL-92.  
DR MIM; 147100; -  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003600; Ig\_like.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00410; Ig\_like; 1.  
DR SMART; SM00407; Igc1; 2.  
DR PROSITE; PS00290; IG\_MHC; 2.  
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
KW 3D-structure.  
FT NON\_TER 1 1  
FT DOMAIN 1 98 CH1.  
FT DOMAIN 99 110 HINGE.  
FT DOMAIN 111 223 CH2.  
FT DOMAIN 224 330 CH3.  
FT DISULFID 27 83  
FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).  
FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).  
FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).  
FT DISULFID 144 204  
FT DISULFID 250 308  
FT CARBOHYD 180 180  
FT MOD\_RES 330 330  
FT VARIANT 97 97  
FT VARIANT 239 239  
FT VARIANT 241 241  
FT STRAND 123 126  
FT HELIX 130 134  
N-LINKED (GLCNAC...).  
REMOVED POST-TRANSLATIONALLY.  
K -> R (IN GLM(3) MARKER).  
/FTid=VAR\_003886.  
D -> E (IN GLM(NON-1) MARKER).  
/FTid=VAR\_003887.  
L -> M (IN GLM(NON-1) MARKER).  
/FTid=VAR\_003888.

FT	TURN	136	137
FT	STRAND	141	148
FT	STRAND	158	162
FT	TURN	163	164
FT	STRAND	165	166
FT	STRAND	175	178
FT	STRAND	183	190
FT	HELIX	193	197
FT	TURN	198	199
FT	STRAND	202	206
FT	STRAND	215	219
FT	STRAND	227	227
FT	STRAND	230	234
FT	STRAND	238	240
FT	HELIX	241	242
FT	STRAND	245	256
FT	STRAND	260	266
FT	TURN	267	268
FT	STRAND	274	276
FT	STRAND	280	281
FT	TURN	283	284
FT	STRAND	287	296
FT	HELIX	297	301
FT	TURN	302	303
FT	STRAND	306	312
FT	TURN	313	314
FT	TURN	316	317
FT	TURN	320	324
SQ	SEQUENCE	330 AA;	3770EE106C2FA33D CRC64;

Query Match 69.8%; Score 1758; DB 1; Length 330;  
Best Local Similarity 99.1%; Pred. No. 1.3e-113;  
Matches 327; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 141 ASTKGPSVPFLAPSSKSTGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200  
Db 1 ASTKGPSVPFLAPSSKSTGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
QY 201 GLYSLSVVTVPSSSISGTYICNVNHPKNTKVDKRVKPKSCDKTHTCCPCAPPELLGG 260  
Db 61 GLYSLSVVTVPSSSISGTYICNVNHPKNTKVDKRVKPKSCDKTHTCCPCAPPELLGG 120  
QY 261 PSVFELPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVVHNAKTKPREEQYN 320  
Db 121 PSVFELPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVVHNAKTKPREEQYN 180  
QY 321 STYRVVSVLTVHLQDWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 380  
Db 181 STYRVVSVLTVHLQDWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240  
QY 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 440  
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300  
QY 441 QOQNVFSCSVMEALHNHYTQKSLSLSPGK 470  
Db 301 QOQNVFSCSVMEALHNHYTQKSLSLSPGK 330

RESULT 2  
GC2\_HUMAN  
ID GC2\_HUMAN STANDARD; PRT; 326 AA.  
AC P01859;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Ig gamma-2 chain C region.  
GN IGHG2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.



OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE OF 2-326 FROM N.A.  
RX MEDLINE=82197621; PubMed=6804948;  
RA Ellinor J.W., Hood L.E.;  
RT "Linkage and sequence homology of two human immunoglobulin gamma  
heavy chain constant region genes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).  
RN [2]  
RP SEQUENCE OF 88-115 FROM N.A.  
RC TISSUE=Fetal liver;  
RX MEDLINE=83001943; PubMed=6811139;  
RA Takahashi N., Ueda S., Obata M., Nikaide T., Nakai S., Honjo T.;  
RT "Structure of human immunoglobulin gamma genes: implications for  
evolution of a gene family.";  
RL Cell 29:671-679(1982).  
RN [3]  
RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.  
RC TISSUE=Fetal liver;  
RX MEDLINE=84235992; PubMed=6329676;  
RA Krawinkel U., Rabbitts T.H.;  
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma  
heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass  
genes.";  
RL EMBO J. 1:403-407(1982).  
RN [4]  
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).  
RX MEDLINE=81007873; PubMed=6774012;  
RA Wang A.-C., Tung E., Fudenberg H.H.;  
RT "The primary structure of a human IgG2 heavy chain: genetic,  
evolutionary, and functional implications.";  
RL J. Immunol. 125:1048-1054(1980).  
RN [5]  
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).  
RX MEDLINE=8001357; PubMed=113060;  
RA Connell G.E., Parr D.M., Hofmann T.;  
RT "The amino acid sequences of the three heavy chain constant region  
domains of a human IgG2 myeloma protein.";  
RL Can. J. Biochem. 57:758-767(1979).  
RN [6]  
RP SEQUENCE OF 238-275 (ZIE).  
RX MEDLINE=80114419; PubMed=118920;  
RA Hofmann T., Parr D.M.;  
RT "A note of the amino acid sequence of residues 381-391 of human  
immunoglobulin gamma chains.";  
RL Mol. Immunol. 16:923-925(1979).  
RN [7]  
RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).  
RA Hofmann T., Parr D.M.;  
RL Submitted (MAR-1980) to the PIR data bank.  
RN [8]  
RP SEQUENCE OF 1-121 (DOT).  
RX MEDLINE=95255298; PubMed=7737190;  
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;  
RT "Characterization of the two unique human anti-flavin monoclonal  
immunoglobulins.";  
RL Eur. J. Biochem. 228:886-893(1995).  
RN [9]  
RP DISULFIDE BONDS.  
RX MEDLINE=72033500; PubMed=4940472;  
RA Milstein C., Frangione B.;  
RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";  
RL Biochem. J. 121:217-225(1971).  
RN [10]  
RP DISULFIDE BONDS.  
RX MEDLINE=69064124; PubMed=5782707;  
RA Frangione B., Milstein C., Pink J.R.L.;  
RT "Structural studies of immunoglobulin G.";  
RL Nature 221:145-148(1969).  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: J00230; AAB59393.1; -;  
DR PIR: A02148; G2HU.  
DR HSP; P01857; 1FC1.  
DR MIM; 147110; -;  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003600; Ig\_like.  
DR Pfam: PF00047; ig; 3.  
DR SMART; SM00410; Ig\_like; 1.  
DR SMART; SM00407; IGc1; 2.  
DR PROSITE; PS00290; IG\_MHC; 2.  
KW Immunoglobulin domain; Immunoglobulin C region.  
FT NON\_TER 1 1  
FT DOMAIN 1 98  
FT CH1.  
FT HINGE.  
FT DOMAIN 99 110  
FT CH2.  
FT DOMAIN 111 219  
FT CH3.  
FT DOMAIN 220 326  
FT INTERCHAIN (WITH A LIGHT CHAIN).  
FT DISULFID 14 14  
FT DISULFID 27 83  
FT DISULFID 102 102  
FT INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 103 103  
FT INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 106 106  
FT INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 109 109  
FT INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 140 200  
FT DISULFID 246 304  
FT SITE 156 156  
FT MOD\_RES 326 326  
FT VARIAT 60 60  
FT CONFLICT 109 109  
FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;  
SQ  
Query Match 64.0%; Score 1610; DB 1; Length 326;  
Best Local Similarity 91.8%; Pred. No. 1.8e-103;  
Matches 303; Conservative 10; Mismatches 13; Indels 4; Gaps 2;  
QY 141 ASTKGPSVPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200  
Db 1 ASTKGPSVPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
QY 201 GLYSLSVVVTPSSSLGTQTYICNVNHPKSNKVDKRVKPSCKDKTHTCPCPAPELGG 260  
Db 61 GLYSLSVVVTPSSSLGTQTYICNVNHPKSNKVDKRVKPSCKDKTHTCPCPAPELGG 116  
QY 261 PSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320  
Db 117 PSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 176  
QY 321 STYRVSVLTVLHQDLWNGKEYCKVSNKALPAPTEKTIKAKGQPREQVYTLPPSRREE 380  
Db 177 STFRVSVLTVLHQDLWNGKEYCKVSNKALPAPTEKTIKAKGQPREQVYTLPPSRREE 236  
QY 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPTPPDLSDGSGFSELYSKLTVDKSRW 440  
Db 237 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPTPPDLSDGSGFSELYSKLTVDKSRW 296  
QY 441 QGQNVFSCSVMHHEALHNHYTQKSLSLSPGK 470  
Db 297 QGQNVFSCSVMHHEALHNHYTQKSLSLSPGK 326  
RESULT 3  
GC4\_HUMAN STANDARD; PRT; 327 AA.  
AC P01861.  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)



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DR InterPro: IPR003597; Ig_c1.
DR SMART; PF00047; Ig; 3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 N -> E (IN REF. 2).
FT CONFLICT 71 71 V -> VPV (IN REF. 2).
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 173 173 N -> D (IN REF. 5).
FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 Q -> E (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 N -> D (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> D (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).
FT CONFLICT 284 284 N -> S (IN REF. 5).
SQ SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;

Query Match 48.9%; Score 1231.5; DB 1; Length 323;
Best Local Similarity 70.0%; Pred. No. 1.6e-77;
Matches 229; Conservative 34; Mismatches 57; Indels 7; Gaps 2;

QY 144 KGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSSGLY 203
DB 4 KAPSVFPLAPCCGTPSTVTLGCLVKGLYPEPTVTVNNTLLNGVTRFSPVQSSGLY 63
QY 204 SLSSWVTPSSSLGTQYICNVNHPKNTKVDKRVKPSCKDTHTCPCPAPELLGGPSV 263
DB 64 SLSSWVSTSS---QPVTGNVAHPATNTKVDKTVAPSTCKSCK---PTCPPPELLGGPSV 116
QY 264 FLPPPKDILMISRTPEVTCVVDVSHEDPEVKFNKYVDGEVHNNAKTKPREQYNSTY 323
DB 117 FIFPKPKDILMISRTPEVTCVVDVSDQDPEVQFTWYINNEQVTRAPPLREQQFNSTI 176
QY 324 RVSVSLTLVHODWLNREYKCKVSNKALPAPIETKSKAGQPREPOVYITLPPSREEMTK 383
DB 177 RVSVSLTLHODWLNREYKCKVSNKALPAPIETKSKAGQPLEKPYITMGPPREELSS 236
QY 384 NQVSLTCLVKGYFSDIAVEHESGQPNENYKTTTPVLDSDGSPFLSKLVKDRSRWQQG 443
DB 237 RSVSLTCLMNGFYPSDISVSEWEKKAEDNYKTTTPVLDSDGSPFLYLNKLSVPTSEWQRG 296
QY 444 NVFSCSVNHEALHNYTKQKLSLSPGK 470
DB 297 DVFTCSVNHEALHNYTKQKLSRSPGK 323

RESULT 5
GC2_CAVPO STANDARD; PRT; 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
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Db 179 ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGYFIPSDIAVEWESSQGPENNYNTTP 238
Qy 419 PVLDSGDSFFLYSLKLTVDKSRWQGNVFCVSMHEALHNHYTKQSLSPGK 470
Db 239 PMLDSGDSFFLYSLKLTVDKSRWQGNVFCVSMHEALHNHYTKQSLSPGK 290

RESULT 7
GCL_RAT
ID GC1_RAT STANDARD; PRT; 326 AA.
AC P20759;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0017; PS0017.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; Ig_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 112 HINGE.
FT DOMAIN 113 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match 45.9%; Score 1155; DB 1; Length 326;
Best Local Similarity 63.4%; Pred. No. 2.8e-72;
Matches 211; Conservative 52; Mismatches 60; Indels 10; Gaps 4;

Qy 141 ASTKGPSVFPLAPSSKSTSGTAALGCLVKDYFPEPTVSNHGALTSVHTFPFAVLQSS 200
Db 1 AETAPSVYPLAPGALKSNMTLGLCVKGYFPEPTVTWNSGALTSVHTFPFAVLQ-S 59

Qy 201 GLYSLSVVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPCPAPELLGG 260
Db 60 GLYTLTSSVTPSWPSQVTCNVNHNKPSNTKVDKVEPKSCDKTHTCPCPAPELLGG 113

Qy 261 ---PSVFLFPPKPKDILMISRTPEVTCVVDVSHEDPEVKFNKVDGVNHNKTPREE 317
Db 114 SEVSVFIFPPKPKDILMISRTPEVTCVVDVSHEDPEVKFNKVDGVNHNKTPREE 173

Qy 318 QYNSTYRVVSVLTVLDHQLNGKEYCKVSNKALPAPIETISKAKGPREPQVYTLPPS 377
Db 174 QFNSTFRVSSELPILTHDQLNGRFRCKVTSAAFPSPSEIETISKAKGPREPQVYTLPPS 233

Qy 378 REEMTKNQVSLTCLVKGYFIPSDIAVEWESSQGPENNYNTTPVLDSDGSFFLYSLKLTVDK 437
Db 234 KEEMTQNEVSLTCLVKGYFIPSDIAVEWESSQGPENNYNTTPVLDSDGSFFLYSLKLTVDK 293
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Qy 438 SRWQGNVFCVSMHEALHNHYTKQSLSPGK 470
Db 294 EKWQGNVFCVSLHEGLNHNHYTKQSLSPGK 326

RESULT 8
GC3_MOUSE
ID GC3_MOUSE STANDARD; PRT; 329 AA.
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A.; Word C.J.; Rimm D.; Der-Balan G.P.; Martinez H.M.;
RA Tucker P.W.; Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
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CC -----
CC EMBL; J00451; -; NOT_ANNOTATED_CDS.
CC PIR; B02156; G3MSC.
CC HSSP; P01857; IFC1.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003597; Ig_cl.
CC InterPro; IPR003600; Ig_like.
CC Pfam; PF00047; Ig; 3.
CC SMART; SM00410; Ig_Like; 1.
CC SMART; SM00407; IGcl; 2.
CC PROSITE; PS00290; Ig_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 45.7%; Score 1150; DB 1; Length 329;
Best Local Similarity 65.0%; Pred. No. 6.2e-72;
Matches 215; Conservative 44; Mismatches 68; Indels 4; Gaps 3;

Qy 142 STKGPSVFPLAPSSKSTSGTAALGCLVKDYFPEPTVSNHGALTSVHTFPFAVLQSSG 201
Db 1 TTTAPSVYPLVPGCSSTSGSSVTLGCLVKGYFPEPTVKNYGNALSSGRTVSSVLQ-SG 59

Qy 202 LYSLSVVVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCP--PCPAPELLG 259
Db 60 FYSLSLVTPSSVTPSWPSQVTCNVNHNKPSNTKVDKVEPKSCDKTHTCP--IPKSTPPGSCPPGNTLG 118

Qy 260 GPSVFLFPPKPKDILMISRTPEVTCVVDVSHEDPEVKFNKVDGVNHNKTPREEQY 319
Db 119 GPSVFIFFPKPKDILMISLTPEVTCVVDVSHEDPEVKFNKVDGVNHNKTPREEQY 178

Qy 320 NSTYRVVSVLTVLDHQLNGKEYCKVSNKALPAPIETISKAKGPREPQVYTLPPSRE 379
Db 179 NSTYRVVSVLTVLDHQLNGKEYCKVSNKALPAPIETISKAKGPREPQVYTLPPSRE 238
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RA Brueggemann M.;  
 RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";  
 RL Gene 74:473-482(1988).  
 DR PIR: PS0018; 7FAB.  
 DR HSP; P01842; 7FAB.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003600; Ig\_1like.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00410; Ig\_Like; 1.  
 DR SMART; SM00407; IGc1; 2.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region.  
 FT NON\_TER 1  
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 27 80  
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 147 207  
 FT DISULFID 253 311  
 SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;  
 Query Match 45.5%; Score 1144.5; DB 1; Length 333;  
 Best Local Similarity 63.7%; Pred. No. 1.5e-71;  
 Matches 214; Conservative 45; Mismatches 68; Indels 9; Gaps 3;  
 Qy 141 ASTGSPVPEPLAPSKSGCTAALGCLVKDYFPEPTVSNVSGALTSVHTPEPAVLQSS 200  
 Db 1 AQTAPSYPIAPLAGCGDTTSVTLGCLVKGYFPEPTVTWNVSGALSDVHTPEPAVLQ-S 59  
 Qy 201 GLYLSVVYTPSSLSGRTQYICNVNHPKSTKVDKRVKPS-----CDKTHTCPCPCA 254  
 Db 60 GLYTLTSSVT--SSTWPSQTVTCNVAPASSTKVDKVERNGGIGHKCPTCPTCHKCPV 117  
 Qy 255 PELGGSPVFLPPKPKDTLMISRTPEVTCVVDVSHDEPKVKNWYVDGVEVHNNAKTKP 314  
 Db 118 PELGGSPVFLPPKPKDILLISQNAKVTCTVVDVSEEPDQVQFSWFFNNVEVHTAQTP 177  
 Qy 315 REEYNTSYRYVSVLTVLVDLQNGKEYCKVSNKALPAPIEKTSKAKGQPREPQVYTL 374  
 Db 178 REEQNTSYRYVSVLPIQHQDMGSEKFKCKVNNKALPSIEKTSKPKGLVRKPPQVYVM 237  
 Qy 375 PPSREEMTKNOVSLTCLVKGYFPEPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLT 434  
 Db 238 GPPTQLTEQTVSLTCLTSGFLPNDIGVEWTNNGHIEKNYKNTPEVMDSDGSFFMYSKLN 297  
 Qy 435 VDKSRWQGNVFCSSVMHEALHNHYTQKSLSLSPGK 470  
 Db 298 VERSRWDSRAPFVCSVHVEGLHNHIVEKISIRPPGK 333  
 RESULT 11  
 GCIM\_MOUSE  
 ID GCIM\_MOUSE STANDARD; PRT; 393 AA.  
 AC P01869;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Ig gamma-1 chain C region, membrane-bound form.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=80045036; PubMed=115593;  
 RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,  
 RA Takahashi N., Mano Y.;  
 RT "Cloning and complete nucleotide sequence of mouse immunoglobulin  
 gamma 1 chain gene.";

RL Cell 18:559-568(1979).  
 RN [2]  
 RP SEQUENCE OF 323-393 FROM N.A.  
 RX MEDLINE=82197626; PubMed=6804950;  
 RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;  
 RT "mRNA for surface immunoglobulin gamma chains encodes a highly  
 RT conserved transmembrane sequence and a 28-residue intracellular  
 RT domain.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).  
 RN [3]  
 RP SEQUENCE OF 323-366 FROM N.A.  
 RX MEDLINE=82115295; PubMed=6799207;  
 RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,  
 RA Eisenberg D., Wall R.;  
 RT "Gene segments encoding transmembrane carboxyl termini of  
 RT immunoglobulin gamma chains.";  
 RL Cell 26:19-27(1981).  
 RN [4]  
 RP SEQUENCE OF 1-44 FROM N.A.  
 RX MEDLINE=8222190; PubMed=6283537;  
 RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;  
 RT "Nucleotide sequences of gene segments encoding membrane domains of  
 RT immunoglobulin gamma chains.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).  
 CC -1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA  
 CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED  
 CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-  
 CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED  
 CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND  
 CC SEGMENT OF MU CHAINS.  
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 DR EMBL; V00793; CAA24172.1; -;  
 DR EMBL; V00793; CAA24173.1; -;  
 DR EMBL; V00793; CAA24174.1; -;  
 DR PIR; P02159; G1MSM.  
 DR HSP; P01842; 7FAB.  
 DR MGD; MGI:96446; Igh-4.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00407; IGc1; 2.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
 KW Alternative splicing; Transmembrane.  
 FT NON\_TER 1  
 FT DOMAIN 1 97 CH1.  
 FT DOMAIN 98 110 HINGE.  
 FT DOMAIN 111 217 CH2.  
 FT DOMAIN 218 324 CH3.  
 FT DISULFID 27 82  
 FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 138 198  
 FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).  
 FT DISULFID 244 302  
 FT TRANSMEM 340 357 POTENTIAL.  
 FT DOMAIN 358 393 CYTOPLASMIC (POTENTIAL).  
 SQ SEQUENCE 393 AA; 43386 MW; 4CC88343B7A1CE27 CRC64;

Query Match 45.3%; Score 1140; DB 1; Length 393;  
 Best Local Similarity 62.2%; Pred. No. 3.7e-71;  
 Matches 206; Conservative 55; Mismatches 60; Indels 10; Gaps 4;





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RX MEDLINE=81223894; PubMed=6787604;
RA Ollo R., Aulfray C., Morchamps C., Rougeon F.;
RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
RT suggests that exons can be exchanged between genes in a multigenic
RT family.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
RN [4]
RP MYELOMA PROTEIN MOPC 173.
RX MEDLINE=74175517; PubMed=4831970;
RA Bourgois A., Fougereau M., Rocca-Serra J.;
RT "Determination of the primary structure of a mouse IgG2a
RT immunoglobulin:amino-acid sequence of the Fc fragment. Implications
RT for the evolution of immunoglobulin structure and function.";
RL Eur. J. Biochem. 43:423-435(1974).
RN [5]
RX DISULFIDE BONDS.
RP MEDLINE=73056887; PubMed=4565406;
RA de Preval C., Fougereau M.;
RT "Determination of the primary structure of a mouse gamma G2a
RT immunoglobulin. Identification of the disulfide bridges.";
RL Eur. J. Biochem. 30:452-462(1972).
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CC -----
DR EMBL; V00798; CAA24178.1; -.
DR PIR; A02152; G2MSA.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG_Like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;

Query Match 44.9%; Score 1129; DB 1; Length 330;
Best Local Similarity 63.9%; Pred. No. 1.7e-70;
Matches 212; Conservative 43; Mismatches 73; Indels 4; Gaps 3;

QY 141 ASTKGPSVFPLAPSSKSTSGGTAALGLVVDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200
DB 1 AKTTAPSVYPLAPCGDTGTSSTGLGLVKGYPPEPTLTWNSGSLSSGVHTFPAVLQSD 60

QY 201 GLYSLSSVTVPSSSLGTQTYICNVNHPKSNKVKDKRVEPKSCDKTHTCPP--CPAPELL 258
DB 61 -LXTLSSSVTVTSSTWPSQSTTCNVNHPASSTKVDKKIEPRG-PTIKPCPPCKCPAPNLL 118

QY 259 GGPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 318
DB 119 GGPSVFIPPKIKDKLVLMISPIVTCVVVDVSDPDVDQVSWFNVEVHTAQTQTHRED 178

QY 319 YNSTYRVSVLTVLHODWLNGEKYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
DB 179 YNSTLVRVSLPIQHODWMSGKEFKCKVKNKDLPAPIERTISKPKGSVRAPQVYTLPPPE 238
```

```
QY 379 EEMTKNOVSLTCLVKGYPSPDIADVENSNGQPPENNYKTPPPVLDSDGSFFLYSLKTVDKS 438
DB 239 EEMTKQVTLTCLVKGYPSPDIADVENSNGQPPENNYKTPPPVLDSDGSFFLYSLKTVDKS 298
QY 439 RWOOGNVFSCVSMHEALHNHYVTKOKLSLSLSPCK 470
DB 299 NWVERNSYSCSVVHEGLHNHHTTKSFRTPKG 330

RESULT 14
GCC_RAT GCC_RAT STANDARD; PRT; 329 AA.
AC P20762;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2C chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88166903; PubMed=3127222;
RA Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
RT region cDNA: extensive homology to mouse gamma 3.";
RL Eur. J. Immunol. 18:317-319(1988).
CC -----
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CC -----
DR EMBL; X07189; CAA30169.1; -.
DR PIR; S00847; S00847.
DR HSSP; P01857; IFC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG_Like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 97 CHI.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 222 CH2.
FT DOMAIN 223 329 CH3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 143 203
FT DISULFID 249 307
SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;

Query Match 44.8%; Score 1127.5; DB 1; Length 329;
Best Local Similarity 62.8%; Pred. No. 2.1e-70;
Matches 209; Conservative 51; Mismatches 66; Indels 7; Gaps 3;

QY 141 ASTKGPSVFPLAPSSKSTSGGTAALGLVVDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200
DB 1 AKTTAPSVYPLVPGCGSTGSLVTLGLCVLKGYPPEPTVKNWNSGALSSGVHTFPAVLQ-S 59

QY 201 GLYSLSSVTVPSSSLGTQTYICNVNHPKSNKVKDKRVEPKSCDKTHTCPP--CPAPEL 257
DB 60 GLYTLSSSVTVPSSTWSSQVTCTVAHPATKSNLIKRIEPR---RPKRPPTDICSDDN 116
```

```
QY 258 LGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREE 317
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 117 LGRPSVFIFPPKPKDILMITLPKTCVVVDVSEEDPDQFSFVNDVRVFTAQTPHEE 176
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 318 QYNSTYRVVSVLTVLDHQLWLNKEYCKKYSNKKALPAPIETKISKAKGQPREPOVYTPPPS 377
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 177 QLNSTYRVVSVLTVLDHQLWLNKEYCKKYSNKKALPAPIETKISKAKGQPREPOVYTPPPS 236
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 378 REEMTKNOVSLTCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDK 437
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 237 RQMSKNKVSVCMTWTFSPASISVEWERNGELEQDQKNTLPVLDSDGSFFLYSLKLSVDT 296
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 438 SRWQGNVFCSCVMHEALHNHYTKQSLSPGK 470
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 297 DSWMRGDIWTCVWHEALHNHYTKQSLSPGK 335
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
GCAB_MOUSE
ID GCAB_MOUSE STANDARD; PRT; 335 AA.
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2A chain C region, B allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
  IgG2a and Ig2ab alleles of the mouse.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN [2]
RP SEQUENCE.
RX MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwereys M., Strosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
  chain Fc regions of Ig1a and Ig1b allotypic forms.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -!- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
  FROM BALB/C MICE, AT 15% OF THE POSITIONS.
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CC -----
DR EMBL; J00479; -; NOT_ANNOTATED_CDS.
DR PIR; A02153; G2MSAB.
DR HSSP; P01857; 1FC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IGCL; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
SQ SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;

Query Match 44.8%; Score 1126.5; DB 1; Length 335;
Best Local Similarity 61.6%; Pred. NO. 2.6e-70;
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Matches 207; Conservative 52; Mismatches 70; Indels 7; Gaps 2;
QY 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSNWSGALTSGVHTFPAVLQSS 200
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 AKTAPSVTPLVPVCGGTGSSVTIGCLVKGFPEPTVTLNWSGSLSSGVHTFPAVLQ-S 59
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 201 GLYSLSVVTVFPSSSLGTQTYICNVNHNKPSNTKVKDKRVEPK-----SCDKHTHCPPCA 254
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 GLYTLSSSVTVTSNTWPSQTITCNVAHPASSTKVDKKIEPRVPIITQNPCHQRPVPCA 119
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 255 PELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTP 314
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 PDLGGPSVFIFPPKPKDILMITLPKTCVVVDVSEEDPDQFSFVNDVRVFTAQTP 179
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 315 REEQYNSTYRVVSVLTVLDHQLWLNKEYCKKYSNKKALPAPIETKISKAKGQPREPOVYTL 374
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 180 HREDYNSTLRVVSALPIQHDWMSGKEFKCKVNNRALPSPIETKISKPRGVPYRAPQVYVL 239
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 375 PPSREEMTKNOVSLTCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLT 434
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 240 PPPAEEMTKKEFSLTCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLT 299
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 435 VDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 470
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 300 VDKSTWERSLFCSCVMHEALHNHYTKQSLSPGK 335
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Search completed: August 14, 2002, 15:23:15
Job time: 688 sec
```



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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:22:16 ; Search time 187.61 Seconds  
(without alignments)  
433.386 Million cell updates/sec

Title: US-09-499-662-145  
Perfect score: 2517  
Sequence: 1 MGWSCIILFLVATATGVHSQ.....MHEALHNYTKSLSPCK 470

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL19.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvrius.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1637.5	65.1	473	11 Q9D8L4	Q9d8l4 mus musculus
2	1626.5	64.6	463	11 Q99LC4	Q99lc4 mus musculus
3	1586.5	63.0	473	11 Q99L25	Q99l25 mus musculus
4	1564	62.1	468	11 Q99L31	Q99l31 mus musculus
5	1435.5	57.0	437	11 Q99IA4	Q99ia4 mus musculus
6	1422.5	56.5	473	11 Q91Z05	Q91z05 mus musculus
7	1263.5	50.2	337	6 Q95M34	Q95m34 equus caball
8	1257	49.9	701	4 Q96PQ8	Q96pq8 homo sapien
9	984	39.1	278	11 Q92L1K1	Q92lk1 mus musculus
10	929.5	36.9	614	4 Q96GAG	Q96gag homo sapien
11	888.5	35.3	481	11 Q91WT3	Q91wt3 mus musculus
12	857	34.0	500	4 Q9BRV0	Q9brv0 homo sapien
13	834.5	33.2	481	11 Q91WT1	Q91wt1 mus musculus
14	818	32.5	488	11 Q91WR1	Q91wr1 mus musculus
15	814.5	32.4	597	4 Q96BB9	Q96bb9 homo sapien
16	806	32.0	496	4 Q96DK0	Q96dk0 homo sapien

17	764.5	30.4	597	4 Q9BU10	Q9bu10 homo sapien
18	760.5	30.2	597	4 Q9BQ88	Q9bqb8 homo sapien
19	758	30.1	484	11 Q99LA6	Q99la6 mus musculus
20	754.5	30.0	618	4 Q96AA6	Q96aa6 homo sapien
21	736	29.2	494	4 Q96K68	Q96k68 homo sapien
22	731	29.0	613	4 Q96EY0	Q96ey0 homo sapien
23	726.5	28.9	487	11 Q99KA4	Q99ka4 mus musculus
24	720.5	28.6	479	11 Q91WP5	Q91wp5 mus musculus
25	702	27.9	486	11 Q91Z07	Q91z07 mus musculus
26	691.5	27.5	480	11 Q91XE1	Q91xe1 mus musculus
27	658	26.1	482	11 Q91X92	Q91x92 mus musculus
28	654	26.0	479	11 Q99M22	Q99m22 mus musculus
29	643	25.5	496	4 Q96KX8	Q96kx8 homo sapien
30	603	24.0	426	11 Q9DCD9	Q9dc9 mus musculus
31	582.5	23.1	416	4 Q9NPP6	Q9np6 homo sapien
32	540.5	21.5	143	11 Q91V67	Q91v67 mus musculus
33	528.5	21.0	143	11 Q92AP9	Q92ap9 mus musculus
34	524	20.8	150	4 Q9Y298	Q9y298 homo sapien
35	515	20.5	142	11 Q92AQ2	Q92aq2 mus musculus
36	511.5	20.3	145	11 Q92AR3	Q92ar3 mus musculus
37	507	20.1	157	4 Q95978	Q95978 homo sapien
38	496.5	19.7	143	11 Q92AQ5	Q92aq5 mus musculus
39	495.5	19.7	159	4 Q96Q50	Q96qs0 homo sapien
40	495	19.7	146	11 Q92AR8	Q92ar8 mus musculus
41	494	19.6	144	11 Q92AP5	Q92ap5 mus musculus
42	493.5	19.6	145	11 Q92AQ7	Q92aq7 mus musculus
43	489.5	19.4	145	11 Q92AR4	Q92ar4 mus musculus
44	487.5	19.4	143	11 Q92AQ0	Q92aq0 mus musculus
45	487	19.3	140	11 Q92AP8	Q92ap8 mus musculus

ALIGNMENTS

RESULT	1
Q9D8L4	
ID	Q9D8L4 PRELIMINARY; PRT; 473 AA.
AC	Q9D8L4; 01-JUN-2001 (TrEMBLrel. 17, Created)
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	1810060009RIK PROTEIN.
GN	IGH-1 OR 1810060009RIK.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX	MEDLINE=21085660; PubMed=11217851;
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA	Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA	Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RT	Hayashizaki Y.;
RT	"Functional annotation of a full-length mouse cDNA collection.";
PL	Nature 409:685-690(2001).
DR	EMBL; AK007918; BAB25349.1; -.
DR	HSSP; P01842; 7FAB.



```
DR SMART: SM00407; IGcl; 3.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match      63.08; Score 1586.5; DB 11; Length 473;
Best Local Similarity 63.4%; Pred. No. 3,7e-125;
Matches 301; Conservative 61; Mismatches 106; Indels 7; Gaps 5;

QY 1 MGWSCIILFLVATATGVHSGVQVLSQSGAEVKKPGASVKVSCKASGYFTSTVWQWVQKAP 60
  ||| : : : ||||| ||| : : ||||| ||| : : ||||| : : ||||| : : |||||
Db 1 MENSWVFLFSLVTTGVHSGVQVLSQSGAEVKKPGASVKVSCKASGYFTTTHHWVQRP 60
  ||||| : : : ||||| ||| : : ||||| ||| : : ||||| ||| : : ||||| : : |||

QY 61 GQLEWNGEIDPSQSYNYNOKFKGKATITVDTSSTAYMELSLRSEDATVYYCARNRD 120
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 61 EQGLEWIGWIDPEGETKYAPFQDKATITADTSNTAYLQLSLTSEDATLIYCARNLL 120
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

QY 121 --YSNN--WYFDVWGQGLTVTVSSASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPV 177
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 121 IYGYGLYIYFDYWGQGLTITVSSAKTTAPSVYPLAPVCGDITGSSVTLGCLVKGYFPEPV 180
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

QY 178 TVNSNGALTSQGVTHFAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKR 237
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 181 TLTWNSGSLSSGVTHFAVLQSD--LYTLSSSVTVTSWPSQSITCNVAHPASSTKVDKK 239
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

QY 238 VEPKCDKTHTCPP--CPAPELGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPE 295
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 240 IEPRG-PTIKPCPCPCAPNLLGGPSVFIIPPKIKDVLMLSLSPMTCVVVDVSEDDPD 298
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

QY 296 VKFNWYDGVVEVHNAKTPREEQVNSYRVVSVLTVLHQQMLNGKEYCKVSNKALPAPI 355
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 299 VQISWFVNNVEVLTAQQTTHREDYNSTLRVVSALPIQHDWMSKEFKCKVNNKALPAPI 358
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

QY 356 EKTISKAKGQPREQVTLTPSREEMTKNQVSLTCLVKGYFSPDIAVWESNGOPENNYK 415
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 359 ERTISKPKGSRAPQVTLVLPPEEMTKKQVTLTCMTVDFMPEDIIYVETWNGKTELNYK 418
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

QY 416 TTPVLDSDGSFFLYSKLTVDKSRWQQGVFSCSVHMEALHNHYTKQSLSLSPGK 470
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 419 NTEPVLDSDGSFYFMSKLRVEKKNNVERNSVSCSVVHGLNHHHTTKSFSRTPGK 473
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

RESULT 4
Q99L31 ID Q99L31 PRELIMINARY; PRT; 468 AA.
AC Q99L31
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AAH03878.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

QY 1 MGWSCIILFLVATATGVHSGVQVLSQSGAEVKKPGASVKVSCKASGYFTSTVWQWVQKAP 60
  ||| : : : ||||| ||| : : ||||| ||| : : ||||| : : ||||| : : |||||
Db 1 MENSWVFLFSLVTTGVHSGVQVLSQSGAEVKKPGASVKVSCKASGYFTTTHHWVQRP 60
  ||||| : : : ||||| ||| : : ||||| ||| : : ||||| ||| : : ||||| : : |||

QY 61 GQLEWNGEIDPSQSYNYNOKFKGKATITVDTSSTAYMELSLRSEDATVYYCARNRD 120
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 61 EQGLEWIGWIDPEGETKYAPFQDKATITADTSNTAYLQLSLTSEDATLIYCARNLL 120
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

QY 121 YSNWYEDVWGQGLTVTVSSASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPVTVS 180
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 121 YGG--YYDWGQGLTITVSSAKTTAPSVYPLAPVCGDITGSSVTLGCLVKGYFPEPVLT 178
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

QY 181 WNSGALTSQGVTHFAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKREP 240
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 179 WNSGSLSSGVTHFAVLQSD--LYTLSSSVTVTSWPSQSITCNVAHPASSTKVDKKIEP 237
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

QY 241 KSCDKTHTCPP--CPAPELGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKF 298
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 238 RG-PTIKPCPCPCAPNLLGGPSVFIIPPKIKDVLMLSLSPMTCVVVDVSEDDPDVQI 296
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

QY 299 NWYVDGVVEVHNAKTPREEQVNSYRVVSVLTVLHQQMLNGKEYCKVSNKALPAPIERT 358
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 297 SWFVNNVEVLTAQQTTHREDYNSTLRVVSALPIQHDWMSKEFKCKVNNKALPAPIERT 356
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

QY 359 ISKAKGQPREQVTLTPSREEMTKNQVSLTCLVKGYFSPDIAVWESNGOPENNYKTPP 418
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 357 ISKPKGSRAPQVTLVLPPEEMTKKQVTLTCMTVDFMPEDIIYVETWNGKTELNYKTE 416
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

QY 419 PVLDSDGSFFLYSKLTVDKSRWQQGVFSCSVHMEALHNHYTKQSLSLSPGK 470
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 417 PVLDSDGSFYFMSKLRVEKKNNVERNSVSCSVVHGLNHHHTTKSFSRTPGK 468
  ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

RESULT 5
Q9RIA4 ID Q9RIA4 PRELIMINARY; PRT; 437 AA.
AC Q9RIA4
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;
```

Query Match 57.0%; Score 1435.5; DB 11; Length 437;  
Best Local Similarity 59.3%; Pred. No. 1.7e-112;  
Matches 268; Conservative 71; Mismatches 96; Indels 17; Gaps 7;

QY 21 VOLVQSGAEVKKPCASVKVSKASGYFTFTSYWQWQYKAPQCGLEWGEIDPDSYTNYN 80  
DB 1 VOLQESGGGLVKGKGLSKLCAASGFTFSYAMSWVRQTPTEKRLWYASF-SGGIIYYT 59  
QY 81 QKFKGRATITVDITSTAYMELSLRSEDYAVYICARNRDYNNWYFDVNGOGTFLTVSS 140  
DB 60 DSVKGRFTIYKDKDRNLSLQMSLSRSEDYAMYYCARG-DYS-----AYGPGTLTVSA 113  
QY 141 ASTKGSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPVYVSNWNGALTSVHTFPVAVLQSS 200  
DB 114 AKTTPSVYPLAPGSAQAQNTSMVTGLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPVAVLQSD 173  
QY 201 GLYSLSVWTVPPSSSLGTQYICNVNHNKPSNTKVDKRVKPCDKTHTCPP--CPAPELL 258  
DB 174 -LVTLSSTVTPSPSTWSPSEFTVCNVAHPASSTKVDKRVKPCDKTHTCPP--CPAPELL 227  
QY 259 GSPSVFLFPKPKDITLMSIRTPVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQ 318  
DB 228 --SSVIFPPKPKDVLITLTPKVTWVVDISKDDPEVQSFVFDVDDVEVHTAQTPREEQ 285  
QY 319 YNTYRVVSVTLVHQDLNGKEYKCKVSNKALPAPIEKTISKAKGQRPQVYITLPPSR 378  
DB 286 FNSTFRSVSELPIMHQDLNGKEYKCKVSNKALPAPIEKTISKAKGQRPQVYITLPPSR 345  
QY 379 EEMTKNOVSLTCLVKGYFPEPSDIKAVENSGQPNENYKTPPVLDSDGSLFLYKSLTVDKS 438  
DB 346 EQMAKDKVSLTCLVKGYFPEPSDIKAVENSGQPNENYKTPPVLDSDGSLFLYKSLTVDKS 405  
QY 439 RWOQGVNFCVSMVHEALHNHYTKSLSPGK 470  
DB 406 NWEAGNTFTCSVLHGLNHNHTEKNLSHSPGK 437

RESULT 6  
Q91205  
ID Q91205 PRELIMINARY; PRT; 473 AA.  
AC Q91205  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DE HYPOTHETICAL 51.9 KDA PROTEIN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC010327; AAH10327.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 56.5%; Score 1422.5; DB 11; Length 473;  
Best Local Similarity 57.1%; Pred. No. 2.3e-111;  
Matches 270; Conservative 74; Mismatches 114; Indels 15; Gaps 5;

QY 7 ILFLVATATGVHSQVLQVSGAEVKKPGASVKVSKASGYFTFTSYWQWQYKAPQCGLEW 66  
DB 7 LVFLVLILKGVQCEVQLVSGGGLVKGKGLSKLCAASGFTFSYAMSWVRQTPTEKRLWYASF 66  
QY 67 MGEIDPDSYTNYNQKFKKATITVDITSTAYMELSLRSEDYAVYICARNRDYNNY 126  
DB 67 VAYINGSGSTIYADYVTKGRFTISRDNKNTLFLQMTLSRSEDYAVYICAREL-----WL 121  
QY 127 --FDVNGOGTFLTVSSASTKGSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPVYVSNWNGALTSVHTFPVAVLQSS 184  
DB 122 RRIDYWGQGTITVSSAKTTPSVYPLAPGCGGDTTGGSVTLGCLVKGYFPEPVYVSNWNG 181

QY 185 ALTSGVHTFPVAVLQSSGLYSLSVWTVPPSSSLGTQYICNVNHNKPSNTKVDKRVKPSQD 244  
DB 182 SLSSVHTFPVAVLQ-SGLYTHSSSVTVPPSTWSPQVTCVSAHPASSTTVDDKLEPSGPI 240  
QY 245 KT-HTCPP-----CPAPELLGGPSVFLFPKPKDITLMSIRTPVTCVVDVSHEDPEVK 297  
DB 241 STINPCPPCKECHKCAPNLEGGPSVFIFFPNIKDVLMLSLTPKVTWVVDVSEDDPDVQ 300  
QY 298 FNNYVDGVEVHNNAKTKPREEQYNTYRVVSVTLVHQDLNGKEYKCKVSNKALPAPIEK 357  
DB 301 ISFVNNVNEVHTAQTQTHREDYNSTIRVSALPIHQDWMGKFEKCKVNNKDLPSPIER 360  
QY 358 TISKAKGQRPQVYITLPPSREEMTKNOVSLTCLVKGYFPEPSDIKAVENSGQPNENYKTT 417  
DB 361 TISKIKGLYRAPQVYITLPPPAEQLSRKDVSLTCLVGFNPGDISVENTSNGHTEENYKDT 420  
QY 418 PPVLDSDGSLFLYKSLTVDKSRWQGVNFCVSMVHEALHNHYTKSLSPGK 470  
DB 421 APVLDSDGSLFLYKSLTVDKSRWQGVNFCVSMVHEALHNHYTKSLSPGK 473

RESULT 7  
Q95M34  
ID Q95M34 PRELIMINARY; PRT; 337 AA.  
AC Q95M34;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE IMMUNOGLOBULIN GAMMA 1 HEAVY CHAIN CONSTANT REGION  
GN (FRAGMENT).  
OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wagner B.;  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9838416; PubMed=9717671;  
RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,  
Leibold W., Radbruch A.;  
RT "Organization of the equine immunoglobulin heavy chain constant region  
genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";  
RL Immunobiology 199;105-119(1998).  
DR EMBL; AJ300675; CAC44624.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;

Query Match 50.2%; Score 1263.5; DB 6; Length 337;  
Best Local Similarity 68.9%; Pred. No. 3.5e-98;  
Matches 233; Conservative 44; Mismatches 52; Indels 9; Gaps 3;

QY 141 ASTKGSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPVYVSNWNGALTSVHTFPVAVLQSS 200  
DB 1 ASTKGSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPVYVSNWNGALTSVHTFPVAVLQSS 60  
QY 201 GLYSLSVWTVPPSSSLGTQYICNVNHNKPSNTKVDKRVKPEP-----KSCDKTHTCPPCPA 254  
DB 61 GFYLSVWTVPPSTWSETYICNVVHAASNFKVDKRIEIPDNHQKCDMS-KCPKCPA 119  
QY 255 PELLGGPSVFLFPKPKDITLMSIRTPVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKP 314  
DB 120 PELLGGPSVFLFPKPKDITLMSIRTPVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKP 179  
QY 315 REEQYNTYRVVSVTLVHQDLNGKEYKCKVSNKALPAPIEKTISKAKGQRPQVYITL 374  
DB 180 KEEQFNSTYRVVSVTLVHQDLNGKEYKCKVSNKALPAPIEKTISKAKGQRPQVYITL 239



QY 375 PPSREEMTKNOVSLTCLVKGYFSPDIAVWESNGQP--ENNYKTTTPVLDSDGSFFLYSK 432  
Db 240 AHPDELKSKSVSTCLVKDFYFPEINIEWQSGNQPLETEKYSTQAQDSGDFLYSK 299  
QY 433 LTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPCK 470  
Db 300 LSVDRNRWQGTTFTCGMHEALHNHYTKQVSKNPK 337

RESULT 8  
Q96PQ8 ID Q96PQ8 PRELIMINARY; PRT; 701 AA.  
AC Q96PQ8; 2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RS SEQUENCE FROM N.A.  
RX MEDLINE=21477448; PubMed=11593034;  
RA Hu Z., Garen A.;  
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor  
cells for immunotherapy in mouse models of prostatic cancer.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).  
DR EMBL: AF272774; AAK58686.1; -.  
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;

Query Match 49.9%; Score 1257; DB 4; Length 701;  
Best Local Similarity 99.1%; Pred. No. 3.5e-97;  
Matches 230; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 239 EPKSCDTHCTCPCPAPDELGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298  
Db 470 EPKSCDTHCTCPCPAPDELGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 529  
QY 299 NWYVDGVEVHNATKPREEOYNSTYRVSVLTVLHQDLNGKEYCKVSKNALPAPIEKT 358  
Db 530 NWYVDGVEVHNATKPREEQNSTYRVSVLTVLHQDLNGKEYCKVSKNALPAPIEKT 589  
QY 359 ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGYFSPDIAVWESNGQPENNYKTTP 418  
Db 590 ISKAKGQPREPQVYTLPPSREELTKNQVSLTCLVKGYFSPDIAVWESNGQPENNYKTTP 649  
QY 419 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTKSLSPCK 470  
Db 650 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTKSLSPCK 701

RESULT 9  
Q921K1 ID Q921K1 PRELIMINARY; PRT; 278 AA.  
AC Q921K1; 2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE UNKNOWN (PROTEIN FOR MGC:18977).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RS SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC012207; AAK12207.1; -.  
SQ SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;

Query Match 39.1%; Score 984; DB 11; Length 278;  
Best Local Similarity 67.1%; Pred. No. 8.8e-75;  
Matches 186; Conservative 33; Mismatches 50; Indels 8; Gaps 3;  
QY 1 MGWSCIILFLVATATGVHSGAELVQSGAEVKKPGASVKASKASGYTFTSYWMQVKAQ 60  
Db 1 MGWNCIILFLVATATGVHSGVQLQOQGAELVKPGASVKASKASGYTFTSYWMHVKORR 60  
QY 61 GQGLEWMEIDPDSYTNYNOKFKGKATITVDSTSTAYMELSLRSDEDTAYVYCARNRD 120  
Db 61 GQGLEWIGNINPNSGGTNYNEKFKKATLAVDKSSITYVMQLSSLTSDSAVYCTRGY 120  
QY 121 YSNWYFDVWGQGLTVTVSSASTKGPSVFPLAPLAPSKSTSGTAAALCLVKDYFPEPVTV 180  
Db 121 Y-DDVYFDVWGAGTIVTVSSAKTTAPSVYPLAPVCGGTGSSVTGLCLVKGYFPEPVTLT 179  
QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKRV 240  
Db 180 WNSGSLSGVHTFPAVLO--SGLYTLSSSVTVTSNWPSTQITCNVAHPASSTKVDKRIE 238  
QY 241 K-----SCDKTHCTCPCPAPPELLGGPSVFLFPPPK 271  
Db 239 RVPITQNPCLPKCEPCCAAPDLLGGPSVFIFPPPSR 275  
RESULT 10  
Q96GA6 ID Q96GA6 PRELIMINARY; PRT; 614 AA.  
AC Q96GA6; 2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE UNKNOWN (PROTEIN FOR MGC:15420).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RS SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC009851; AAK09851.1; -.  
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match 36.9%; Score 929.5; DB 4; Length 614;  
Best Local Similarity 36.7%; Pred. No. 1.1e-69;  
Matches 212; Conservative 84; Mismatches 166; Indels 115; Gaps 17;  
QY 1 MGWSCIILFLVATATGVHSGAELVQSGAEVKKPGASVKASKASGYTFTSYWMQVKAQ 60  
Db 1 MDWTIRILFLVAAATDAYSQMLVQSGAEVKKTGSVKVSKASGYTFTYRLHWVRQAP 60  
QY 61 GQGLEWMEIDPDSYTNYNOKFKGKATITVDSTSTAYMELSLRSDEDTAYVYCARNRD 120  
Db 61 GQALEWGWITPFGNTNTYAAQKFDQRTITRDRSMNTAYMELSLRSDEDTAYVYCARG-- 118  
QY 121 YSNW--YEDVWGQGLTVTVSSASTKGPSVFPLAPSSKSTSG-GTAAALCLVKDYFPEPV 177  
Db 119 YSSWDDAFDIWGQGTWTVSSGSASAPTLFPLVSCENSPSDTSSVAVGCLAQFLPDSI 178  
QY 178 TVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSL--GTQTY-ICNVNHRKPSN- 231  
Db 179 TFSWKYKNNSDISSTRGFPVLR-GGKYAATSQVLLPSSKDVWQGTDEHVCKVQHPGNK 237  
QY 232 -----TKVDKRVPEKS-----CDKTHCTCP----- 250  
Db 238 EKNVPLPVIABLPKVSFVFPDRGFGNPRKSKLICQATGFSRQIQVSWLREGQVGS 297  
QY 251 -----PCPAPELLGGPS----- 262  
Db 298 GVTTDQVOAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDRHGLTFTQONASSMCMV 357

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QY 263 -----VLFPPPKKOTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 316
   ||  :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 358 QDFAIRFAIPPS-FASIFLTKSTKLTCLVTLDTYD-SVTISWTRQNGEAVKTHNISE 415
QY 317 EQNSTYRVVSVLTVLHQDLNKEKEYCKVKSNKALPAPIEKTIKAKGPQ-REPQVYTL 375
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 416 SHPNATFSAVGEASICEDDWNSEGERCTVTHTDLPSPKLTQTSRKPGRVALLHPRDVL 475
QY 376 PSREMT-KNOVSLTCLVKGFPDIAVWESNGQP--ENNYKTTTPVLD--SDGSFFELY 430
   ||:: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 476 PAREQNLRESATITCLVTFSPADVFVQNMQRGQPLSPKPYVTSAPMPEQAPGRIFAH 535
QY 431 SKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLS 467
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 536 SILTVSEEWNTGETYTCVVAHEALPNRVTERTVDKS 572

RESULT 11
Q91WT3 PRELIMINARY; PRT; 481 AA.
AC Q91WT3;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE HYPOTHETICAL 52.0 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-COLON;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC013488; RAH13488.1; -.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52022 MW; 4EB5C253038B718 CRC64;
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Query Match 35.3%; Score 888.5; DB 11; Length 481;
Best Local Similarity 42.7%; Pred. No. 2.1e-66;
Matches 206; Conservative 73; Mismatches 172; Indels 31; Gaps 16;

QY 1 MGNSCIILFLVATATGVHISOVLQSGAEVKKPGASVKYCKASGYTFTSYWQWVKQAP 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MRWSCIILFLVATATGVNSQVQLQPGAEIVREGASVKLSCKTSGYTFDYWNNWVKQRP 60
QY 61 GOGLEWMGIDPSDSTNTYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYICARNRD 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 GOGLEWIGAIDPDSYTSYNQKFKG--TTLTVDTSASSAYMLLSLTSEDSAVYFCARGPR 119
QY 121 YSNWVFDVWGOGTLTVTSSASTKGPSVFLAPSSKTSGGTAALGCLVKDYFPE-PVTV 179
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Db 120 DSGYF---WGOGTLTVTSSAPAREPTIYPLT-FPOALSSDPVIIGCLLHDYFPSTGMV 175
QY 180 SNWNGALTSGVTHFPVAVLQSSGLYSLSVTVTPSSSLGT-QTYICNVNHNKPSNTKVDKR 238
   ||: ||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 176 TWGKSGKDIITVNFPPALASGGRYTNSSQLTLPVCEPGESEVKCSQVH-DSNPVQELNV 234
QY 239 EPKSCDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VK 297
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 235 NCPGIGSPPTTPPPSCQ----PSLSLQRPALD-LLLGSDASITCTLNGL--RDEGAV 287
QY 298 FNVYDGVGVHNAKTKPREEQINST---YRVVSVLTVLHQDLNKGKEYCKVSNKALPAP 354
   ||: ||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 288 FTW-----EPSTGDAVQKKAQVNSCGCYSVSVLPGPCAERNWNSGASFKCTVTHPESDT- 341
QY 355 IEKTIKAKGPQREPQVYTLPPSREMTKNQ-VSLTCLVKGFYPSDIAVWESNGO---P 410
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Db 342 LTGTAKTAVTNVFPQVHLLPPSEALNELVSLTCLVRAENPREVLVRLHGNELSP 401
QY 411 ENNYKTTTPVLDSDG--SFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSP 468
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Db 402 ESYLVEPLKPEGEGATVLTSLVRSABIRKQDQYSVMGVGHEALPMNFTQRTIDRLS 461
QY 469 GK 470
Db 462 GK 463

RESULT 12
Q9BRV0 PRELIMINARY; PRT; 500 AA.
AC Q9BRV0;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE HYPOTHETICAL 54.2 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PROSTATE;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC005951; AAH05951.1; -.
DR HSSP: P01789; 1MCP.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003600; Ig_like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_4.
DR SMART: SM00409; Ig_4.
DR SMART: SM00407; IGc1; 2.
DR SMART: SM00406; Igv; 1.
DR SMART: SM00410; IG-like; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

Query Match 34.0%; Score 857; DB 4; Length 500;
Best Local Similarity 40.9%; Pred. No. 9.9e-64;
Matches 205; Conservative 69; Mismatches 177; Indels 50; Gaps 18;

QY 1 MGNSCIILFLVATATGVHISOVLQSGAEVKKPGASVKYCKASGYTFTSYWQWVKQAP 60
   ||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MDWTSILFLVAAATGAQSOVLVQSGAEVWSPGASVRVSCKTSGYAFHYTSIIVRQAP 60
QY 61 GOGLEWMGIDPSDSTNTYNQKFKGKATITVDTSTSTAYMELSSLRSEDTAVYICARNR- 119
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 61 GOGLEWMGWISFSSDNTREAFKFGQGRVTLTDTSTSTVYMELESLRSDDTAVYICARRY 120
QY 120 DYS---NNWYF---DVWGOGTLTVTSSASTKGPSVFLAPSSKTSGGTAALGCLVKDYF 173
   ||: ||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 121 SYSSCONDYIIYMDVWGKGTITVSSASPTSPKVPPLSLCS-TQPDGNVVIACLVGQGF 179
QY 174 P-EPYTVSNNSGALTSGVHTFPVAVLQSSG-LYSLSSVTVTPSSS-LGTOTYICNVNHNKPS 230
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 180 POEPLSVTVWSESGQGVTAARNFPPSQDASGDLYTTSQLTLPATQCLAGKSVTCHVKHY-T 238
QY 231 NTKVDKRVEPKSCDKTHTCPAPPELLGGPSVFLFPPKPK-----DTLM 275
   ||: ||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 239 NPSQDVTV-----PCVPSTPTTPSPST-PPTPSPSCCHPRLSLHRAPELDDL 285
QY 276 ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYNSTYRVVSVLTVLHQD 335
   ||: ||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 286 LGSEANLTCTLGL-RDASGVTFWTTPSSGK--SAVGPPDRDLGCGYSVSSVSLGCAEP 342
QY 336 WLNGKEYCKVSNKALPAPIEKTIKAKGPQREPQVYTLPPSREMTKNQ-VSLTCLVK 394
   ||: ||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 343 WNHGKTFCTTAAYPESKTPTLTATLSKS-GNTFRPEVHLLPPPESEALNELVTLTCLARG 401
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:15:38 ; Search time 230.21 Seconds  
(without alignments)  
226.770 Million cell updates/sec

Title: US-09-499-662-147

Perfect score: 2517

Sequence: 1 MGWSCIILFLVATATGVHSQ.....MHEALHNYTKLSLSLSPCK 470

Scoring table:

BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_032802.\*

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- 2: /SIDSL/gcgdata/hold-geneseq/geneq-emb1/AA1981.DAT.\*
- 3: /SIDSL/gcgdata/hold-geneseq/geneq-emb1/AA1982.DAT.\*
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- 19: /SIDSL/gcgdata/hold-geneseq/geneq-emb1/AA1998.DAT.\*
- 20: /SIDSL/gcgdata/hold-geneseq/geneq-emb1/AA1999.DAT.\*
- 21: /SIDSL/gcgdata/hold-geneseq/geneq-emb1/AA2000.DAT.\*
- 22: /SIDSL/gcgdata/hold-geneseq/geneq-emb1/AA2001.DAT.\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2517	100.0	470	21	AAW90935 Humanised anti-Fas
2	2514	99.9	470	21	AAW90933 Humanised anti-Fas
3	2512	99.8	470	21	AAW90934 Humanised anti-Fas
4	2511	99.8	470	19	AAW83037 Anti-Fas humanised
5	2511	99.8	470	21	AAW84779 Humanised anti-Fas
6	2511	99.8	470	21	AAW90929 Humanised HFE7A de
7	2498	99.2	470	19	AAW83036 Anti-Fas humanised
8	2498	99.2	470	21	AAW84776 Humanised anti-Fas
9	2498	99.2	470	21	AAW90926 Humanised HFE7A de
10	2498	99.2	470	21	AAW90936 Humanised HFE7A de
11	2349.5	93.3	731	22	AAW52156 Humanised HMFG-1 h

12	2349.5	93.3	741	22	AAW52159	Humanised HMFG-1 h
13	2344.5	93.1	729	22	AAW52158	Humanised HMFG-1 h
14	2344.5	93.1	739	22	AAW52161	Humanised HMFG-1 h
15	2338.5	92.9	730	22	AAW52157	Humanised HMFG-1 h
16	2338.5	92.9	740	22	AAW52160	Humanised HMFG-1 h
17	2307	91.7	652	19	AAW48650	Heavy chain of hMA
18	2293.5	91.1	465	22	AAW72228	Humanised 323/A3 (
19	2288.5	90.9	464	22	AAW72232	Humanised 323/A3 (
20	2284	90.7	470	21	AAW80826	A dimeric anti-CD2
21	2283	90.7	466	22	AAW03755	Chimeric 2403 IgG
22	2258	89.7	476	20	AAW88464	Monoclonal antibody
23	2254.5	89.6	481	13	AAW24442	Sequence of antibody
24	2251	89.4	472	20	AAW50166	Human reshaped F19
25	2235	88.8	449	14	AAW43339	Completely humanis
26	2235	88.8	449	14	AAW49816	Amino acid sequenc
27	2233	88.7	476	14	AAW31023	Antibody D heavy c
28	2236.5	88.5	583	22	AAW83156	Ganglioside GM2 an
29	2205.5	87.6	467	22	AAW36210	Human immune syste
30	2203.5	87.5	452	20	AAW29458	Recombinant immuno
31	2203.5	87.5	452	21	AAW30322	Humanised anti-IL-
32	2203.5	87.5	452	21	AAW77667	Humanised anti-IL-
33	2203	87.5	472	20	AAW50157	Chimeric mouse/hum
34	2194.5	87.2	452	19	AAW69316	Anti-IL-8 humanise
35	2191.5	87.1	473	22	AAW64475	Human type anthum
36	2190	87.0	592	22	AAW83838	Amino acid sequenc
37	2189	87.0	474	22	AAW14177	Human novel protei
38	2188.5	86.9	473	22	AAW64471	Human type anthum
39	2187	86.9	595	20	AAW86003	Anti-5T4 single ch
40	2184.5	86.8	475	22	AAW63640	Amino acid sequenc
41	2183.5	86.8	473	22	AAW64469	Human type anthum
42	2176.5	86.5	473	22	AAW64473	Human type anthum
43	2174	86.4	468	20	AAW85689	D9D10 heavy chain
44	2174	86.4	711	20	AAW85692	MoTABII fusion pro
45	2165	86.0	470	13	AAW22757	Reshaped CAMPATH-1

#### ALIGNMENTS

RESULT 1

AAW90935

ID AAW90935 standard; Protein; 470 AA.

AC AAW90935;

XX XX

DT 08-AUG-2000 (first entry)

XX XX

DE Humanised anti-Fas designed heavy chain Heu 3 protein.

XX XX  
Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;  
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;  
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;  
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

XX Synthetic.

OS EP990663-A2.

XX PN

XX PD

XX PD

XX PF

XX PF

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PR

XX PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 XX DR WPI: 2000-258930/23.  
 XX DR N-PSDB; AAAL1646.  
 XX PT New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 XX PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 XX PT cells with abnormal Fas-Fas ligand systems -  
 XX PS Claim 2; Page 180-182; 263pp; English.  
 XX CC This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,  
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis, myasthenia gravis, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody heavy chain construct designated Heu 3  
 CC which is described in the method of the invention.  
 XX Sequence 470 AA;

Query Match 100.0%; Score 2517; DB 21; Length 470;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-144;  
 Matches 470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGVSCIIILFLVATATGVIHQVQVGVGAEVKKPGASVKVSKASGYTFTSYMQWVRQAP 60  
 DB 1 MGVSCIIILFLVATATGVIHQVQVGVGAEVKKPGASVKVSKASGYTFTSYMQWVRQAP 60  
 QY 61 GQGLEWMMGEIDPSDVTYNNQKFKGKATLTVDTSSTAYMELSSLRSEDVAVYYCARNRD 120  
 DB 61 GQGLEWMMGEIDPSDVTYNNQKFKGKATLTVDTSSTAYMELSSLRSEDVAVYYCARNRD 120  
 QY 121 YSNNNYFDVWGGTGLTVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVVS 180  
 DB 121 YSNNNYFDVWGGTGLTVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVVS 180  
 QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYTCNVNHPKSTNKKVRPEP 240  
 DB 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYTCNVNHPKSTNKKVRPEP 240  
 QY 241 KSCDTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300  
 DB 241 KSCDTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300  
 QY 301 YVDGVEVHNNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYCKKVKSNKALPAPIEKTIS 360  
 DB 301 YVDGVEVHNNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYCKKVKSNKALPAPIEKTIS 360  
 QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 420  
 DB 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 420

Db 361 kakgqprepqvtytlppsrreemtknqvsltclvkgyfypsdiavewesngqpennyktppv 420  
 QY 421 LDSGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALNHHYTKQKLSLSLSPGK 470  
 Db 421 ldsdgsfflyskltvdksrwqgnvfscsvmhealnhytqkslsispgk 470  
 RESULT 2  
 AAW90933  
 ID AAW90933 standard; Protein; 470 AA.  
 XX AC AAW90933;  
 XX DT 08-AUG-2000 (first entry)  
 DE Humanised anti-Fas designed heavy chain Heu 1 protein.  
 XX KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;  
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;  
 KW hepatotropic; apoptosis; systemic lupus erythematosus;  
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
 KW Goodpasture syndrome; Crohn's disease; myasthenia gravis;  
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
 XX Synthetic.  
 OS EP990663-A2.  
 PN 05-APR-2000.  
 PD 29-SEP-1999; 99EP-0307711.  
 XX 30-SEP-1998; 98JP-0276881.  
 PR 30-SEP-1998; 98JP-0276882.  
 XX (SANY ) SANKYO CO LTD.  
 PA Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 XX WPI: 2000-258930/23.  
 DR N-PSDB; AAAL1644.  
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems -  
 XX Claim 2; Page 169-170; 263pp; English.

CC This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,  
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively

CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
CC cells. They bind to both human and murine Fas, so can be evaluated in  
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
CC the native ligand, do not induce liver disease, and have reduced risk of  
CC inducing a human anti-murine antibody response. This sequence represents  
CC a humanised anti-Fas antibody heavy chain construct designated Heu 1  
CC which is described in the method of the invention.

XX SQ Sequence 470 AA;

Query Match 99.9%; Score 2514; DB 21; Length 470;  
Best Local Similarity 99.8%; Pred. No. 2.6e-144; Mismatches 0; Indels 0; Gaps 0;  
Matches 468; Conservative 1;

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DB 1 mgwsciiilflvatatgshsqvqlvqsgaevkpkgsasvkvsckasgytftsywmqvqkqap 60  
QY 61 GQGLEWMGEIDPDSYNTYNNQKFKGKATLTVDTSSTAYMELSSLRSEDVAVYICARNRD 120  
DB 61 gqglewmgeidpsdysntynqkfkgtatltvdtststaymelsslrseavvyicarnrd 120  
QY 121 YSNWYFDVWGQGLTVTVSSASTKGPVFLAPSKSTSGCTAALGCLVKDYFPEPTVTS 180  
DB 121 ysnwyfdvwgqglvtvtvssastkgspsvflapsskstsggtaalgclvkdypfepvts 180  
QY 181 WNSGALTSVHTFPAVLQSSGLYSLSSVTVTPSSSLGTTQYICNVNHPKSNTKVDKRVPE 240  
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DB 301 yvdgvevhnatkpreqynstyrvvsvltvlhqdwlngkeyckvsnkalpapietkis 360  
QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEFESNQGNPNVKTTPPV 420  
DB 361 kkgqprepytytlppsreemtknqvsltcvkgfypsdiavefesnqgnpnvktppv 420  
QY 421 LDSGSEFLYSLKLTVDKSRWQGNVFCSSVMHEALHNHYTQKSLSLSPGK 470  
DB 421 ldsdgsfplyslkltvdksrwqgnvfscsvmhcalhnhytqkslsispkg 470

### RESULT 3

AAW90934 standard; Protein; 470 AA.

XX AC AAW90934;

XX DT 08-AUG-2000 (first entry)

XX DE Humanised anti-Fas designed heavy chain Heu 2 protein.

XX KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
XX KW anti-allergic; human; anti-arthritis; antiviral; immunomodulatory; cardiac;  
XX KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
XX KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;  
XX KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
XX KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
XX KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
XX KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
XX KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
XX KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
XX KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
XX OS Synthetic.

XX PN EP990663-A2.

XX 05-APR-2000.

XX 29-SEP-1999; 99EP-0307711.

XX 30-SEP-1998; 98JP-0276881.

XX 30-SEP-1998; 98JP-0276882.

XX (SANY ) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

XX WPI: 2000-259930/23.

XX N-PSDB; AAA11645.

XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
XX inflammatory or autoimmune disease, induces apoptosis selectively in  
XX cells with abnormal Fas-Fas ligand systems

XX Claim 2 ; Page 174-176; 263pp; English.

XX This invention describes a novel humanized anti-Fas antibody-like  
XX molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
XX ligand system, by binding to Fas on the cell surface, and prevents  
XX apoptosis in cells with a normal system, by inhibiting binding between  
XX Fas and its ligand. The products of the invention have anti-inflammatory,  
XX anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
XX immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
XX antirheumatic, nephrotropic, antiinfertility, neuroprotective,  
XX antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce  
XX apoptosis by binding to cell surface Fas or inhibit it by competitive  
XX inhibition of ligand binding. (I) are used to treat and/or prevent  
XX diseases associated with the Fas/Fas ligand system, especially systemic  
XX lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
XX versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
XX anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
XX disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
XX multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
XX dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
XX cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
XX (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
XX inhibit apoptosis in normal cells but selectively induce it in abnormal  
XX cells. They bind to both human and murine Fas, so can be evaluated in  
XX murine disease models. (I) act on the active site of Fas, i.e. they mimic  
XX the native ligand, do not induce liver disease, and have reduced risk of  
XX inducing a human anti-murine antibody response. This sequence represents  
XX a humanised anti-Fas antibody heavy chain construct designated Heu 2  
XX which is described in the method of the invention.

XX SQ Sequence 470 AA;

Query Match 99.8%; Score 2512; DB 21; Length 470;  
Best Local Similarity 99.6%; Pred. No. 3.5e-144;  
Matches 468; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCIIILFLVATATGHSQVQLVQSGAEVKKPKGASVKVSKASGYTFTSYWMQVRQAP 60  
DB 1 mgwsciiilflvatatgshsqvqlvqsgaevkpkgsasvkvsckasgytftsywmqvqkqap 60  
QY 61 GQGLEWMGEIDPDSYNTYNNQKFKGKATLTVDTSSTAYMELSSLRSEDVAVYICARNRD 120  
DB 61 gqglewmgeidpsdysntynqkfkgtatltvdtststaymelsslrseavvyicarnrd 120  
QY 121 YSNWYFDVWGQGLTVTVSSASTKGPVFLAPSKSTSGCTAALGCLVKDYFPEPTVTS 180  
DB 121 ysnwyfdvwgqglvtvtvssastkgspsvflapsskstsggtaalgclvkdypfepvts 180  
QY 181 WNSGALTSVHTFPAVLQSSGLYSLSSVTVTPSSSLGTTQYICNVNHPKSNTKVDKRVPE 240  
DB 181 wnsгалtsvhtfpavlsqssglyslssvstvtpssslgttqyicnvnhpksntkvdkrvpe 240  
QY 241 KSCDKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300







CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, anti-diabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,  
 CC antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocardiitis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (A, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody HFE7A designed heavy chain which is used in  
 CC the method described in the invention.

XX SQ Sequence 470 AA;

Query Match 99.8%; Score 2511; DB 21; Length 470;  
 Best Local Similarity 99.6%; Pred. No. 4e-144;  
 Matches 468; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVATATGVHSGVQLVQSGAEVKKPGASVKYSCKASGVTFTSYMMQWVROAP 60  
 Db 1 mgwscilflvatatgvhsqqlvqsgaevkpgasvksckasgytftsymbmqwkqap 60

QY 61 GQGLEWNGEIDPSDSTYNNQKFKGKATLTVDFTSTAYMELSSLRSEDPAVYYCARNRD 120  
 Db 61 gqglewngelidpsdstynynqkfkgtatltvdtststaymelsslrseidpavyyccarnrd 120

QY 121 YSNWYFDVWGQGLTVTVSSASKPGSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180  
 Db 121 ysnwyfdvwgqglvtvssaskpgsvplapsskstsaggtaalgclvkdyfpeptvts 180

QY 181 WNSGALTSGVHTFPAVLQSGGSLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240  
 Db 181 wnsгалtsgvhtfpavllqsggslyslssvstvpssslgtqtyicnvnhkpsntkvdkrvep 240

QY 241 KSCDKHTCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNW 300  
 Db 241 kscdkhtccpcpapelggpsvflfppkpkdtlmisrtpetvctcvvvdvshedpevkfnw 300

QY 301 YVDGVEVHNAKTKPREEQVNSITRVVSVLTVLTQDMLNGKEYKCKVSNKALPAPIEKTIS 360  
 Db 301 yvdgvevhnaktkpreeqvnsitrvvsvltvltqldmlngkeykckvsnkalpapiektis 360

QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTPPV 420  
 Db 361 kkgqprepqvylppsreemtknqvsltclvkgyfypsdiavewesngopennyktppv 420

QY 421 LQSDGFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470  
 Db 421 ldsdgsfflyskltvdksrwqgnvfscsvmhéalhnhytqkslsispkg 470

RESULT 7

AAW83036  
 ID AAW83036 standard; Protein; 470 AA.

XX AC AAW83036;

XX DT 15-MAR-1999 (first entry)

XX

DE Anti-Fas humanised antibody HFE7A heavy chain.  
 XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;  
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;  
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;  
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;  
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;  
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;  
 KW atopy; arteriosclerosis; myocardiitis; cardiomyopathy; AIDS;  
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
 KW transplant rejection; therapy.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FH Peptide 1..19 /label= Sig\_peptide  
 FT Protein 20..470 /label= Mat\_protein  
 FT Region 20..140 /label= Variable  
 FT Region 141..464 /label= Constant  
 FT Region 50..54 /label= CDR\_H1  
 FT /note= "Claim 9"  
 FT Region 69..84 /label= CDR\_H2  
 FT /note= "Claim 9"  
 FT Region 118..129 /label= CDR\_H3  
 FT /note= "Claim 9"  
 XX AU9859701-A.  
 XX 08-OCT-1998.  
 XX 30-MAR-1998; 98AU-0059701.  
 XX 08-OCT-1997; 97JP-0276064.  
 PR 01-APR-1997; 97JP-0082953.  
 PR 25-JUN-1997; 97JP-0169088.  
 XX (SANY ) SANKYO CO LTD.  
 XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;  
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;  
 DR WPI: 1998-543440/47.  
 DR N-PSDB; AAV70079.  
 XX New antibodies and proteins bind conserved epitope of Fas antigen -  
 PT used to evaluate drugs in animal models and to treat Fas-associated  
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
 PT myocardiitis, hepatitis and AIDS  
 XX Claim 22; Page 212-213; 292pp; English.  
 XX This is the amino acid sequence of the VD type humanised heavy  
 CC chain of murine anti-human Fas monoclonal antibody HFE7A. E. coli  
 CC pGHS17A62 SANK 73397 harbors plasmid pGHS17A62 carrying a fusion  
 CC fragment of the humanised VD type HFE7A heavy chain and DNA  
 CC encoding human IgG1 constant region (see AAV70079), and is deposited  
 CC as FERM BP-6074 (claimed). The invention provides methods for  
 CC producing humanised antibodies by culturing host cells. Humanised  
 CC versions of HFE7A (see AAW83031-37), like native HFE7A, are capable  
 CC of inducing apoptosis in abnormal cells expressing Fas, and of  
 CC inhibiting Fas-induced apoptosis in normal cells. The humanised  
 CC antibodies are used to evaluate, in animal models, treatments of  
 CC diseases that involve Fas/Fas ligand interactions, and also to

CC treat such diseases, including autoimmune disease (e.g. systemic  
CC lupus erythematosus, Hashimoto's disease, graft versus host disease,  
CC Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,  
CC Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,  
CC autoimmune haemolytic anaemia, sterility, myasthenia gravis,  
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, and  
CC insulin-dependent diabetes), allergies, atopy, arteriosclerosis,  
CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic  
CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).  
XX  
SQ Sequence 470 AA;

Query Match 99.2%; Score 2498; DB 19; Length 470;  
Best Local Similarity 99.1%; Pred. No. 2.5e-143;  
Matches 466; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MGWSCIILFLVATATGVSQVQLVQSGAEVKKPGASVKVSCKASGYFTSYMMQWVRQAP 60  
Db 1 mgwsciilflvatatgvsqvlvqsgaevkpgasvkvsckasgyftsywmgwvkqap 60  
QY 61 GQGLEWMEIDPDSYNTYNNOKFKGKATLTVDTSSTAYMELSLRSEDATVYICARNRD 120  
Db 61 gqglewmeidpsdysntynngkfkgkatltvdtstastaymelslrse dtavyyicarnrd 120  
QY 121 YSNWNYFDVWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180  
Db 121 ysnwnyfdvWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180  
QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHKPSNTKVDKRV 240  
Db 181 wnsGALTsgvhtfpavliqsglyslssvvtvpssslgtqtyicnvnhkpsntkvdkrv 240  
QY 241 KSCDKHTCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVYVDVSHEDPEVKFNW 300  
Db 241 kscdkhtccpCpapelLggsVflfppkpkdtlmiSrtpEvTcvYvdvshEdpeVkfNw 300  
QY 301 YVDGVEVHNATKPREQYNSTYRVSVLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 360  
Db 301 yvdgvevhnatkpreEqynstYrvsvltclvKgfYpsdiAVEwESngqpennYkttppv 360  
QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420  
Db 361 kaKgqprePqvYtlppSreEmtknQvslTclvKgfYpsdiAVEwESngqpennYkttppv 420  
QY 421 LDSGSPFLYSLKLTVDKSRWQGNVFSCSVNHEALHNHYTQKSLSLSPGK 470  
Db 421 ldsGsflyslkltvdKsrwGgnvfscsvnhealhnhytqkslsispgk 470

RESULT 8  
AAB14776  
ID AAB14776 standard; Protein; 470 AA.  
AC AAB14776;  
XX  
XX  
XX  
XX 24-NOV-2000 (first entry)  
XX Humanised anti-Fas antibody heavy chain, SEQ ID NO:89.  
XX  
XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;  
KW human Fas; Fas ligand; apoptosis modulator; determining region; CDR;  
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;  
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;  
KW hepatitis; AIDS; graft rejection; heavy chain.  
XX  
OS Chimeric - Mus musculus.  
OS Chimeric - Homo sapiens.  
XX  
PN JP2000169393-A.  
XX  
XX 20-JUN-2000.

XX 30-SEP-1999; 99JP-0278301.  
XX  
XX 30-SEP-1998; 98JP-0276883.  
PR  
XX (SANY ) SANKYO CO LTD.  
XX  
XX WPI; 2000-485645/43.  
DR N-PSDB; AAA72159.  
XX  
PT Preventive or treating agent for the diseases caused by an abnormality  
PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains  
PT anti-Fas antibody -  
XX  
XX Claim 21; Page 95-96; 139pp; Japanese.  
XX  
XX The invention relates to compositions for the prevention or treatment  
XX or diseases caused by an abnormality in the Fas/Fas ligand system  
XX containing an anti-Fas antibody as the active component. The anti-Fas  
XX antibody is either the murine anti-human Fas monoclonal antibody HFE7A,  
XX or a humanised version of HFE7A containing identical CDRs  
XX (complementarity determining regions) to antibody HFE7A. Via its  
XX interaction with Fas, the antibody of the invention acts as a modulator  
XX of apoptosis. The compositions of the invention may therefore be used in  
XX the treatment or prevention of conditions such as autoimmune diseases,  
XX allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,  
XX glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS  
XX and organ graft rejection. Sequences AAB14775-B14776 and AAB14779  
XX represent the heavy chains (or fragments thereof) of various humanised  
XX HFE7A-derived anti-Fas antibodies.  
XX  
SQ Sequence 470 AA;

Query Match 99.2%; Score 2498; DB 21; Length 470;  
Best Local Similarity 99.1%; Pred. No. 2.5e-143;  
Matches 466; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MGWSCIILFLVATATGVSQVQLVQSGAEVKKPGASVKVSCKASGYFTSYMMQWVRQAP 60  
Db 1 mgwsciilflvatatgvsqvlvqsgaevkpgasvkvsckasgyftsywmgwvkqap 60  
QY 61 GQGLEWMEIDPDSYNTYNNOKFKGKATLTVDTSSTAYMELSLRSEDATVYICARNRD 120  
Db 61 gqglewmeidpsdysntynngkfkgkatltvdtstastaymelslrse dtavyyicarnrd 120  
QY 121 YSNWNYFDVWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180  
Db 121 ysnwnyfdvWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180  
QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHKPSNTKVDKRV 240  
Db 181 wnsGALTsgvhtfpavliqsglyslssvvtvpssslgtqtyicnvnhkpsntkvdkrv 240  
QY 241 KSCDKHTCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVYVDVSHEDPEVKFNW 300  
Db 241 kscdkhtccpCpapelLggsVflfppkpkdtlmiSrtpEvTcvYvdvshEdpeVkfNw 300  
QY 301 YVDGVEVHNATKPREQYNSTYRVSVLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 360  
Db 301 yvdgvevhnatkpreEqynstYrvsvltclvKgfYpsdiAVEwESngqpennYkttppv 360  
QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420  
Db 361 kaKgqprePqvYtlppSreEmtknQvslTclvKgfYpsdiAVEwESngqpennYkttppv 420  
QY 421 LDSGSPFLYSLKLTVDKSRWQGNVFSCSVNHEALHNHYTQKSLSLSPGK 470  
Db 421 ldsGsflyslkltvdKsrwGgnvfscsvnhealhnhytqkslsispgk 470

RESULT 9  
AAW90926



XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 XX WPI: 2000-258930/23.  
 DR N-PSDB; AAA11655.  
 XX  
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
 PT inflammatory or autoimmune disease, induces apoptosis selectively in  
 PT cells with abnormal Fas-Fas ligand systems -  
 XX  
 XX Claim 2: Page 188-189; 263pp; English.  
 XX  
 XX This invention describes a novel humanized anti-Fas antibody-like  
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
 CC ligand system, by binding to Fas on the cell surface, and prevents  
 CC apoptosis in cells with a normal system, by inhibiting binding between  
 CC Fas and its ligand. The products of the invention have anti-inflammatory,  
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,  
 CC immunomodulatory, dermatological, immunosuppressive, thrombolytic,  
 CC antirheumatic, nephrotropic, antinfertility, neuroprotective,  
 CC antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce  
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
 CC inhibition of ligand binding. (I) are used to treat and/or prevent  
 CC diseases associated with the Fas/Fas ligand system, especially systemic  
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic  
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
 CC cells. They bind to both human and murine Fas, so can be evaluated in  
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
 CC the native ligand, do not induce liver disease, and have reduced risk of  
 CC inducing a human anti-murine antibody response. This sequence represents  
 CC a humanised anti-Fas antibody HFE7A heavy chain construct HHH type  
 CC which is described in the method of the invention.  
 XX  
 XX Sequence 470 AA;

Query Match 99.2%; Score 2498; DB 21; Length 470;  
 Best Local Similarity 98.9%; Pred. No. 2.5e-143;  
 Matches 465; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 MGWSCIIIFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVRQAP 60  
 Db 1 mgwsciliflvatatgvhsqvlvqsgaevkpgasvkvsckasytftsytmmqwrqap 60  
 Qy 61 GQGLEWMGEIDPDSYNTYNNQKFKGKATLTVDTSSTAYMELSSLRSEDVAVYICARNRD 120  
 Db 61 ggglewmgeidpsdyntynqkfgkgrvtitrdtststaymelslrsedtavvycarnrd 120  
 Qy 121 YSNWYFDVWQGLTIVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180  
 Db 121 ysnwfyfdwqegltivtvssastkgpsvfplapssksgtgtaalgclvkdypfepvtvs 180  
 Qy 181 WNSGALTSVGHTEFPAVLQSSGLYSLSSVTVTPSSSLGQTQYICNVNHHKPSNTKVDKRVPE 240  
 Db 181 wnsгалtsvghtfpavlgssglyslssvstvtpssslgqtqyicnvnhkpsntkvdkrvpe 240  
 Qy 241 KSCDKHTCCPPAPELGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300  
 Db 241 kscdkhtccppapellggpsvflfppkpkdtlmisrtpevtcvvvdshedpevkfnw 300  
 Qy 301 YVDGVEVHNATKPREEQYNSTYRVVSVLTVLDHDLNGKYEKCKVSNKALPAPIEKTIS 360  
 Db 301 yvdgvevhnatkpreeqynstyrvvsvltvlhdwlngkyekckvsnkalpapiektis 360  
 Qy 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 420  
 Db 361 kakgqprepqvtytlppsreemtknqvsltclvkgfypsdiavewesngqpennkytppv 420

Db 361 kakgqprepqvtytlppsreemtknqvsltclvkgfypsdiavewesngqpennkytppv 420  
 Qy 421 LDSGCSFFLYSKLTVDKSRWQQGNVFCSVHAEALHNHYTQKSLSLSPK 470  
 Db 421 ldsqgsfflyskltvdksrwqqgnvfscsvmhealhnhytqkslslsppgk 470  
 RESULT 11  
 AAM52156  
 ID AAM52156 standard; Protein; 731 AA.  
 XX  
 AC AAM52156;  
 XX  
 DT 05-FEB-2002 (first entry)  
 XX  
 DE Humanised HMFG-1 heavy chain/DNase I fusion protein 1.  
 XX  
 KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;  
 KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200174905-A1.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PD 26-MAR-2001; 2001WO-GB01324.  
 XX  
 PF 03-APR-2000; 2000GB-0008049.  
 XX  
 PR 02-OCT-2000; 2000US-237159P.  
 XX  
 XX (ANTI-) ANTISOMA RES LTD.  
 XX  
 YI Young RJ;  
 XX  
 DR WPI: 2001-662969/76.  
 XX  
 PT Novel compound used to treat cancer has target cell-specific portion  
 PT comprising humanised monoclonal antibody having specificity for  
 PT polymorphic epithelial mucin, and cytotoxic portion having  
 PT endonucleolytic activity -  
 XX  
 PS Claim 20; Figure 7; 176pp; English.  
 XX  
 CC The invention relates to a compound which comprises a target  
 CC cell-specific portion, comprising an humanised monoclonal antibody,  
 CC having specificity for polymorphic epithelial mucin (PEM) or its antigen  
 CC binding fragment and a cytotoxic portion having endonucleolytic activity,  
 CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The  
 CC compound has cytostatic activity useful for treating cancer and acting as  
 CC a potential inducer of apoptosis.  
 XX  
 SQ Sequence 731 AA;

Query Match 93.3%; Score 2349.5; DB 22; Length 731;  
 Best Local Similarity 93.2%; Pred. No. 3.8e-134;  
 Matches 438; Conservative 19; Mismatches 10; Indels 3; Gaps 1;  
 Qy 1 MGWSCIIIFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVRQAP 60  
 Db 1 mgwsciliflvatatgvhsqvlvqsgaevkpgasvkvsckasytftsytmmqwrqap 60  
 Qy 61 GQGLEWMGEIDPDSYNTYNNQKFKGKATLTVDTSSTAYMELSSLRSEDVAVYICARNRD 120  
 Db 61 ggglewmgeidpsdyntynqkfgkgrvtitrdtststaymelslrsedtavvycarsyd 120  
 Qy 121 YSNWYFDVWQGLTIVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180  
 Db 121 fa---wfywqggltivtvssastkgpsvfplapssksgtgtaalgclvkdypfepvtvs 177  
 Qy 181 WNSGALTSVGHTEFPAVLQSSGLYSLSSVTVTPSSSLGQTQYICNVNHHKPSNTKVDKRVPE 240

Db 178 wnsqaltsgvhtfpavilgsglyslssvvtvpssslgtqtyicnvnhkpsntckvdkkvep 237  
 QY 241 KSCDKTHTCPCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNM 300  
 Db 238 kscdkthtccpcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw 297  
 QY 301 YVDGVEVHNAKTPREEOYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 360  
 Db 298 yvdgvevhnaktkpreeqnystyrsvsvltvlhqdwlngkeyckvsnkalpapietkis 357  
 QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420  
 Db 358 kagqgprepqvvtlppsrdeitknqvsitclvkgfypsdiavewesngqpennnykttppv 417  
 QY 421 LQSDGSFFLYSKLTVDKSRWQQGNVPCSMVHEALHNNHYTQKLSLSLSPGK 470  
 Db 418 ldsdgsfflyskltvdksrwggnvfscsmvhealhnhytqklsispsgk 467

## RESULT 12

AAW52159  
 ID AAW52159 standard; Protein; 741 AA.

AC AAW52159;

DT 05-FEB-2002 (first entry)

DE Humanised HMFG-1 heavy chain/DNase I fusion protein 4.

XX Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;

KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.

OS Homo sapiens.

OS Synthetic.

PN WO200174905-A1.

PD 11-OCT-2001.

PF 26-MAR-2001; 2001WO-GB01324.

XX 03-APR-2000; 2000GB-0008049.

PR 02-OCT-2000; 2000US-237159P.

XX (ANTI-) ANTISOMA RES LTD.

XX Young RJ;

XX WPI; 2001-662969/76.

XX Novel compound used to treat cancer has target cell-specific portion

PT comprising humanised monoclonal antibody having specificity for

PT polymorphic epithelial mucin, and cytotoxic portion having

PT endonucleolytic activity -

XX Claim 20; Figure 10; 176pp; English.

XX The invention relates to a compound which comprises a target

CC cell-specific portion, comprising an humanised monoclonal antibody,

CC having specificity for polymorphic epithelial mucin (PEM) or its antigen

CC binding fragment and a cytotoxic portion having endonucleolytic activity,

CC exemplified by AAW52154-AAW52168 and encoded by ABA02682-ABA02728. The

CC compound has cytostatic activity useful for treating cancer and acting as

CC a potential inducer of apoptosis.

XX Sequence 741 AA;

## Query Match

Best Local Similarity 93.3%; Score 2349.5; DB 22; Length 741;

Matches 438; Conservative 19; Mismatches 10; Indels 3; Gaps 1;

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 Db 1 mgwscililflvatgvhsqvlvsgaevkpgasvkscaksgyftfaywiewvraqp 60  
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 Db 61 gkglewvgeilpgsnnsrynefkgrvtvtrdtstntaymelsslrsestavyycarsyd 120  
 QY 121 YSNWYFDVWGQGLTVTVSSASTKGPSVPLAPSSKSTSGGTAALGCLVLDKDFPEPVTVS 180  
 Db 121 fa---wfywvggtlvtvssastkgpsvplapsskstsggtaalgclvldkdfpepvtvs 177  
 QY 181 WNSGALTSGVHTFPVAVLQSSGLYSLSVVTVPSSSSLGTQTYICNVNHNKPSNTKVDKRVEP 240  
 Db 178 wnsqaltsgvhtfpavilgsglyslssvvtvpssslgtqtyicnvnhkpsntckvdkkvep 237  
 QY 241 KSCDKTHTCPCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNM 300  
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 QY 421 LQSDGSFFLYSKLTVDKSRWQQGNVPCSMVHEALHNNHYTQKLSLSLSPGK 470  
 Db 418 ldsdgsfflyskltvdksrwggnvfscsmvhealhnhytqklsispsgk 467

## RESULT 13

AAW52158  
 ID AAW52158 standard; Protein; 729 AA.

AC AAW52158;

DT 05-FEB-2002 (first entry)

DE Humanised HMFG-1 heavy chain/DNase I fusion protein 3.

XX Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;

KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.

OS Homo sapiens.

OS Synthetic.

PN WO200174905-A1.

PD 11-OCT-2001.

PF 26-MAR-2001; 2001WO-GB01324.

XX 03-APR-2000; 2000GB-0008049.

PR 02-OCT-2000; 2000US-237159P.

XX (ANTI-) ANTISOMA RES LTD.

XX Young RJ;

XX WPI; 2001-662969/76.

XX Novel compound used to treat cancer has target cell-specific portion

PT comprising humanised monoclonal antibody having specificity for

PT polymorphic epithelial mucin, and cytotoxic portion having

PT endonucleolytic activity -

XX Claim 20; Figure 9; 176pp; English.

XX The invention relates to a compound which comprises a target

CC cell-specific portion, comprising an humanised monoclonal antibody,

CC having specificity for polymorphic epithelial mucin (PEM) or its antigen  
 CC binding fragment and a cytotoxic portion having endonucleolytic activity,  
 CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The  
 CC compound has cytostatic activity useful for treating cancer and acting as  
 CC a potential inducer of apoptosis.  
 XX  
 SQ Sequence 729 AA;

Query Match 93.1%; Score 2344.5; DB 22; Length 729;  
 Best Local Similarity 93.2%; Pred. No. 7.5e-134;  
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 Db 1 mgwscililflvatatgvsqvlvqsgaevkpgasvkvsckasgytftsawiewvrdqap 60  
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 Db 61 gglewmeidpdsytnynokfkgkatltvdststaymelslsrseadtavyycarsyd 120  
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 Db 121 fa---wfaywgggtlvtvssastkgpsvfplapsskstsggtaalgclvkdypfepvtvs 177  
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 Db 178 wnsгалтsgvitfpavldssglsyslvstvtpssslgtqtyicnvnhkpsntkvdckv 237  
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 Db 238 kscdkthcpccpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw 297  
 Qy 301 YVDGVEVHNATKPREOYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360  
 Db 298 yvdgvevhnatkpreedynstyrvvsvltvlhqdwlngkeyckvskvsnkalpapiektis 357  
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 Db 358 kkgqprepqvytlppsrdeitknqvsitclvkgyfypsdiavewesngqpennykttppv 417  
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 ID AAM52161 standard; Protein; 739 AA.  
 XX  
 AC AAM52161;  
 XX  
 DT 05-FEB-2002 (first entry)  
 XX  
 DE Humanised HMFg-1 heavy chain/DNase I fusion protein 6.  
 XX  
 KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;  
 KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200174905-A1.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 26-MAR-2001; 2001WO-GB01324.  
 XX  
 PR 03-APR-2000; 2000GB-0008049.  
 PR  
 PR 02-OCT-2000; 2000US-237159P.  
 XX  
 PA (ANTI-) ANTISOMA RES LTD.  
 XX

PI Young RJ;  
 XX  
 DR WPI; 2001-662969/76.  
 XX  
 PT Novel compound used to treat cancer has target cell-specific portion  
 PT comprising humanised monoclonal antibody having specificity for  
 PT polymorphic epithelial mucin, and cytotoxic portion having  
 PT endonucleolytic activity -  
 XX  
 PS Claim 20; Figure 12; 176pp; English.  
 XX  
 CC The invention relates to a compound which comprises a target  
 CC cell-specific portion, comprising an humanised monoclonal antibody,  
 CC having specificity for polymorphic epithelial mucin (PEM) or its antigen  
 CC binding fragment and a cytotoxic portion having endonucleolytic activity,  
 CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The  
 CC compound has cytostatic activity useful for treating cancer and acting as  
 CC a potential inducer of apoptosis.  
 XX  
 SQ Sequence 739 AA;

Query Match 93.1%; Score 2344.5; DB 22; Length 739;  
 Best Local Similarity 93.2%; Pred. No. 7.6e-134;  
 Matches 437; Conservative 19; Mismatches 10; Indels 3; Gaps 1;  
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 Db 298 yvdgvevhnatkpreedynstyrvvsvltvlhqdwlngkeyckvskvsnkalpapiektis 357  
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 Db 358 kkgqprepqvytlppsrdeitknqvsitclvkgyfypsdiavewesngqpennykttppv 417  
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 Db 418 ldsdgsfflyskltvdksrwqgnvfscsvmhealhnyhtqkslsispg 466

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 ID AAM52157 standard; Protein; 730 AA.  
 XX  
 AC AAM52157;  
 XX  
 DT 05-FEB-2002 (first entry)  
 XX  
 DE Humanised HMFg-1 heavy chain/DNase I fusion protein 2.  
 XX  
 KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;  
 KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.  
 XX  
 OS Homo sapiens.  
 OS

Search completed: August 14, 2002, 15:15:40  
Job time: 838 sec

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OS Synthetic.
XX WO200174905-A1.
XX PD
XX PD
XX 11-OCT-2001.
XX 26-MAR-2001; 2001WO-GB01324.
XX
XX 03-APR-2000; 2000GB-0008049.
XX 02-OCT-2000; 2000US-237159P.
XX
XX (ANTI-) ANTISOMA RES LTD.
XX
XX Young RJ;
XX WPI; 2001-662969/76.
XX
XX Novel compound used to treat cancer has target cell-specific portion
XX comprising humanised monoclonal antibody having specificity for
XX polymorphic epithelial mucin, and cytotoxic portion having
XX endonucleolytic activity
XX
XX Claim 20; Figure 8; 176pp; English.
XX
XX The invention relates to a compound which comprises a target
XX cell-specific portion, comprising an humanised monoclonal antibody,
XX having specificity for polymorphic epithelial mucin (PEM) or its antigen
XX binding fragment and a cytotoxic portion having endonucleolytic activity,
XX exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
XX compound has cytostatic activity useful for treating cancer and acting as
XX a potential inducer of apoptosis.
XX
XX Sequence 730 AA;
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Query Match 92.9%; Score 2338.5; DB 22; Length 730;
Best Local Similarity 93.2%; Pred. No. 1.7e-133;
Matches 436; Conservative 19; Mismatches 10; Indels 3; Gaps 1;
QY 1 MGWSCIILFLVATATGVHSGVQLVQSGAEVKKPGASVKVCKASGYTFTSYWQWVQRAP 60
DB 1 mgwscililflvatatgvhsqqlvqsgaevkpgasvkvsckasgytfsaywiewvraqp 60
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DB 61 gqglewvegilpgsnnsrynekfgrvtvtrdtstntaymelsslrse dtavvycarsyd 120
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DB 121 fa---wfywgggtlvtvssastkgpsvfplapsskstsggtaalgclvkdyfpeptvts 177
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DB 178 wnsгалtsghvtfpavlqsglysisvvtvpssslgtqyicnvnhkpsntkvdkkvep 237
QY 241 KSCDKTHTCTPCPCAPAPPELLGGPSVFLPPPKPKDTLMISRPETVCVVVDVSHEDPEVKFNM 300
DB 238 kscdkthtctpcpapellggpsvflfppkpkdtlmisrtpetvcvvdvshedpevkfnw 297
QY 301 YVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 15:17:06 ; Search time 82.88 Seconds  
(without alignments)  
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Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2235	88.8	449	1	US-08-458-516-13
2	2233	88.7	476	2	US-08-378-939-10
3	2205.5	87.6	467	4	US-09-049-672A-8
4	2203.5	87.5	452	3	US-09-027-449-71
5	2203.5	87.5	452	4	US-09-026-985-71
6	2174	86.4	468	4	US-09-485-737B-67
7	2174	86.4	711	4	US-09-485-737B-90
8	2158.5	85.8	454	2	US-07-934-373C-22
9	2158.5	85.8	454	3	US-08-437-642B-22
10	2158.5	85.8	454	5	PCT-US93-07832-22
11	2147	85.3	472	4	US-08-793-450-8
12	2127	84.5	451	2	US-08-887-352B-14
13	2127	84.5	451	2	US-08-887-352B-16
14	2127	84.5	451	3	US-08-466-151-65
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17	2127	84.5	451	4	US-09-296-005-14
18	2127	84.5	451	4	US-09-296-005-16
19	2124	84.4	478	3	US-08-487-550-8
20	2119	84.2	451	2	US-08-887-352B-18
21	2119	84.2	451	4	US-09-109-207C-18
22	2119	84.2	451	4	US-09-282-505-2
23	2119	84.2	451	4	US-09-054-255-2
24	2119	84.2	451	4	US-09-296-005-18
25	2108	83.8	453	3	US-08-466-151-8
26	2108	83.8	453	4	US-08-466-163B-8
27	2106.5	83.7	467	2	US-07-916-098A-45

28	2105.5	83.7	449	4	US-09-679-397-2	Sequence 2, Appl
29	2102.5	83.5	552	5	PCT-US93-07832-23	Sequence 23, Appl
30	2099.5	83.4	469	2	US-07-934-373C-23	Sequence 23, Appl
31	2099.5	83.4	469	3	US-08-437-642B-23	Sequence 23, Appl
32	2096	83.3	451	4	US-09-247-352-3	Sequence 3, Appl
33	2093.5	83.2	459	1	US-08-157-101A-7	Sequence 7, Appl
34	2073.5	82.5	467	1	US-08-704-744-81	Sequence 81, Appl
35	2073.5	82.4	473	4	US-09-049-672A-4	Sequence 4, Appl
36	2063.5	82.0	445	4	US-08-341-560B-17	Sequence 17, Appl
37	2057.5	81.7	446	3	US-08-397-411-7	Sequence 7, Appl
38	2057	81.7	476	3	US-08-487-550-12	Sequence 12, Appl
39	2025	80.5	442	5	PCT-US98-10043-9	Sequence 9, Appl
40	2025	80.5	476	3	US-08-487-550-4	Sequence 4, Appl
41	2013	80.0	442	1	US-08-461-968A-5	Sequence 5, Appl
42	2013	80.0	442	2	US-08-462-571-5	Sequence 5, Appl
43	1998.5	79.4	450	2	US-08-788-800-12	Sequence 12, Appl
44	1989	79.0	442	1	US-08-480-036-2	Sequence 2, Appl
45	1989	79.0	442	1	US-08-461-968A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-08-458-516-13  
; Sequence 13, Application US/08458516  
; Patent No. 5777085  
; GENERAL INFORMATION:  
; APPLICANT: Co, Man Sung  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Humanized Antibodies Reactive with  
; TITLE OF INVENTION: GPIIB/IIIA  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/458,516  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/059,159  
; FILING DATE: 03-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-37-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 449 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-458-516-13

Query Match 88.8%; Score 2235; DB 1; Length 449;  
Best Local Similarity 93.3%; Pred. No. 6.6e-159;  
Matches 421; Conservative 13; Mismatches 15; Indels 2; Gaps 2;

QY 20 QVOLVSGAEVKKPGASVKVSKASGYTFTSYWMQVRAQPGGLEWMEGIDPSDYTNV 79  
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Db 179 SGLYSLSVVTVPSVSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCCPPCAPPELLG 238  
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Db 359 ELTKNQVSLTCLVKGPYPSDIAVWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSR 418  
QY 440 WQGNVFCFSVMHEALHNHYTKLSLSPGK 470  
Db 419 WQGNVFCFSVMHEALHNHYTKLSLSPGK 449

## RESULT 2

US-08-378-939-10  
; Sequence 10, Application US/08378939  
; Patent No. 5876961  
; GENERAL INFORMATION:  
; APPLICANT: CROWE, JAMES SCOTT  
; APPLICANT: LEWIS, ALAN PETER  
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ  
; STREET: 555 THIRTEENTH ST. N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: U.S.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/378,939  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/952640  
; FILING DATE: 01-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ERNST, BARBARA G  
; REGISTRATION NUMBER: 30,377  
; REFERENCE/DOCKET NUMBER: 1808-118  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 783-6040  
; TELEFAX: (202) 783-6031  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 476 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

; MOLECULE TYPE: protein  
US-08-378-939-10

Query Match 88.7%; Score 2233; DB 2; Length 476;  
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QY 1 MGWSCIILFLVATATQVHQSQVQLVQSGAEVKKPGASVKVSKASGYTFTSYWMQVRAQ 60  
Db 1 MDWTRFLFVAAATQVQSQVQVQVQSGAEVKKPGSSVTVSKASGGTFSNYAISWVRAQ 60  
QY 61 GQGLEWMEIDPSDYSYNTNKKFKGKATLVDTSTAYMELSLRSEDATAYYCARNR- 119  
Db 61 GQGLEWMEIDPSDYSYNTNKKFKGKATLVDTSTAYMELSLRSEDATAYYCARNR- 120  
QY 120 -----DYSNNWTFDVMWGQGTTLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGLVKDYFP 174  
Db 121 RQANFDRARVGVFDPWGQGTTLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGLVKDYFP 180  
QY 175 EPTVTVSWNSGALTSGVHTFPAVLQSSSLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKV 234  
Db 181 EPTVTVSWNSGALTSGVHTFPAVLQSSSLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKV 240  
QY 235 DKRVEPKSCDKTHTCCPPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 294  
Db 241 DKRVEPKSCDKTHTCCPPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300  
QY 295 EVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVKVSNKALPAP 334  
Db 301 EVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVKVSNKALPAP 360  
QY 355 IEKTSKAKGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNY 414  
Db 361 IEKTSKAKGQPREPOVYTLPPSREDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNY 420  
QY 415 KTTTPVLDSDGSFPLYSKLTVDKSRWQGNVFCFSVMHEALHNHYTKLSLSPGK 470  
Db 421 KTTTPVLDSDGSFPLYSKLTVDKSRWQGNVFCFSVMHEALHNHYTKLSLSPGK 476

## RESULT 3

US-09-049-672A-8  
; Sequence 8, Application US/09049672A  
; Patent No. 6135941  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Yue, Henry  
; APPLICANT: Au-Young, Janice  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; APPLICANT: Baughn, Mariah R.  
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/049,672A  
; FILING DATE: HEREWITH  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ceirone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGUT11
; CLONE: 2747531
; US-09-049-672A-8

Query Match      87.6%; Score 2205.5; DB 4; Length 467;
Best Local Similarity 89.4%; Pred. No. 1.1e-156;
Matches 415; Conservative 18; Mismatches 28; Indels 3; Gaps 1;

Qy 7 ILFLVATATGVHVSQVLQVSGAEYKPKGASVKSCASGYTFTSYMMQWVRQAPQGGLW 66
Db 7 ILFLVAAATGTHAQVLQVSGAEYKPKGASVQVSGFTLSDLVHVMVRQAPQGGLW 66

Qy 67 MGEIDPSDSTNYNQKFKGKATLVDTSTAYMELSLRSEDYAVYCARNRDYSNNY 126
Db 67 MGLAPENGEAYAKFLGRLTSEDYADTAYMFLNNGSDESAIYYCARQH---YDF 123

Qy 127 FDVWGQGLTVTVSSASVKGPSVFLAPSSKSTSGTAAALGCLVKDYRPPETVSNWNGAL 186
Db 124 FDFWGQGTMTVTVSSASVKGPSVFLAPSSKSTSGTAAALGCLVKDYRPPETVSNWNGAL 183

Qy 187 TSGVHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKYDKRVEPKSCDKT 246
Db 184 TSGVHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKYDKRVEPKSCDKT 243

Qy 247 HTCPCPAPELLGSPVFLFPKPKDTLMISRTPETVCVVVDVSHEDPEVKFNWYVDGVE 306
Db 244 HTCPCPAPELLGSPVFLFPKPKDTLMISRTPETVCVVVDVSHEDPEVKFNWYVDGVE 303

Qy 307 VHNKTKPREQYNTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGP 366
Db 304 VHNKTKPREQYNTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGP 363

Qy 367 REPOVYTLPPSREMTKNQVSLTCLVKGFPYSDIAVWESNGQPENNYKTTTPVLDSDGS 426
Db 364 REPOVYTLPPSREMTKNQVSLTCLVKGFPYSDIAVWESNGQPENNYKTTTPVLDSDGS 423

Qy 427 FFYLSKLTVDKSRQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 470
Db 424 FFYLSKLTVDKSRQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 467

RESULT 4
US-09-027-449-71
; Sequence 71, Application US/09027449
; Patent No. 6025158
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way

```

```

; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,449
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074,330
; FILING DATE: 22-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,664
; FILING DATE: 21-Feb-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: PI085R3-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-027-449-71

Query Match      87.5%; Score 2203.5; DB 3; Length 452;
Best Local Similarity 90.3%; Pred. No. 1.5e-156;
Matches 408; Conservative 26; Mismatches 17; Indels 1; Gaps 1;

Qy 20 QVLVQSGAEYKPKGASVKSCASGYTFTSYMMQWVRQAPQGGLWGEIDPSDSTNY 79
Db 1 EVQLVQSGGLVQPGSLRLSCAASGYSFSSHYMHWRQAPGKGLWYGYIDPSNGEITY 60

Qy 80 NQKFKGKATLVDTSTAYMELSLRSEDYAVYCAR-NRDYSNNWYFDVWGQGLTVTV 138
Db 61 NQKFKGRTLSRDNSKNTAYLQMNLSRAEDYAVYCARGDYRYNGDWFVWGQGLTVTV 120

Qy 139 SSASTKGPSVFLAPSSKSTSGTAAALGCLVKDYRPPETVSNWNGALTSGVHTFPVAVLQ 198
Db 121 SSASTKGPSVFLAPSSKSTSGTAAALGCLVKDYRPPETVSNWNGALTSGVHTFPVAVLQ 180

Qy 199 SSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKYDKRVEPKSCDKTHTCPCPAPELL 258
Db 181 SSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKYDKRVEPKSCDKTHTCPCPAPELL 240

Qy 259 GGPSVFLPPPKPKDTLMISRTPETVCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQ 318
Db 241 GGPSVFLPPPKPKDTLMISRTPETVCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQ 300

Qy 319 YNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGPREPOVYTLPPSR 378
Db 301 YNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGPREPOVYTLPPSR 360

Qy 379 EEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 438
Db 361 EEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420

Qy 439 RWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 470
Db 421 RWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 452

RESULT 5
US-09-026-985-71

```

; Sequence 71, Application US/09026985  
; Patent No. 6133426

; GENERAL INFORMATION:

; APPLICANT: Gonzalez, Tania R.

; APPLICANT: Leong, Steven R.

; APPLICANT: Presta, Leonard G.

; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and

; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies

; NUMBER OF SEQUENCES: 72

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech,

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/026,985

; FILING DATE: 20-Feb-1998

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Love, Richard B.

; REGISTRATION NUMBER: 34,659

; REFERENCE/DOCKET NUMBER: P1085R3-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-5530

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 71:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 452 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

; US-09-026-985-71

Query Match 87.5%; Score 2203.5; DB 4; Length 452;

Best Local Similarity 90.3%; Pred. No. 1.5e-156;

Matches 408; Conservative 26; Mismatches 17; Indels 1; Gaps 1;

QY 20 QYLVQSGAEVKKPGASVVKSCASGYFTSYMMQVVRQAPGQGLWMCIDPSISYNN 79

DB 1 EVQLVQSGGGLVQPGGSLRLCAASGYSFSSHHMHWVRQAPGKGLWVGVIIDPSNGETTY 60

QY 80 NQKFKGKATLVDTSTSTAYMELSLRSEDATVYICAR-NRDYSNNWYFDVWGQGTLLTV 138

DB 61 NQKFKGRFTLSRDNSKNTAYLQMNSLRAREDATVYICARGDYRNGDWFFDVWGQGTLLTV 120

QY 139 SSASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTTTPAVLQ 198

DB 121 SSASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTTTPAVLQ 180

QY 199 SSGLSLSSVWTVVPSSSLGTQYICNVNHPKSNKTKVDRKVEPKSCDKTHTCPCPAPELL 258

DB 181 SSGLSLSSVWTVVPSSSLGTQYICNVNHPKSNKTKVDRKVEPKSCDKTHTCPCPAPELL 240

QY 259 GGPSVFLFPKPKDLMISRTPVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREQ 318

DB 241 GGPSVFLFPKPKDLMISRTPVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREQ 300

QY 319 YNSTRVVSVLVHODWLNKKEYCKVSNKALPAIEKTIISKAGCOPREPQVYTLPPSR 378

DB 301 YNSTRVVSVLVHODWLNKKEYCKVSNKALPAIEKTIISKAGCOPREPQVYTLPPSR 360

QY 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKS 438

DB 361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKS 420

QY 439 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470

DB 421 RWOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 452

RESULT 6

US-09-485-737B-67

; Sequence 67, Application US/09485737B

; Patent No. 6350860

; GENERAL INFORMATION:

; APPLICANT: Buyse, Marie-Ange

; APPLICANT: Sablon, Erwin

; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,

; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS

; FILE REFERENCE: INNS:015

; CURRENT APPLICATION NUMBER: US/09/485,737B

; CURRENT FILING DATE: 2000-02-14

; PRIOR APPLICATION NUMBER: PCT/EP 98/05165

; PRIOR FILING DATE: 1998-08-14

; PRIOR APPLICATION NUMBER: EPO 98870139.7

; PRIOR FILING DATE: 1998-06-18

; PRIOR APPLICATION NUMBER: EPO 97870122.5

; PRIOR FILING DATE: 1997-08-18

; NUMBER OF SEQ ID NOS: 104

; SOFTWARE: Patentin version 3.0

; SEQ ID NO 67

; LENGTH: 468

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: SYNTHETIC

; US-09-485-737B-67

Query Match 86.4%; Score 2174; DB 4; Length 468;

Best Local Similarity 88.0%; Pred. No. 2.5e-154;

Matches 409; Conservative 21; Mismatches 31; Indels 4; Gaps 1;

QY 6 IILFLVATATGTVHSGVQLVQSGAEVKKPGASVVKSCASGYFTSYMMQVVRQAPGQGLE 65

DB 7 IFSELLISASVILSQVLQVQSGSELKPKGASVKISKASGYFTDYGMNVKQAPQGGLK 66

QY 66 WNGEIDPSISYNNQKFKGKATLVDTSTSTAYMELSLRSEDATVYICARNRDYSNNW 125

DB 67 WNGWINTYTGESTYVDDDFGKGFVFLDTSVSAAYLQISLKAEDTATYFCARRGFYA--- 123

QY 126 YFDVWGQGTLLTVVSSASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSNNSGA 185

DB 124 -MDYWGQGTLLTVVSSASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSNNSGA 182

QY 186 LTSGVHTTTPAVLQSSGLYSLSSVTVVPSSSLGTQYICNVNHPKSNKTKVDRKVEPKSCDK 245

DB 183 LTSGVHTTTPAVLQSSGLYSLSSVTVVPSSSLGTQYICNVNHPKSNKTKVDRKVEPKSCDK 242

QY 246 THTCPPCPAPELLGSPVFLFPKPKDLMISRTPVTCVVDVSHEDPEVKFNWYVDGV 305

DB 243 THTCPPCPAPELLGSPVFLFPKPKDLMISRTPVTCVVDVSHEDPEVKFNWYVDGV 302

QY 306 EYHNKTKPREQYNSTYRVVSVTLVHODWLNKKEYCKVSNKALPAIEKTIISKAGQ 365

DB 303 EYHNKTKPREQYNSTYRVVSVTLVHODWLNKKEYCKVSNKALPAIEKTIISKAGQ 362

QY 366 PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 425

DB 363 PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 422

QY 426 SFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470

DB 423 SFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 467

RESULT 7

US-09-485-737B-90

; Sequence 90, Application US/09485737B

; Patent No. 6350860  
; GENERAL INFORMATION:  
; APPLICANT: Buyse, Marie-Ange  
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,  
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS  
; FILE REFERENCE: INNS:015  
; CURRENT APPLICATION NUMBER: US/09/485,737B  
; CURRENT FILING DATE: 2000-02-14  
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165  
; PRIOR FILING DATE: 1998-08-14  
; PRIOR APPLICATION NUMBER: EPO 98870139.7  
; PRIOR FILING DATE: 1998-06-18  
; PRIOR APPLICATION NUMBER: EPO 97870122.5  
; PRIOR FILING DATE: 1997-08-18  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 90  
; LENGTH: 711  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC  
US-09-485-737B-90

Query Match 86.4%; Score 2174; DB 4; Length 711;  
Best Local Similarity 88.0%; Pred. No. 4.3e-154;  
Matches 409; Conservative 21; Mismatches 31; Indels 4; Gaps 1;

QY 6 IILFLVATGVSQVQVOSGAEVKKPGASVKASCKASGYTFTSYWQVVRQAPQGGL 65  
Db 7 IFGLISASVILVSQVQVOSGSELKPGASVKISCKASGYTFTDYGNNVYKQAPQGGL 66  
QY 66 WMGEIDPSDYTNKQFKKATLTVDSTSTAYMELSSRLSEDTAVIYCARNRDYSNNW 125  
Db 67 WMGWINTYTGESYVDVDFGRFVSLDTSVAAYLQISSLKAEATATYFCARRGFVA--- 123  
QY 126 YFDVWQOGLTVYSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGA 185  
Db 124 -MDYWGQGTFTVYSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGA 182  
QY 186 LTSVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKYDKRVEPKSCDK 245  
Db 183 LTSVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKYDKRVEPKSCDK 242  
QY 246 THTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 305  
Db 243 THTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 302  
QY 306 EVHNAKTKPREQYNSTIRYVSVLTCLVHQLDNLNGKEYCKKVSNAKALPAPIETKISRAKQ 365  
Db 303 EVHNAKTKPREQYNSTIRYVSVLTCLVHQLDNLNGKEYCKKVSNAKALPAPIETKISRAKQ 362  
QY 366 PREPQYTLPPSREEMTKNQVSLTCLVKGYPSDIAVEWESNGOPENNYKTTTPVLDSDG 425  
Db 363 PREPQYTLPPSREEMTKNQVSLTCLVKGYPSDIAVEWESNGOPENNYKTTTPVLDSDG 422  
QY 426 SFFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSLSPGK 470  
Db 423 SFFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTKLSLSLSPGK 467

RESULT 8  
US-07-934-373C-22  
; Sequence 22, Application US/07934373C  
; Patent No. 5821337

; GENERAL INFORMATION:  
; APPLICANT: Paul J. Carter  
; APPLICANT: Leonard G. Presta  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 48  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/934,373C  
; FILING DATE: 21-Aug-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05126  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA: 07/715272  
; APPLICATION NUMBER:  
; FILING DATE: 14-JUN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0709P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1994  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 454 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-07-934-373C-22

Query Match

85.8%; Score 2159.5; DB 2; Length 454;

Best Local Similarity 89.2%; Pred. No. 3.4e-153;

Matches 405; Conservative 18; Mismatches 28; Indels 3; Gaps 1;

QY 20 QVQLVQSGAEVKKPGASVKASCKASGYTFTSYWQVVRQAPQGGLWMEGETDPSDSTNY 79  
Db 1 QVQLQSGPELVKPGASVKISCKTSGYTFEYTHHWKQSHGKSLWIGFENPKNGSSH 60  
QY 80 NQKFKGKATLTVDSTSTAYMELSSRLSEDTAVIYCARNRDYSNNW---YFDVWQOGLTV 136  
Db 61 NQKFKGKATLTVDSTSTAYMELSSRLSEDTAVIYCARNRDYSNNW---YFDVWQOGLTV 120  
QY 137 TVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTTTPAV 196  
Db 121 TVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTTTPAV 180  
QY 197 LQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKYDKRVEPKSCDKTKTCPCPAPE 256  
Db 181 LQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKYDKRVEPKSCDKTKTCPCPAPE 240  
QY 257 LLGSPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVEVHNAKTKPRE 316  
Db 241 LLGSPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVEVHNAKTKPRE 300  
QY 317 EQYNSTIRYVSVLTCLVHQLDNLNGKEYCKKVSNAKALPAPIETKISKAGQPREPQYTLPP 376  
Db 301 EQYNSTIRYVSVLTCLVHQLDNLNGKEYCKKVSNAKALPAPIETKISKAGQPREPQYTLPP 360  
QY 377 SREEMTKNQVSLTCLVKGYPSDIAVEWESNGOPENNYKTTTPVLDSDGSEFFLYSLKLTVD 436  
Db 361 SREEMTKNQVSLTCLVKGYPSDIAVEWESNGOPENNYKTTTPVLDSDGSEFFLYSLKLTVD 420  
QY 437 KSRWQGNVFCSCVMHEALHNHYTKLSLSLSPGK 470  
Db 421 KSRWQGNVFCSCVMHEALHNHYTKLSLSLSPGK 454

[illegible]



Db 61 NQFMDKATLAVDKSTSTAYMELSLTSEDSGIIYICARWGLNYGFDVRYFDWAGGTV 120  
Qy 137 TVSSASTKSPVFPPLAPSSKTSGGTAALGCLVKDYFPEPVTVSWNSGALTSQVHTFPV 196  
Db 121 TVSSASTKSPVFPPLAPSSKTSGGTAALGCLVKDYFPEPVTVSWNSGALTSQVHTFPV 180  
Qy 197 LQSSGLYSLSSVTVVPSSSLGTQYIYICNVNKKPNTKVDKVEPKSCDKTHTCPCPAPE 256  
Db 181 LQSSGLYSLSSVTVVPSSSLGTQYIYICNVNKKPNTKVDKVEPKSCDKTHTCPCPAPE 240  
Qy 257 LLGSPSVFLFPKPKDTHMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNKTRPRE 316  
Db 241 LLGSPSVFLFPKPKDTHMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNKTRPRE 300  
Qy 317 EQYNSTYRVSVLTVLHODWLNKREYKCKVSNKALPAPIEKTSKAKGQPREPOVYTLPP 376  
Db 301 EQYNSTYRVSVLTVLHODWLNKREYKCKVSNKALPAPIEKTSKAKGQPREPOVYTLPP 360  
Qy 377 SREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVD 436  
Db 361 SREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKLTVD 420  
Qy 437 KSRWQOGNVFSCSVMHREALHNNHYTKLSLSPGK 470  
Db 421 KSRWQOGNVFSCSVMHREALHNNHYTKLSLSPGK 454

RESULT 11  
US-08-793-450-8  
; Sequence 8, Application US/08793450  
; Patent No. 6312690  
; GENERAL INFORMATION:  
; APPLICANT: EDELMAN, LENA  
; APPLICANT: MARGARITTE, CHRISTEL  
; APPLICANT: KACZOREK, MICHEL  
; APPLICANT: CHABRIHL, HASSAN  
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/793,450  
; FILING DATE: 03-MAR-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 94/10566  
; FILING DATE: 02-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT  
; TELEPHONE: 703-413-3000  
; TELEFAX: 703-413-2220  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 472 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-793-450-8

Query Match 85.3%; Score 2147; DB 4; Length 472;  
Best Local Similarity 85.18; Pred. No. 2.6e-152;  
Matches 404; Conservative 26; Mismatches 37; Indels 8; Gaps 3;  
Qy 1 MGWSCIIILFLVATATGVHSGAELVQSGAEVKKPGASVKVSKKASGYTFTSYMMQWRQAP 60  
Db 1 MGWSCIIILFLVATATGVHSGAELVQSGAEVKKPGASVKVSKKASGYTFTSYMMQWRQAP 60  
Qy 61 GQGLEWMEIDPSDSTNYNQKFKGKATLTVDSTSTAYMELSSRLSDEDTAVYICARNRD 120  
Db 61 GQGLEWMEIDPSDSTNYNQKFKGKATLTVDSTSTAYMELSSRLSDEDTAVYICARPE 119  
Qy 121 YSNWN-----YFDVMGQGLTVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPE 175  
Db 120 Y--KWKYHGWDWDFWQGGTTTVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPE 177  
Qy 176 PVTYSWNSGALTSQVHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQYIYICNVNKKPNTKVD 235  
Db 178 PVTYSWNSGALTSQVHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQYIYICNVNKKPNTKVD 237  
Qy 236 KRVEPKSCDKTHTCPCPAPELLGSPVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPE 295  
Db 238 KKAEPKSCDKTQTCPCPAPELLGSPVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPE 297  
Qy 296 VKFNWYVDGVEVHNKTRPREOYNSTYRVSVLTVLHODWLNKREYKCKVSNKALPAPI 355  
Db 298 VKFNWYVDGVEVHNKTRPREOYNSTYRVSVLTVLHODWLNKREYKCKVSNKALPAPI 357  
Qy 356 EKTISKAKGQPREPVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 415  
Db 358 EKTISKAKGQPREPVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 417  
Qy 416 TTPVLDSDGSPFLYSKLTVDKSRWQOGNVFSCSVMHREALHNNHYTKLSLSPGK 470  
Db 418 TTPVLDSDGSPFLYSKLTVDKSRWQOGNVFSCSVMHREALHNNHYTKLSLSPGK 472  
RESULT 12  
US-08-887-352B-14  
; Sequence 14, Application US/08887352B  
; Patent No. 5994511  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
; TITLE OF INVENTION: Improving Polypeptides  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,352B  
; FILING DATE: 03-Jul-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P1123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 451 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-887-352B-14

Query Match 84.5%; Score 2127; DB 2; Length 451;  
Best Local Similarity 87.8%; Pred. No. 7.4e-151;  
Matches 397; Conservative 23; Mismatches 30; Indels 2; Gaps 2;

QY 20 QVQLVSGAEVKPGASVKSCASGYTFTS-YVMQWVROAPQGLGWGEIDPDSYTN 78  
Db 1 EVLVESGGGLVQPGGSLRLSCAVSYISITSGYSWNIROAPQGLGWVASI-TYDGSN 59  
QY 79 YNOKFKGKATLVTDSTAYMELSLRSEDATVYYCARNRDYSNNWYFDVWGQGLTVTV 138  
Db 60 YNPVSKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHHFAVWGQGLTVTV 119  
QY 139 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWGALTSGVHTFPAVLQ 198  
Db 120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWGALTSGVHTFPAVLQ 179  
QY 199 SSGLYSLSSVTVTPSSSLGTQTYICNVNKPSTKVDKRVKPKSCDKTHTCPPCPAPELL 258  
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNKPSTKVDKRVKPKSCDKTHTCPPCPAPELL 239  
QY 259 GGPVFLFPFKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQ 318  
Db 240 GGPVFLFPFKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQ 299  
QY 319 YNSTYRWVSVLVTHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378  
Db 300 YNSTYRWVSVLVTHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359  
QY 379 EEMTKNQVSLTCLVKGFYPSDIAVEHESGQPENNYKTTTPVLDSDGSFSLYKLTVDKS 438  
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEHESGQPENNYKTTTPVLDSDGSFSLYKLTVDKS 419  
QY 439 RMQOGNVFSCVSMHEALHNNHYTKLSLSPGK 470  
Db 420 RMQOGNVFSCVSMHEALHNNHYTKLSLSPGK 451

RESULT 13  
US-08-887-352B-16  
; Sequence 16, Application US/08887352B  
; Patent No. 5994511  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IGE Antibodies and Method of  
; TITLE OF INVENTION: Improving Polypeptides  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,352B  
; FILING DATE: 03-Jul-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P1123

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 451 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-887-352B-16

Query Match 84.5%; Score 2127; DB 2; Length 451;  
Best Local Similarity 87.8%; Pred. No. 7.4e-151;  
Matches 397; Conservative 23; Mismatches 30; Indels 2; Gaps 2;

QY 20 QVQLVSGAEVKPGASVKSCASGYTFTS-YVMQWVROAPQGLGWGEIDPDSYTN 78  
Db 1 EVLVESGGGLVQPGGSLRLSCAVSYISITSGYSWNIROAPQGLGWVASI-TYDGSN 59  
QY 79 YNOKFKGKATLVTDSTAYMELSLRSEDATVYYCARNRDYSNNWYFDVWGQGLTVTV 138  
Db 60 YNPVSKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHHFAVWGQGLTVTV 119  
QY 139 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWGALTSGVHTFPAVLQ 198  
Db 120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSNWGALTSGVHTFPAVLQ 179  
QY 199 SSGLYSLSSVTVTPSSSLGTQTYICNVNKPSTKVDKRVKPKSCDKTHTCPPCPAPELL 258  
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNKPSTKVDKRVKPKSCDKTHTCPPCPAPELL 239  
QY 259 GGPVFLFPFKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQ 318  
Db 240 GGPVFLFPFKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQ 299  
QY 319 YNSTYRWVSVLVTHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378  
Db 300 YNSTYRWVSVLVTHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359  
QY 379 EEMTKNQVSLTCLVKGFYPSDIAVEHESGQPENNYKTTTPVLDSDGSFSLYKLTVDKS 438  
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEHESGQPENNYKTTTPVLDSDGSFSLYKLTVDKS 419  
QY 439 RMQOGNVFSCVSMHEALHNNHYTKLSLSPGK 470  
Db 420 RMQOGNVFSCVSMHEALHNNHYTKLSLSPGK 451

RESULT 14  
US-08-466-151-65  
; Sequence 65, Application US/08466151  
; Patent No. 6037453  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,151  
; FILING DATE:  
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39, 044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-65

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Query Match      84.5%; Score 2127; DB 3; Length 451;
Best Local Similarity 87.8%; Pred. No. 7.4e-151;
Matches 397; Conservative 23; Mismatches 30; Indels 2; Gaps 2;

Qy  20 OVQLVQSGAEVKKPGASVKASKGTYFTTS-YMQWVVRQAPGQGLEWMGEIDPSDSYTN 78
Db  1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSCYSNNWIRQAPGKLEWVASI-TYDGSN 59

Qy  79 YNQKFKGKATLTVDSTSTAYMELSSLRSEDTAVYYCARNRDYNNWYFDVWGQGLTVTV 138
Db  60 YNPVKGRITISRDSDSKNTFYLMNSLRSEDVAVYYCARGSHYFGHWFAVWGQGLTVTV 119

Qy  139 SSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLIQ 198
Db  120 SSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLIQ 179

Qy  199 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKRVKPKSCDKHTHTCCPCPAPELL 258
Db  180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKRVKPKSCDKHTHTCCPCPAPELL 239

Qy  259 GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 318
Db  240 GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 299

Qy  319 YNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 378
Db  300 YNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 359

Qy  379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS 438
Db  360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS 419

Qy  439 RWOQGNVFSCSYMHHEALHNHYTQKSLSLSPGK 470
Db  420 RWOQGNVFSCSYMHHEALHNHYTQKSLSLSPGK 451

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```

RESULT 15
US-09-109-207C-14
; Sequence 14, Application us/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide

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; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAEL1
US-09-109-207C-14

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Query Match      84.5%; Score 2127; DB 4; Length 451;
Best Local Similarity 87.8%; Pred. No. 7.4e-151;
Matches 397; Conservative 23; Mismatches 30; Indels 2; Gaps 2;

Qy  20 OVQLVQSGAEVKKPGASVKASKGTYFTTS-YMQWVVRQAPGQGLEWMGEIDPSDSYTN 78
Db  1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSCYSNNWIRQAPGKLEWVASI-TYDGSN 59

Qy  79 YNQKFKGKATLTVDSTSTAYMELSSLRSEDTAVYYCARNRDYNNWYFDVWGQGLTVTV 138
Db  60 YNPVKGRITISRDSDSKNTFYLMNSLRSEDVAVYYCARGSHYFGHWFAVWGQGLTVTV 119

Qy  139 SSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLIQ 198
Db  120 SSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLIQ 179

Qy  199 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKRVKPKSCDKHTHTCCPCPAPELL 258
Db  180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKRVKPKSCDKHTHTCCPCPAPELL 239

Qy  259 GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 318
Db  240 GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 299

Qy  319 YNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 378
Db  300 YNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 359

Qy  379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS 438
Db  360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS 419

Qy  439 RWOQGNVFSCSYMHHEALHNHYTQKSLSLSPGK 470
Db  420 RWOQGNVFSCSYMHHEALHNHYTQKSLSLSPGK 451

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Search completed: August 14, 2002, 15:17:08  
Job time: 691 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 15:19:01 ; Search time 108.64 Seconds  
(without alignments)  
415.703 Million cell updates/sec

Title: US-09-499-662-147  
Perfect score: 2517  
Sequence: 1 MGWSCIIILFLVATATGVHSQ.....MHEALHNHYTKQSLSLSPCK 470

Scoring table:  
BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues  
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR.71.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1758	69.8	330	1 GHU	Ig gamma-1 chain C
2	1639.5	65.1	377	2 A23511	Ig gamma-3 chain C
3	1637.5	65.1	377	2 A60764	Ig gamma-3 chain C
4	1610.5	64.0	469	2 S37483	Ig gamma-2a chain
5	1610	64.0	326	1 G2HU	Ig gamma-2 chain C
6	1599.5	63.5	327	1 G4HU	Ig gamma-4 chain C
7	1546	61.4	474	1 G2MS11	Ig gamma-2b chain
8	1544	61.3	446	2 S40295	Ig gamma-2a chain
9	1501.5	59.7	475	2 S01321	Ig gamma-2b chain
10	1477	58.7	470	2 S22080	Ig heavy chain pre
11	1470	58.4	472	2 S31459	Ig gamma-1 chain -
12	1435	57.0	374	2 S69339	Ig heavy chain v r
13	1429.5	56.8	444	2 PC4436	monoclonal antibod
14	1267	50.3	328	2 I47159	Ig gamma 2a chain
15	1261	50.1	328	2 I47160	Ig gamma 2b chain
16	1253	49.8	255	4 S31866	Ig gamma-1 chain C
17	1245	49.5	234	2 PT0207	Ig gamma chain C r
18	1235	49.1	328	2 I47158	Ig gamma 1 chain C
19	1231.5	48.9	323	1 GHRB	Ig gamma chain C r
20	1231	48.9	328	2 I47161	Ig gamma-3 chain C
21	1210.5	48.1	329	1 G2GP	Ig gamma-2 chain C
22	1165.5	46.3	308	2 C30554	Ig heavy chain C r
23	1157	46.0	289	1 G3HUI	Ig gamma-3 heavy c
24	1155	45.9	326	2 PS0017	Ig gamma-1 chain C
25	1150	45.7	329	1 G3MSC	Ig gamma-3 chain C
26	1145	45.5	324	1 G1MS	Ig gamma-1 chain C
27	1144.5	45.5	333	2 PS0018	Ig gamma-2b chain
28	1140	45.3	333	1 G1MSM	Ig gamma-1 chain C
29	1139	45.3	398	1 G3MSM	Ig gamma-3 chain C

RESULT 1  
GHU

Ig gamma-1 chain C region - human  
C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence\_revision 18-Aug-1982 #text\_change 16-Jul-1999  
C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146  
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.  
Nucleic Acids Res. 10, 4071-4079, 1982  
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.  
A:Reference number: A93433; MUID:82274238  
A:Accession: A93433  
A:Molecule type: DNA  
A:Residues: 1-330 <ELL>  
A:Cross-references: EMBL:Z17370  
A:Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) marker  
A:Note: Lys-330 is removed after translation  
R:Harris, L.J.  
submitted to the EMBL Data Library, October 1992

ALIGNMENTS

30 1129 44.9 330 1 G2MSA  
31 1127.5 44.8 329 2 S00847  
32 1126.5 44.8 335 1 G2MSAB  
33 1124 44.7 399 1 G2MSAM  
34 1115 44.3 322 2 PS0019  
35 1093.5 43.4 327 2 S06611  
36 1080 42.9 405 1 G2MSBM  
37 1070 42.5 277 2 I47162  
38 999 39.7 548 2 S38864  
39 946 37.6 627 2 S14683  
40 925.5 36.8 549 2 S04845  
41 870.5 34.6 241 2 S69131  
42 851 33.8 246 2 S38950  
43 801 31.8 220 2 A49444  
44 765.5 30.4 249 2 S69340  
45 762.5 30.3 572 2 B46529  
Ig gamma-2a chain  
Ig gamma-2c chain  
Ig gamma-2a chain  
Ig gamma-2a chain  
Ig gamma-2a chain  
Ig gamma-2 chain C  
Ig gamma-2b chain C  
Ig gamma 4 chain c  
Ig epsilon chain c  
Ig mu chain precu  
Ig heavy chain pre  
Ig heavy chain (DO  
Ig gamma chain - m  
Ig gamma-1 heavy c  
Ig heavy chain VHI  
Ig Y heavy chain (

Ig gamma-1 chain C  
R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.  
Cell 29, 671-679, 1982  
A:Title: Structure of human immunoglobulin gamma genes: Implications for evolution of  
A:Reference number: S33887; MUID:83001943  
A:Accession: S33887  
A:Molecule type: DNA  
A:Residues: 2-330 <HAR>  
A:Cross-references: EMBL:Z17370  
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman  
Biochemistry 9, 3161-3170, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq  
A:Reference number: A90563; MUID:71064024  
A:Contents: myeloma protein Eu  
A:Accession: B90563  
A:Molecule type: protein  
A:Residues: 1-96, 'R', 98-135 <CUN>  
A:Note: this sequence has the G1m(3) marker, 97-Arg  
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.  
Biochemistry 9, 3171-3181, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se  
A:Reference number: A90564; MUID:71064025  
A:Contents: Eu  
A:Accession: A90564  
A:Molecule type: protein  
A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 2  
A:Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met  
R:Ponstingl, H.; Hilschmann, N.  
Hoppe-Seyler's z. Physiol. Chem. 357, 1571-1604, 1976  
A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein N1

igen Primaerstruktur.  
A:Reference number: A91668; MUID:77070269  
A:Contents: myeloma protein Nie  
A:Accession: B91668  
A:Molecule type: protein  
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27  
A:Note: this sequence has the Gln(17) and Gln(1) markers  
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
A:Title: Die Primaerstruktur des kristallinsierbaren monoklonalen Immunglobulins IgG1 KOI  
A:Reference number: A91723; MUID:83289131  
A:Contents: myeloma protein KOI; disulfide bonds  
A:Accession: A91723  
A:Molecule type: protein  
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH  
A:Note: this sequence has the Gln(3) and Gln(non-1) markers  
R:Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid  
A:Reference number: A90565; MUID:71064027  
A:Contents: annotation; disulfide bonds  
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976  
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob  
enbromide cleavage products, and the disulfide bridges.  
A:Reference number: A91667; MUID:77070267  
A:Contents: annotation; disulfide bonds  
C:Genetics:  
A:Gene: GDB:IGHG1  
A:Cross-references: GDB:120085; OMIM:147100  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1; 114/1; 224/1  
A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:137-310/Domain: immunoglobulin homology <IM2>  
F:243-310/Domain: immunoglobulin homology <IM3>  
F:27-83, 144-204, 250-308/Disulfide bonds: #status experimental  
F:103/Disulfide bonds: interchain (to light chain) #status experimental  
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 69.8%; Score 1758; DB 1; Length 330;  
Best Local Similarity 99.1%; Pred. No. 3.3e-93;  
Matches 327; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 141 ASTKGPSVEPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSNWSGALTSGVHTFPAVLQSS 200  
Db 1 ASTKGPSVEPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSNWSGALTSGVHTFPAVLQSS 60

QY 201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVK 260  
Db 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVK 120

QY 261 PSVFLPPPKPDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN 320  
Db 121 PSVFLPPPKPDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN 180

QY 321 STYRVSVLTIVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 380  
Db 181 STYRVSVLTIVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

QY 381 WTKNQVSLTCLVKGYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 440  
Db 241 LTKNQVSLTCLVKGYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300

QY 441 QCGNVFSCSVMHAEALHNHYTQKSLSLSPGK 470  
Db 301 QCGNVFSCSVMHAEALHNHYTQKSLSLSPGK 330

Query Match 65.1%; Score 1639.5; DB 2; Length 377;  
Best Local Similarity 82.8%; Pred. No. 2.1e-86;  
Matches 312; Conservative 7; Mismatches 11; Indels 47; Gaps 1;

QY 141 ASTKGPSVEPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSNWSGALTSGVHTFPAVLQSS 200  
Db 1 ASTKGPSVEPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSNWSGALTSGVHTFPAVLQSS 60

QY 201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVK 238  
Db 61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVK 120

QY 239 -----EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKPKDT 273  
Db 121 DTPPCPCPCPEPKSCDTPPPCPCPEPKSCDTPPPCPCPEPKSCDTPPPCPCPEPKPKDT 180

QY 274 LMSRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYNSTYRVSVLTIVLH 333  
Db 181 LMSRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYNSTYRVSVLTIVLH 240

QY 334 QDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVK 393  
Db 241 QDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVK 300

QY 394 GFPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSSVMHE 453  
Db 301 GFPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSSVMHE 360

QY 454 ALHNHYTQKSLSLSPGK 470  
Db 361 ALHNHYTQKSLSLSPGK 377

RESULT 3  
A0764  
Ig gamma-3 chain C region, form LAT - human  
C:Species: Homo sapiens (man)  
C:Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 16-Jul-1999  
R:Huck, S.; Lefranc, G.; Lefranc, M.P.  
Immunogenetics 30, 250-257, 1989  
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 con  
A:Reference number: A60764; MUID:90007613  
A:Accession: A60764  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-377 <HUC>  
C:Superfamily: immunoglobulin C region; immunoglobulin homology

RESULT 2  
A23511  
Ig gamma-3 chain C region (allotype G3m(b)) - human  
C:Species: Homo sapiens (man)  
C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 23-Jul-1999  
C:Accession: A23511  
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.  
Nucleic Acids Res. 14, 1779-1789, 1986  
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene  
A:Reference number: A23511; MUID:86148507  
A:Accession: A23511  
A:Molecule type: DNA  
A:Residues: 1-377 <HUC>  
A:Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056  
C:Genetics:  
A:Gene: GDB:IGHG3  
A:Cross-references: GDB:119339; OMIM:147120  
A:Map position: 14q32.33-14q32.33  
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IMM>

**C; Keywords:** immunoglobulin

F; 20-85/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 65.1%; Score 1637.5; DB 2; Length 377;  
Best Local Similarity 82.8%; Pred. No. 2.8e-86;  
Matches 312; Conservative 7; Mismatches 11; Indels 47; Gaps 1;

QY 14:1 ASTKGPSVFPLAPSSKSTSCGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLSS 200

Db 1 ASTKPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVITFPAVLQSS 60

QY 201 GLYSLSSVTVPSSSLGTOTYICNVNHKPSNTKVDPKRV----- 238

Db 61 GLYSLSVTVVSSSLGTQTYTCNVNKKPSNTKVDKRVLEKLTPLGDTHTTCPRCPKSC 120

QY 239 -----EPKSCDKTHTCPPCPAPELGGPSVFLFPPKPKDT 273

Db 121 DTppPCRCPEPKSCDTPPPCPRCPBKSCDTPPPCPRCPAPELLGGPSVLEFPFKPKDT 180

QY 274 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVHL 333

181 LMISRPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTPREEQINSTRFVVSVLTVLH 240

QY 334 QDWLNGKEYKCKVSNKALPAPIEKTISAKGPREPQVYTLPPSREEMTKNOVSLTCLVK 393

Db 241 QDWLNGKEYKCKVSNKALPAPIEKTISKTKGPREPQVYTLPPSREEMTKNQVSLTCLVK 300

QY 394 GFYPSDIAVEWESNGQPENNYKTTTPVPLDSDGSEFFLYSKLTVDKSRWQQGNVFSCSVMHE 453

Db 301 GFYPDIAVESSGQPENNYNTTPVLDSDGSFFLYSKLTVDKSRWQEGNVFSCSYMHE 360

QY 454 ALHNHYTOKSLSLSPGK 470

7

## RESULT 4

S37483

Ig gamma-2a chain - mouse

C; Species: *Mus musculus* (house mouse)

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999

C; Accession: S37483  
R: Divanool F F D

R; Ducancel, F.F.D. submitted to the E

A: Reference number: S37483

A;Accession: S37483

A; Status: preliminary

**A; Molecule type: mRNA**

A; Residues: 1-469 &lt;DUC

A; Cross-references: EMBL  
C. Guirfami; Immunology

C;superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin

F;276-345/Domain: immunoglobulin homolog <IMM>

### 3.2.2.2. *Phylogenetic analysis*

Query Match 64.0%; Score 1610.5; DB 2; Length 469;  
Best Local Similarity 64.4%; Pred. No. 1.2e-84;  
Matches 304; Conservative 60; Mismatches 103; Indels 5; Gaps 4;

QY 1 MGWSCIIILFLVATATGVHSQVLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVROAP 60

1 MGWSWIFLFLLLSTAGVHCOIQLOQSGPELVKPGASVKLSCKASGYTFETDYINWVKQK 60

QY 61 GQGLEWNGEIDPSDSYNTNNQKFKGKATLTVDTSTSTAYMELSSLRSEDVAVYCARNRD 120

```

Db
61 GQGLKWIGWIYPASGNTKYNNFKGATLVTSSSTAYMQLSSLTSEDATVFCARAMG 120

```

QY 121 YSNWYFDWGQGTLTVTSSASTKGPSVFPLPSSKSTSGGTAALGCLVKDYFPEPTVS 180

```
Db 121 -ATATLLDYGQGTTLTVSSAKTTAFSVYPLAPVCGDTTGSSVTGLCLVKGYFPEPVLT 179
```

Q7 191 WNSCATESCUTTERAW CCCCC VCT CCNWTWDCSCY CCEMYTCNNINIKDCNTWKVCKEVEDR 240

Nature 221, 145-148, 1969  
A:Title: Structural studies of immunoglobulin G.  
A:Reference number: A93157; MUID:69064124  
A:Contents: annotation; Sa, disulfide bonds  
C:Genetics:  
A:Gene: IGHG2

A:Cross-references: GDB:119338; OMIM:147110  
A:Map position: 14q32.33-14q32.33  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) and two identical heavy (lambda) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:133-202/Domain: immunoglobulin homology <IM2>  
F:239-306/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83,140-200,246-304/Disulfide bonds: #status experimental  
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 64.0%; Score 1610; DB 1; Length 326;  
Best Local Similarity 91.8%; Pred. No. 8.6e-85;  
Matches 303; Conservative 10; Mismatches 13; Indels 4; Gaps 2;

QY 141 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPVQLQSS 200  
DB 1 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPVQLQSS 60  
QY 201 GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNKVDKRRPEKSCDKTHTCPPCPAPPELLGG 260  
DB 61 GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNKVDKRRPEKSCDKTHTCPPCPAPPELLGG 116  
QY 261 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVFNHAKTKPREEQN 320  
DB 117 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVFNHAKTKPREEQN 176  
QY 321 STYRVVSVLTVLHODWLNKCKYKCKVSNKALPAPIETKISKAKQPREPOVYTLPPSREE 380  
DB 177 STYRVVSVLTVLHODWLNKCKYKCKVSNKALPAPIETKISKAKQPREPOVYTLPPSREE 236  
QY 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKTVDKSRW 440  
DB 237 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKTVDKSRW 296  
QY 441 QGQNVFSCSVMHENHNTQKSLSPGK 470  
DB 297 QGQNVFSCSVMHENHNTQKSLSPGK 326

RESULT 6  
G4HU  
Ig gamma-4 chain C region - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 16-Jul-1999  
C:Accession: A90933; A90249; A02150  
R:Ellison, J.; Buxbaum, J.; Hood, L.  
DNA 1, 11-18, 1981  
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.  
A:Reference number: A90933; MUID:83157104  
A:Accession: A90933  
A:Molecule type: DNA  
A:Residues: 1-327 <ELL>  
A>Note: the sequence was determined from the germline gene  
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.  
Biochem. J. 117, 33-47, 1970  
A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant region of the heavy chain of human gamma2b chain gene cloned from a human myeloma cell line.  
A:Reference number: A90249; MUID:70207560  
A:Accession: A90249  
A:Molecule type: protein  
A:Residues: 1-30; 81-326 <PIN>  
C:Genetics:  
A:Gene: IGHG4

A:Cross-references: GDB:119340; OMIM:147130  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1; 111/1; 221/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) and two identical heavy (lambda) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:99-110/Region: hinge  
F:134-203/Domain: immunoglobulin homology <IM2>  
F:240-307/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83,141-201,247-305/Disulfide bonds: #status predicted  
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 63.5%; Score 1599.5; DB 1; Length 327;  
Best Local Similarity 91.8%; Pred. No. 3.4e-84;  
Matches 303; Conservative 9; Mismatches 15; Indels 3; Gaps 1;

QY 141 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPVQLQSS 200  
DB 1 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPVQLQSS 60  
QY 201 GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNKVDKRRPEKSCDKTHTCPPCPAPPELLGG 260  
DB 61 GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNKVDKRRPEKSCDKTHTCPPCPAPPELLGG 117  
QY 261 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVFNHAKTKPREEQN 320  
DB 118 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVFNHAKTKPREEQN 177  
QY 321 STYRVVSVLTVLHODWLNKCKYKCKVSNKALPAPIETKISKAKQPREPOVYTLPPSREE 380  
DB 178 STYRVVSVLTVLHODWLNKCKYKCKVSNKALPAPIETKISKAKQPREPOVYTLPPSREE 237  
QY 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKTVDKSRW 440  
DB 238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKTVDKSRW 297  
QY 441 QGQNVFSCSVMHENHNTQKSLSPGK 470  
DB 298 QGQNVFSCSVMHENHNTQKSLSPGK 327

RESULT 7  
G2MS11  
Ig gamma-2b chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Mar-1980 #sequence\_revision 01-Dec-2000 #text\_change 01-Dec-2000  
C:Accession: S25057; A02157; A26235; A26233; A53598  
R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.  
submitted to the EMBL Data Library, July 1992  
A:Description: Production of a tobacco mosaic virus (TMV) inactivating neotop specific  
A:Reference number: S25057  
A:Accession: S25057  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-474 <FIS>  
A:Cross-references: EMBL:X67210; NID:954826; PIDN:CAA47649.1; PID:954827  
R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.  
Nature 283, 786-789, 1980  
A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from a mouse myeloma cell line.  
A:Reference number: A02157; MUID:80120716  
A:Accession: A02157  
A:Molecule type: DNA  
A:Residues: 138-161, 'L', 163-189, 'Fp', 193-474 <YAM>  
A:Cross-references: GB:J00461  
A>Note: the sequence was determined from the germline gene  
R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.  
Science 206, 1299-1303, 1979



A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b heavy chain  
A:Reference number: A26235; MUID:80081501  
A:Contents: MPC 11  
A:Accession: A26235  
A:Molecule type: mRNA  
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU1>  
A:Note: Lys-474 is probably removed posttranslationally  
R:Trucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.  
Science 206, 1303-1306, 1979  
A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglobulin heavy chain  
A:Reference number: A26232; MUID:80081502  
A:Accession: A26232  
A:Molecule type: DNA  
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU2>  
R:Ollo, R.; Rougeon, F.  
Nature 296, 761-763, 1982  
A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma2b heavy chain genes  
A:Reference number: A26233; MUID:82173203  
A:Contents: b allele  
A:Accession: A26233  
A:Molecule type: DNA  
A:Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLL>  
A:Cross-references: GB:J00461  
R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi, J.  
J. Biol. Chem. 269, 12345-12350, 1994  
A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.  
A:Reference number: A53598; MUID:94216359  
A:Accession: A53598  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 234-251 <KIM>  
C:Comment: The a allele sequence is shown.  
C:Genetics:  
A:Introns: 138/1; 236/1; 258/1; 368/1  
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:157-222/Domain: immunoglobulin C region; immunoglobulin homology  
F:157-222/Domain: immunoglobulin C region; immunoglobulin homology  
F:281-350/Domain: immunoglobulin C region; immunoglobulin homology  
F:281-350/Domain: immunoglobulin C region; immunoglobulin homology  
F:152/Disulfide bonds: interchain (to light chain) #status predicted  
F:164-220,288-348,394-452/Disulfide bonds: #status predicted  
F:247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted  
F:324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 61.48; Score 1546; DB 1; Length 474;  
Best Local Similarity 61.29; Pred. No. 5.8e-81;  
Matches 292; Conservative 67; Mismatches 108; Indels 10; Gaps 3;

Qy 1 MGWSCIILFLVATATGTVHSGVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVRQAP 60  
Db 1 MENSWIFLLSLGAGVHSEVQLQSGPELVNPGASVKMSCKASGYTFTSYMMHWKQKP 60

Qy 61 QGGLWEMGEIDPSYTNYNOKFGKATLVDTSTAYMELSLRSEDATVYYCARNRD 120  
Db 61 QGGLWIGIYNPNKDGTKFNEKFKGKATLVDSKSNATYMEELSLTSDSAVYICARDYD 120

Qy 121 YSNWYFDVWQGLTLVTVSSASTKGPVPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180  
Db 121 YD---WFAYWYOGGLTVTVSSAATTPPSYIPLAPGDDTGTSSVTSGLVKGYFPESVNT 177

Qy 181 WNSGALTSVHTFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNNHKPSNTKVDKRVPE 240  
Db 178 WNSGSLSSVHTLSQLQSSGLYTMSSSVTPSSVWPSQTWCSVAHPASSTTVDDKLEP 237

Qy 241 KSCDKT-HTCPP-----CPAPELLGSPSVFLPPPKPDKTLMISRTPEVTVCVVDVSHED 293  
Db 238 SGPISTINPCPKCKECHKCAPNLEGGPSVFIFPNKIDVLMISITPKYTCVVDVSDDD 297

Qy 294 PEVFNWTVDGVVHNAKTKPREQYNSTYRKVSVLTVLHODWLNKGKEYCKVSNKALPA 353

Db 298 PDVQISWFWNNVEVHTAQOTQTHREDYNTIRVVSFLPIQHDQWMSGKFKCVNNKDLPS 357  
Qy 354 PIEKTISKAGOPREPQVYITLPPSREEMTKNOVSLTCLVGFYPSDIAVEMSGNQEPNN 413  
Db 358 PIERTISKIKGLVRAPQVYITLPPPAEQLSRKDVSLTCLVGFNPGDISVETWSNGHTEEN 417  
Qy 414 YKTPPVLDSDGSFLLYSKLTVDKSRWQGVNFGSCVMHEALHNNHYTKSLSPGK 470  
Db 418 YKDTAPVLDSDGSFYISKLNKTKWEKTDSESCNVRHGLKNYLLKTKTISRSPGK 474

RESULT 8  
S40295  
Ig gamma-2a chain (mAb735) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 16-Jul-1999  
C:Accession: S40295  
R:Kiebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; submitted to the EMBL Data Library, January 1993  
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 agl.in  
A:Reference number: S40295  
A:Accession: S40295  
A:Molecule type: protein  
A:Residues: 1-446 <KLE>  
C:Genetics:  
A:Map position: 12  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglyutamic acid  
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>  
F:1-117/Domain: V-D-J region <VDJ>  
F:118-446/Domain: C region <CHR>  
F:118-214/Domain: C1 region <CH1>  
F:215-230/Region: hinge  
F:231-340/Domain: C2 region <CH2>  
F:341-446/Domain: C3 region <CH3>  
F:360-427/Domain: immunoglobulin homology <IMM>  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted  
F:132/Disulfide bonds: interchain (to light chain) #status predicted  
F:224,227,229/Disulfide bonds: interchain #status predicted  
F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 61.38; Score 1544; DB 2; Length 446;  
Best Local Similarity 64.4%; Pred. No. 7e-81;  
Matches 291; Conservative 59; Mismatches 94; Indels 8; Gaps 4;

Qy 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVRQAPGQGLEWMGEIDPSDSYTN 79  
Db 1 QIQLQQSGPELVNPGASVKISCKASGYTFTDYIHWVKQRPGEGLWIGIYVPGSGNTKY 60

Qy 80 NOKFKGKATLVDTSTAYMELSLRSEDATVYYCARNRDYNNWYFDVWQGLTVTVS 139  
Db 61 NEKTAGKATLVDTSSSTAYMQLSSTSDSAVYFCARGKFA---MDYWGQGSYTVS 116

Qy 140 SASKTGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSVHTFPAVLQS 199  
Db 117 SAKTAPSVYPLAPVCGDGTGSSVTLGCLVKGYPPEPTVLTWNSGSLSSGVHTFPAVLQS 176

Qy 200 SGLYSLSVTVTPSSSLGTQTYICNNHKPSNTKVDKRVKPEKCDKTHTCPP--CPAPEL 257  
Db 177 D-LYTLSSSVTVTSSTWPSQSITCNVAHPASSTVDDKKEIPRG-PTIKPCPPCKCAPNL 234

Qy 258 LGGSPVFLFPKPKDKTLMISRTPEVTVCVVDVSHEDPEVKFNWYDGVVHNAKTKPRE 317  
Db 235 LGGSPVFIIPKIKIDVLMISLSPMVTVCVVDVSDDDPDQISFWNNVEVLTQAQTTHRE 294

Qy 318 QYNSTIRVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTIKAKGPRPQVYITLPPS 377  
Db 295 DYNSTIRVSVLTVLHODWLNKGKEYCKVSNKALPAPIERTISKPGSVRAQVYVLP 354

Qy 378 REEMTKNOVSLTCLVKGYPVSDIAVEMSGNQEPNNYKTPPVLDSDSGSFFLYSKLTVDK 437



A; Cross-references: EMBL:X81695  
C; Superfamily: immunoglobulin C region; immunoglobulin homology

QY 136 VTSSASTKGPVSFFPLAPSSKSTSGGTAALGCLVRDYFPEPYVSNWNSGALTSGVHTFPA 19

QY 196 VLOSSGLYSSVVVTPSSSLGTQTYICNVNHPKNTKVDKRVKPCSDKTHTCPP--CP 253  
Db 176 VLOSD-LYTLSSVTPSSWPSTTCNVNHPASSKVDKIVPRDCG---CKPCICT 230  
QY 254 APELLGGPSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 313  
Db 231 VPEV---SSVFIPEPKPKDVLTLTPKVKVVDVSKDDPEVQFWSFVDDVEVHTAQTQ 287  
QY 314 PREEQNSTYRVSVLTVLHQDLNKGKCKVSNKALPAPIEKTIISKAKGQPREPOVYT 373  
Db 288 PREEQNSTYRVSELPIMHQDLNKGKCKVSNKALPAPIEKTIISKAKGQPREPOVYT 347  
QY 374 LPRESREMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 433  
Db 348 IPPPKQEMAKDKVSLTCMIIDFPEPITVEWQWNGQPAENYKNTQPIMDTDGSEFYVSKL 407  
QY 434 TVDKSRMQGNVFSVCSVMHEALHNHYTQKSLSLSPGK 470  
Db 408 NVQKSNWEAGNTFTCSVLHLEGLHNHTKSLSPGK 444  
RESULT 14  
I47159  
Ig gamma 2a chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47159  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A:Reference number: I47158; MUID:95015845  
A:Accession: I47159  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <AC>  
C:Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124  
C:Superfamily: Immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IMM>  
Query Match 50.3%; Score 1267; DB 2; Length 328;  
Best Local Similarity 69.9%; Pred. No. 2.9e-65;  
Matches 232; Conservative 42; Mismatches 52; Indels 6; Gaps 2;  
QY 141 ASTKGPSVPLAPSSKSTSGTAAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPVAVLQSS 200  
Db 1 APTAPSVIPLAPCSRDTSGPNVALGLASSYFPEPTVTWNSGALTSGVHTFPVAVLQSS 60  
QY 201 GLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKRVKPCSDKTHTCPPCAPPELLGG 260  
Db 61 GLYSLSSMTVTPASSLSKSYTCNVNHPATTTKVDKRVGTRKTPPCPICPACESP---G 116  
QY 261 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320  
Db 117 PSVFIPEPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHTAQTREPKKEQFN 176  
QY 321 STYRVSVLTVLHQDLNKGKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPSREE 380  
Db 177 STYRVSVLPIQHDLNKGKCKVSNKALPAPIETRIISKAKGQTRPEQVYTLPPHAAE 236  
QY 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTTPPVLDSDGSFFLYSKLTVDKS 438  
Db 237 LRSKSVSIITCLVIGFYPPDDIDVEWQNGQPEPEGNRYRTTPQDDVDGTYFLYSKFSVDKA 296  
QY 439 RWQOGNVFSCVSMHEALHNHYTQKSLSLSPGK 470  
Db 297 SWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328

RESULT 15  
I47160

Ig gamma 2b chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47160  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of  
A:Reference number: I47158; MUID:95015845  
A:Accession: I47160  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <AC>  
C:Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126  
C:Genetics:  
C:Superfamily: Immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IMM>  
Query Match 50.1%; Score 1261; DB 2; Length 328;  
Best Local Similarity 69.6%; Pred. No. 6.4e-65;  
Matches 231; Conservative 41; Mismatches 54; Indels 6; Gaps 2;  
QY 141 ASTKGPSVPLAPSSKSTSGTAAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPVAVLQSS 200  
Db 1 APTAPSVIPLAPCSRDTSGPNVALGLASSYFPEPTVTWNSGALTSGVHTFPVAVLQSS 60  
QY 201 GLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKRVKPCSDKTHTCPPCAPPELLGG 260  
Db 61 GLYSLSSMTVTPASSLSKSYTCNVNHPATTTKVDKRVGTRKTPPCPICPACESP---G 116  
QY 261 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320  
Db 117 PSVFIPEPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHTAQTREPKKEQFN 176  
QY 321 STYRVSVLTVLHQDLNKGKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPSREE 380  
Db 177 STYRVSVLPIQHDLNKGKCKVSNKALPAPIETRIISKAKGQTRPEQVYTLPPHAAE 236  
QY 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTTPPVLDSDGSFFLYSKLTVDKS 438  
Db 237 LRSKSVSIITCLVIGFYPPDDIDVEWQNGQPEPEGNRYRTTPQDDVDGTYFLYSKFSVDKA 296  
QY 439 RWQOGNVFSCVSMHEALHNHYTQKSLSLSPGK 470  
Db 297 SWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328

Search completed: August 14, 2002, 15:19:02  
Job time: 690 sec



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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:23:15 ; Search time 53.64 Seconds  
(without alignments)  
339.265 Million cell updates/sec

Title: US-09-499-662-147

Perfect score: 2517

Sequence: 1 MGWSCIILFVATATGVHSQ.....MHEALHHYTKSLSPGK 470

Scoring table:  
BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1758	69.8	330	1	GC1_HUMAN
2	1610	64.0	326	1	GC2_HUMAN
3	1599.5	63.5	327	1	GC4_HUMAN
4	1231.5	48.9	323	1	GC_RABIT
5	1210.5	48.1	329	1	GC2_CAVPO
6	1162	46.2	290	1	GC3_HUMAN
7	1155	45.9	326	1	GC1_RAT
8	1150	45.7	329	1	GC3_MOUSE
9	1145	45.5	324	1	GC1_MOUSE
10	1144.5	45.5	333	1	GC1_MOUSE
11	1140	45.3	393	1	GC1_MOUSE
12	1139	45.3	398	1	GC3_MOUSE
13	1129	44.9	330	1	GC2_MOUSE
14	1127.5	44.8	329	1	GC2_MOUSE
15	1126.5	44.8	335	1	GC2_MOUSE
16	1124	44.7	399	1	GC2_MOUSE
17	1115	44.3	322	1	GC2_MOUSE
18	1085	43.1	336	1	GC2_MOUSE
19	1080	42.9	405	1	GC2_MOUSE
20	559.5	22.2	139	1	GC2_MOUSE
21	525	20.9	117	1	GC2_MOUSE
22	524.5	20.8	137	1	GC2_MOUSE
23	521	20.7	138	1	GC2_MOUSE
24	513	20.4	117	1	GC2_MOUSE
25	507	20.1	140	1	GC2_MOUSE
26	501	19.9	117	1	GC2_MOUSE
27	488	19.4	117	1	GC2_MOUSE
28	486.5	19.3	429	1	GC2_MOUSE
29	486	19.3	428	1	GC2_MOUSE
30	485	19.3	117	1	GC2_MOUSE
31	480	19.1	117	1	GC2_MOUSE
32	479	19.0	117	1	GC2_MOUSE
33	479	19.0	136	1	GC2_MOUSE

RESULT	1	GC1_HUMAN	STANDARD;	PRT;	330 AA.
AC	P01857;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Ig gamma-1 chain C region.				
GN	IGHG1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=82274238; PubMed=6287432;				
RA	Edelson J.W., Berson B.J., Hood L.E.;				
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene."				
RL	Nucleic Acids Res. 10:4071-4079(1982).				
RN	[2]				
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).				
RX	MEDLINE=71064024; PubMed=5489771;				
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,				
RT	Waxdal M.J., Edelman G.M.;				
RL	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."				
RN	[3]				
RP	SEQUENCE OF 136-329 (EU).				
RX	MEDLINE=71064025; PubMed=5530842;				
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,				
RT	Edelman G.M.;				
RL	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."				
RN	[4]				
RP	SEQUENCE (MYELOMA PROTEIN NIE).				
RX	MEDLINE=77070269; PubMed=826475;				
RA	Ponstingl H., Hilschmann N.;				
RT	"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."				
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).				
RN	[5]				
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.				
RX	MEDLINE=83289131; PubMed=6884994;				
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;				
RT	"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."				
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).				
RN	[6]				
RP	DISULFIDE BONDS.				
RX	MEDLINE=71064027; PubMed=4923144;				
RA	Gall W.E., Edelman G.M.;				
RT	"The covalent structure of a human gamma G-immunoglobulin. X.				

P06336 mus musculus  
P01743 homo sapien  
P06329 mus musculus  
P01756 mus musculus  
P01757 mus musculus  
P01744 homo sapien  
P01747 mus musculus  
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P01871 homo sapien  
P03988 oryctolagus  
P01745 mus musculus  
P01873 mus musculus





OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE OF 2-326 FROM N.A.  
RX MEDLINE=82197621; PubMed=6804948;  
RA Ellison J.W., Hood L.E.;  
RT "Linkage and sequence homology of two human immunoglobulin gamma  
heavy chain constant region genes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).  
RN [2]  
RP SEQUENCE OF 88-115 FROM N.A.  
RX TISSUE=Fetal liver;  
RC MEDLINE=83001943; PubMed=6811139;  
RA Takahashi N., Ueda S., Ohta M., Nikaido T., Nakai S., Honjo T.;  
RT "Structure of human immunoglobulin gamma genes: implications for  
evolution of a gene family.";  
RL Cell 29:671-679(1982).  
RN [3]  
RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.  
RX TISSUE=Fetal liver;  
RC MEDLINE=84235992; PubMed=6329676;  
RA Krawinkel U., Rabbitts T.H.;  
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma  
heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass  
genes.";  
RL EMBO J. 1:403-407(1982).  
RN [4]  
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).  
RX MEDLINE=81007873; PubMed=6774012;  
RA Wang A.-C., Tung E., Fudenberg H.H.;  
RT "The primary structure of a human IgG2 heavy chain: genetic,  
evolutionary, and functional implications.";  
RL J. Immunol. 125:1048-1054(1980).  
RN [5]  
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).  
RX MEDLINE=80001357; PubMed=113060;  
RA Connell G.E., Parr D.M., Hofmann T.;  
RT "The amino acid sequences of the three heavy chain constant region  
domains of a human IgG2 myeloma protein.";  
RL Can. J. Biochem. 57:758-767(1979).  
RN [6]  
RP SEQUENCE OF 238-275 (ZIE).  
RX MEDLINE=80114419; PubMed=118920;  
RA Hofmann T., Parr D.M.;  
RT "A note of the amino acid sequence of residues 381-391 of human  
immunoglobulins gamma chains.";  
RL Mol. Immunol. 16:923-925(1979).  
RN [7]  
RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).  
RA Hofmann T., Parr D.M.;  
RL Submitted (MAR-1980) to the PIR data bank.  
RN [8]  
RP SEQUENCE OF 1-121 (DOT).  
RX MEDLINE=95255298; PubMed=7737190;  
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;  
RT "Characterization of the two unique human anti-flavin monoclonal  
immunoglobulins.";  
RL Eur. J. Biochem. 228:886-893(1995).  
RN [9]  
RP DISULFIDE BONDS.  
RX MEDLINE=72033500; PubMed=4940472;  
RA Milstein C., Frangione B.;  
RT "Disulfide bridges of the heavy chain of human immunoglobulin G2.";  
RL Biochem. J. 121:217-225(1971).  
RN [10]  
RP DISULFIDE BONDS.  
RX MEDLINE=69064124; PubMed=5782707;  
RA Frangione B., Milstein C., Pink J.R.L.;  
RT "Structural studies of immunoglobulin G.";  
RL Nature 221:145-148(1969).  
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CC EMBL; J00230; AAB59393.1; -.  
CC PIR; A02148; G2HU.  
CC HSSP; P01857; 1FC1.  
CC -----  
DR EMBL; J00230; AAB59393.1; -.  
DR PIR; A02148; G2HU.  
DR HSSP; P01857; 1FC1.  
DR MIM; 147110; -.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003597; Ig\_ci.  
DR InterPro; IPR003600; Ig\_like.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00410; IG\_Like; 1.  
DR SMART; SM00407; IGcl; 2.  
DR PROSITE; PS00290; IG\_MHC; 2.  
KW Immunoglobulin domain; Immunoglobulin C region.  
FT NON\_TER 1  
FT DOMAIN 1 98 CH1.  
FT DOMAIN 99 110 HINGE.  
FT DOMAIN 111 219 CH2.  
FT DOMAIN 220 326 CH3.  
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).  
FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 140 200  
FT DISULFID 246 304  
FT SITE 156 156  
FT MOD\_RES 326 326  
FT VARIANT 60 60  
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Query Match 64.0%; Score 1610; DB 1; Length 326;  
Best Local Similarity 91.8%; Pred. No. 8.9e-104;  
Matches 303; Conservative 10; Mismatches 13; Indels 4; Gaps 2;  
Qy 141 ASTKGPSVFPLAPSSKSTSGGTAALGLVLDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200  
Db 1 ASTKGPSVFPLAPCSRSTSESTAALGLVLDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60  
Qy 201 GLYSLSVVTVPSSSLGTQYICNVNHRKPSNTKVDKVEPKSCDKHTHTCPCPAPPELLGG 260  
Db 61 GLYSLSVVTVPSSNFGQTYTCNVDHAPSNTKVDKVEPKSCDKHTHTCPCPAPPELLGG 116  
Qy 261 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320  
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Qy 321 STYRVSVLTVLDHQLNGKEYKCKVSKNALKPAPIEKTIKAKGQPREPQVYTLPPSREE 380  
Db 177 STFRVSVLTITVVDHQLNGKEYKCKVSKNGLPAPIEKTIKAKGQPREPQVYTLPPSREE 236  
Qy 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 440  
Db 237 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 296  
Qy 441 QQGNVFCFSVMHEALHNHYTQKSLSLSPGK 470  
Db 297 QQGNVFCFSVMHEALHNHYTQKSLSLSPGK 326  
RESULT 3  
ID GC4\_HUMAN  
AC P01861; STANDARD; PRG; 327 AA.  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)  
Ig gamma-4 chain C region.  
IGHG4.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=83157104; PubMed=6299662;  
RA Ellison J.W., Buxbaum J.N., Hood L.E.;  
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";  
RL DNA 1:11-18(1981).  
RN [2]  
RN SEQUENCE OF 1-30 AND 81-326.  
RX MEDLINE=70207560; PubMed=4192699;  
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;  
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the  
constant region of a gamma 4 chain.";  
RL Biochem. J. 117:33-47(1970).  
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DR PIR; A02150; G4HU.  
DR HSSP; P01842; 7FAB.  
DR MIM; 147130; -.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003597; Ig\_C1.  
DR InterPro; IPR003600; Ig\_Like.  
DR Pfam; PF00047; Ig\_3.  
DR SMART; SM00410; IG\_Like; 1.  
DR SMART; SM00407; IGC1; 2.  
DR PROSITE; PS00290; IG\_MHC; 2.  
KW Immunoglobulin domain; Immunoglobulin C region.  
FT NON\_TER 1  
FT DOMAIN 1 98 CH1.  
FT DOMAIN 99 110 HINGE.  
FT DOMAIN 111 220 CH2.  
FT DOMAIN 221 327 CH3.  
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).  
FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 141 201  
FT DISULFID 247 305  
SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;

Query Match 63.5%; Score 1599.5; DB 1; Length 327;  
Best Local Similarity 91.8%; Pred. No. 4.7e-103;  
Matches 303; Conservative 9; Mismatches 15; Indels 3; Gaps 1;

QY 141 ASTKPSVFPPLAPSKSTSGGTAALGCLVKDYFPPVTVSNWNSGALTSVHTFPVAVLSS 200  
|||||  
1 ASTKPSVFPPLAPSKSTSGGTAALGCLVKDYFPPVTVSNWNSGALTSVHTFPVAVLSS 60  
201 GLYSSVVTVFSSSLGTQTCVNNHPSNTKVDKRPKSCDTHRCPCPAPPELLGG 260  
|||||  
61 GLYSSVVTVFSSSLGTQTCVNNHPSNTKVDKRPKSCDTHRCPCPAPPELLGG 117  
261 PSVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTPREEQYN 320  
118 PSVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTPREEQFN 177  
321 STYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQRPQVYTLPPSREE 380  
|||||

Db 178 STYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQRPQVYTLPPSREE 237  
QY 381 MTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 440  
|||||  
Db 238 MTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 297  
QY 441 QGQNVFSCSVMEALHNNHYTKQSLSPGK 470  
I:|||||  
Db 298 QGQNVFSCSVMEALHNNHYTKQSLSPGK 327  
RESULT 4  
GC RABIT STANDARD; PRT; 323 AA.  
ID GC RABIT  
AC P01870;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig gamma chain C region.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=84030930; PubMed=6313520;  
RA Bernstein K.E., Alexander C.B., Mage R.G.;  
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant  
F-I haplotype.";  
RL Immunogenetics 18:387-397(1983).  
RN [2]  
RN SEQUENCE OF 1-128.  
RX MEDLINE=76135469; PubMed=1243651;  
RA Pratt D.M., Mole L.E.;  
RT "Sequence studies on the constant region of the Fd sections of rabbit  
immunoglobulin G of different allotype.";  
RL Biochem. J. 151:337-349(1975).  
RN [3]  
RN SEQUENCE OF 88-266 FROM N.A.  
RX MEDLINE=83299917; PubMed=6193512;  
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;  
RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma  
heavy chain and identification of two genomic C gamma genes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).  
RN [4]  
RN SEQUENCE OF 132-161.  
RX MEDLINE=70110015; PubMed=5461106;  
RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;  
RT "Sequence studies of the Fd section of the heavy chain of rabbit  
immunoglobulin G.";  
RL Biochem. J. 116:249-259(1970).  
RN [5]  
RN SEQUENCE OF 129-131 AND 155-322.  
RA Hill R.L., Lebowitz H.E., Fellows R.E. Jr., Delaney R.;  
RL (In) Killander J. (eds.);  
RL Gamma globulins, Nobel symp. 3, pp.109-127, Almquist and Wiksell,  
Stockholm (1967).  
CC -!- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,  
104-THR, AND THE E14 MARKER. 185-THR. REF.3 HAS THE D11 AND E15  
MARKERS, AND REF.5 THE E15 MARKER.  
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CC -----  
DR EMBL; M16426; AAA31289.1; -.  
DR PIR; A02161; GHRB.  
DR HSSP; P01857; 1FC1.  
DR InterPro; IPR003006; Ig\_MHC.

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DR InterPro; IPR003597; Ig_cl.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Igc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 N -> E (IN REF. 2).
FT CONFLICT 71 71 V -> VPV (IN REF. 2).
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 173 173 N -> D (IN REF. 5).
FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 Q -> E (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 N -> D (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> D (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).
FT CONFLICT 284 284 N -> S (IN REF. 5).
SQ SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;

Query Match 48.9%; Score 1231.5; DB 1; Length 323;
Best Local Similarity 70.0%; Pred. No. 9.1e-78;
Matches 229; Conservative 34; Mismatches 57; Indels 7; Gaps 2;

QY 144 KGPSVFPLAPSSKSTSGGTAAALGLVDFPEPTVSVNSGALTSGVHTFPAVLQSSGLY 203
DB 4 KAPSVFPLAPCCGTPSTVTLGLGVGLPEPTVTWNSGTLTNGVTFPSVRQSSGLY 63
QY 204 SLSSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKRVKPKSCDKTHTCPCPAPPELLGGPSV 263
DB 64 SLSSVSVTSSTSS---QPVCNVHPATNTKVDKTVASTCSK-----PTCPPPELLGGPSV 116
QY 264 FLFPKPKADTLIMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVVHNNAKTKPRSQYNSTY 323
DB 117 FIFPKPKADTLIMISRTPEVTCVVVDVSDQDPEVQFTWYINNEQVTRTARPLPREGQFNSI 176
QY 324 RVSVSLTVLHODWLNKGEYKCKVGNKALPAPIETKISKAKGPREPQVYTLPPSREEMTK 383
DB 177 RVSVSLTVLHODWLNKGEYKCKVGNKALPAPIETKISKAKGPREPQVYTLPPSREEMTK 383
QY 384 NOVSLTCLVKGFPYSDIAVENESGQPNKYKTPPPVLDSDGSPFLYSKLVVDKSRWQOG 443
DB 237 RVSILTCMNGFYPSDISVEKNGKAEDNYKTTTPAVLSDSGSYFLYNKLSVPTSEWQRG 296
QY 444 NVFSCSVMEALHNHYTKSLSPGK 470
DB 297 DVFTCSVMHEALHNHYTKSLSPGK 323

RESULT 5
GC2_CAVPO STANDARD; PRT; 329 AA.
AC GC2_CAVPO
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;

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RA Birshtein B.K., Hussain Q.Z., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT half-cystine joining heavy and light chains.";
RT Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT and hinge region cyanogen bromide fragments.";
RT Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
RT antibodies.";
RT Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
RT antibodies.";
RT Biochemistry 13:4804-4811(1974).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:26-31(1971).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC 13 INBRED GUINEA PIGS.
DR PIR: A02151; G2GP.
DR HSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; Igc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 48.1%; Score 1210.5; DB 1; Length 329;
Best Local Similarity 69.8%; Pred. No. 2.6e-76;
Matches 233; Conservative 30; Mismatches 62; Indels 9; Gaps 4;

QY 140 SASTKGPSVFPLAPSSKSTSGGTAAALGLVDFPEPTVSVNSGALTSGVHTFPAVLQ 199
DB 1 SARTTAPSVFPLAASCVDTSGMTLGLVKGYPPEPTVKVNSGALTSGVHTFPAVLQ- 59
QY 200 SGLYSLSVSVVFPSSSLGTQTYICNVNHPKSNKTKVDKRVKPKSCDKTH--TCPPCPAPEL 257
DB 60 SGLYSLSVSVVFPSSSLGTQTYICNVNHPKSNKTKVDKRVKPKSCDKTH--TCPPCPAPEL 257
QY 258 LGGPSVFLFPKPKDITLMSIRTPETVCVVVDVSHEDPEVKFNKYVDGVVHNNAKTKPRE 317
DB 116 LGGPSVFLFPKPKDITLMSIRTPETVCVVVDVSHEDPEVKFNKYVDGVVHNNAKTKPRE 317

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Db 179 ISKTGQPREQVYTLPPSREMTKQVSLTCLVKGYFPPYSDIAVEWESSGQPENNYNTTP 238  
 Qy 419 PVLDSGSEFFLYSLKTLVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470  
 Db 239 PMLDSGSEFFLYSLKTLVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 290

RESULT 7  
 GC1\_RAT  
 ID GC1\_RAT STANDARD; PRT; 326 AA.  
 AC P20759;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig gamma-1 chain C region.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89232738; PubMed=3149946;  
 RA Brueggemann M.;  
 RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";  
 RL Gene 74:473-482(1988).  
 DR HSP; PS0017; PS0017.  
 DR HSP; P01842; 7FAB.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003597; Ig\_cl.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00407; IGcl; 2.  
 DR PROSITE; PS00290; Ig\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 97 CH1.  
 FT DOMAIN 98 112 HINGE.  
 FT DOMAIN 113 219 CH2.  
 FT DOMAIN 220 326 CH3.  
 FT DISULFID 27 82  
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 140 200  
 FT DISULFID 246 304  
 FT CARBOHYD 176 176  
 SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match 45.9%; Score 1155; DB 1; Length 326;  
 Best Local Similarity 63.4%; Pred. No. 1.7e-72;  
 Matches 211; Conservative 52; Mismatches 60; Indels 10; Gaps 4;

Qy 141 ASTKGPSVPEPLAPSSKSTSGGTAALCLVKGYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200  
 Db 1 AETAPSYPLAPGALKSNWTLGLVKGYFPEPVTVTWNSGALSSGVHTFPAVLQ-S 59

Qy 201 GLYLSVVTVPSSSLGQTQYICNVNHNKPSNTKVDKRVKPSGCDKTHCP-PCPAPPELLGG 260  
 Db 60 GLYLTSSVTVPSWSPQTVTCNVNHNKPSNTKVDKRVKPSGCDKTHCP-PCPAPPELLGG 113

Qy 261 ---PSVFLFPKPKDTHLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNHNAKTPREE 317  
 Db 114 SEVSSVFIPPKPKDVLITLTLPKVTCTCNVHAPASSTKVDKRVKPSGCDKTHCP-PCPAPPELLGG 173

Qy 318 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPTEKTIKAKGQPREPQVYTLPPS 377  
 Db 174 QFNSTFRSVLPLVHQDWLNGRTFRCKVTCTCNVHAPASSTKVDKRVKPSGCDKTHCP-PCPAPPELLGG 233

Qy 378 REEMTKQVSLTCLVKGYFPPYSDIAVEWESSGQPENNYNTTPVLDSDGSEFFLYSLKTLVDK 437  
 Db 234 KEEMTKQVSLTCLVKGYFPPYSDIAVEWESSGQPENNYNTTPVLDSDGSEFFLYSLKTLVDK 293

Qy 438 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470  
 Db 294 EKQWQGNFTCTSVLHEGLNHNHTEKSLSHSPGK 326

RESULT 8  
 GC3\_MOUSE  
 ID GC3\_MOUSE STANDARD; PRT; 329 AA.  
 AC P22436;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ig gamma-3 chain C region, secreted form.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85027161; PubMed=6092053;  
 RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,  
 RA Tucker P.W., Blattner F.R.;  
 RT "Structural analysis of the murine IgG3 constant region gene.";  
 RL EMBO J. 3:2041-2046(1984).  
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 CC EMBL; J00451; -; NOT\_ANNOTATED\_CDS.  
 DR PIR; B02156; G3MSC.  
 DR HSP; P01857; 1FC1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003597; Ig\_cl.  
 DR InterPro; IPR003600; Ig\_like.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00410; IG\_Like; 1.  
 DR SMART; SM00407; IGcl; 2.  
 DR PROSITE; PS00290; Ig\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.  
 KW Transmembrane; Alternative splicing.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 97 CH1.  
 FT DOMAIN 98 113 HINGE.  
 FT DOMAIN 114 223 CH2.  
 FT DOMAIN 224 327 CH3.  
 SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 45.7%; Score 1150; DB 1; Length 329;  
 Best Local Similarity 65.0%; Pred. No. 3.7e-72;  
 Matches 215; Conservative 44; Mismatches 68; Indels 4; Gaps 3;

Qy 142 STKGPSVPEPLAPSSKSTSGGTAALCLVKGYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 201  
 Db 1 TTTAPSVPLPGCDSTSGSSVTLGLVKGYFPEPVTVKWNIGALSSGVTVSSVLQ-SG 59

Qy 202 LYSLSVVTVPSSSLGQTQYICNVNHNKPSNTKVDKRVKPSGCDKTHCP-PCPAPPELLGG 259  
 Db 60 FYSLSLVTVPSWSPQTVTCNVNHNKPSNTKVDKRVKPSGCDKTHCP-PCPAPPELLGG 118

Qy 260 GPSVFLFPKPKDTHLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNHNAKTPREEQY 319  
 Db 119 GPSVFIFFPKPKDTHLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNHNAKTPREEQY 178

Qy 320 NSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPTEKTIKAKGQPREPQVYTLPPSRE 379  
 Db 179 NSTFRVVSALPIQHDWNRGKEFKCKVNNKALPAPIERTISKPKGQRAQTPQVYTIPTPPRE 238

QY 380 EMTKNQVSLCLVKGFPDIAVWESNGQPNKYKTPPVLDSGDSFFLYSKLTVDKSR 439  
 Db 239 QMSKKVSLTCLVNFSEALSISWERNGELEQDYKKTPTILDSGDFYFLYSLKLTVDKSR 298  
 QY 440 WQSGNVFSCVMHEALHNHYTKSLSPGK 470  
 Db 299 WLOGEFTCSVHEALHNHYTKSLSPGK 329

RESULT 9  
 GCL\_MOUSE STANDARD; PRT; 324 AA.  
 AC P01868;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Ig gamma-1 chain C region.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=80045036; PubMed=115593;  
 RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,  
 RA Takahashi N., Mano Y.;  
 RT "Cloning and complete nucleotide sequence of mouse immunoglobulin  
 gamma 1 chain gene";  
 RL Cell 18:559-568(1979).  
 RN [2]  
 RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).  
 RX MEDLINE=80202559; PubMed=6769752;  
 RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,  
 RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;  
 RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences  
 cloned in a bacterial plasmid";  
 RL Gene 9:87-97(1980).  
 RN [3]  
 RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).  
 RX MEDLINE=80012837; PubMed=113776;  
 RA Rogers J., Clarke P., Salser W.;  
 RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin  
 heavy chain";  
 RL Nucleic Acids Res. 6:3305-3321(1979).  
 RN [4]  
 RP SEQUENCE (MYELOMA PROTEIN MOPC 21).  
 RX MEDLINE=78242288; PubMed=98524;  
 RA Adegugbo K.;  
 RT "Evolution of immunoglobulin subclasses. Primary structure of a  
 murine myeloma gamma1 chain";  
 RL J. Biol. Chem. 253:6068-6075(1978).  
 RN [5]  
 RP DISULFIDE BONDS (MOPC 21).  
 RX MEDLINE=73008889; PubMed=5073237;  
 RA Svasti J., Milstein C.;  
 RT "The disulphide bridges of a mouse immunoglobulin G1 protein";  
 RL Biochem. J. 126:837-850(1972).  
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 CC -----  
 DR EMBL; V00793; CAA24172.1; -  
 DR EMBL; V00793; CAA24173.1; -  
 DR EMBL; V00793; CAA24174.1; -  
 DR EMBL; V00793; CAA24175.1; -  
 DR EMBL; V00795; CAA24176.1; -  
 DR PIR; A02159; GIMS.  
 DR HSSP; P01842; 7FAB.

DR GlycoSuiteDB: P01868; -  
 DR MGD: MGI:96446; Igh-4.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003597; Ig\_CL.  
 DR Pfam: PF00047; Ig; 3.  
 DR SMART: SM00407; IGH1; 2.  
 DR PROSITE: PS00290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
 KW Alternative splicing.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 97 CH1.  
 FT DOMAIN 98 110 HINGE.  
 FT DOMAIN 111 217 CH2.  
 FT DOMAIN 218 324 CH3.  
 FT DISULFID 27 82  
 FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 138 198  
 FT CARBOHYD 174 174 N-LINKED (GLCNAC...).  
 FT FTID-CAR\_000055.  
 FT DISULFID 244 302  
 FT MOD\_RES 324 324 REMOVED POST-TRANSLATIONALLY.  
 FT CONFLICT 276 276 N -> D (IN REF. 3).  
 FT CONFLICT 278 278 N -> D (IN REF. 3).  
 SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;  
 Query Match 45.5%; Score 1145; DB 1; Length 324;  
 Best Local Similarity 62.3%; Pred. No. 8.1e-72;  
 Matches 207; Conservative 55; Mismatches 60; Indels 10; Gaps 4;  
 QY 141 ASFKGSPVPLAPSSKTSSTGTAALCLVKGYPPEPTVTSWNSGALTSVHTTPAVLQSS 200  
 Db 1 AKTPPSVPLAPGSAQAQTNMSVTLGLVKGYPPEPTVTSWNSGSLSSGHTTPAVLQSD 60  
 QY 201 GLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVKPKCDKTHTCPP--CPAPELL 258  
 Db 61 -LYTLSSVTVTPSSPRPSEITVTCNVAHPASSTKVDKKIVPRDCG---CKPCICTVPEV- 114  
 QY 259 GGSVFLFPKPKDMLMSRTPEVTCVVDVSHEDPEVKFNWYVDGVEVINATKKPREEQ 318  
 Db 115 --SSVFIFPPKPKDVLITLTPKVTCTVVDVSHEDPEVKFNWYVDGVEVINATKKPREEQ 172  
 QY 319 YNSTYRWVSVLTVLHODWLNKKEYCKVSNKALPAPTEKTIKAKGQPPPEQVYTLPPSR 378  
 Db 173 FNSTFRSVSELPIMHQDWLNKKEFKVNSAAPPAPIEKTISTKGRPKAPQVYTIPTPK 232  
 QY 379 EEMTKNQVSLCLVKGFPDIAVWESNGQPNKYKTPPVLDSGDSFFLYSKLTVDKSR 438  
 Db 233 EQMAKDKVSLTCMTDFFPEDITVWQNGQPAENYKNTQPIINTNGSYFVSKLVNYS 292  
 QY 439 RWOQGNVFCVMHEALHNHYTKSLSPGK 470  
 Db 293 NWEAGNTFTCSVLHEGLHNHHTKSLSPGK 324  
 RESULT 10  
 GCB\_RAT STANDARD; PRT; 333 AA.  
 AC P20761;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig gamma-2B chain C region.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89232738; PubMed=3149946;

RA Brueggemann M.;  
 RL "Evolution of the rat immunoglobulin gamma heavy-chain gene family";  
 DR Gene 74:473-482(1988).  
 DR PIR; PS0018;  
 DR HSP; P01842; 7FAB.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003597; Ig\_cl.  
 DR InterPro; IPR003600; Ig-like.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00410; IG\_Like; 1.  
 DR SMART; SM00407; IGcl; 2.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region.  
 FT NON\_TER 1  
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 27 80  
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 147 207  
 FT DISULFID 253 311  
 SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;  
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 Best Local Similarity 63.7%; Pred. No. 9e-72;  
 Matches 214; Conservative 45; Mismatches 68; Indels 9; Gaps 3;  
 QY 141 ASTGSPVEPLAPSSKTSGLTALGLVDYFPPEVTYVNSGALTSVHTFFAVLQSS 200  
 Db 1 AQTAPSYVLPAGCGDTSTSTVLGCLVGYFPPEVTYVNSGALSSDVHTFFAVLQ-S 59  
 QY 201 GLYSLSSVTVTPSSSLGTQYICNVNHNKPSNTKVDKVRPKS-----CDKTHRCPPCPA 254  
 Db 60 GYLTLTSSVT--STWSPQYVTCNVHPASTKVDKVKVERNGGIGHKCTPCPCCHKCPV 117  
 QY 255 PELGGSPVFPPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKTP 314  
 Db 118 PELLGGSPVFPPPKPKDILLISQNAKVCVVDVSEEDPDVQSFVFNWVNVHTAQTPQ 177  
 QY 315 REEQNSTYRVVSVLTVHQLWNLGKEYCKVSNKALPAPEIKTSIRAKGQPREPOVYTL 374  
 Db 178 REEQNSTYRVVSVLTVHQLWNLGKEYCKVSNKALPAPEIKTSIRAKGQPREPOVYVM 237  
 QY 375 PPSREEMTKNOVSLTCLVKGPYPSDIAVEWESNGOPENNYKTTTPVLDSDGSEFLYSKLT 434  
 Db 238 GPPEQLTEQTVSLTCLTSGFLPDNDIGVEWTSNGHIEKNYKNTPEVMDSDGSEFLYSKLN 297  
 QY 435 VDKSRWQGNVFCSSVMHEALHNHYTKLSLSPEK 470  
 Db 298 VERSRWSDRAPFCVSVVHEGLNHHVBEKSIKRPCK 333  
 RESULT 11  
 GCIM\_MOUSE STANDARD; PRT; 393 AA.  
 AC P01869;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Ig gamma-1 chain C region, membrane-bound form.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=80045036; PubMed=115593;  
 RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,  
 RA Takahashi N., Mano Y.;  
 RT "Cloning and complete nucleotide sequence of mouse immunoglobulin  
 gamma 1 chain gene.";

RL Cell 18:559-568(1979).  
 RN [2]  
 RP SEQUENCE OF 323-393 FROM N.A.  
 RX MEDLINE=82197626; PubMed=6804950;  
 RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;  
 RT "mRNA for surface immunoglobulin gamma chains encodes a highly  
 conserved transmembrane sequence and a 28-residue intracellular  
 domain";  
 RT Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).  
 RN [3]  
 RP SEQUENCE OF 323-366 FROM N.A.  
 RX MEDLINE=82115295; PubMed=6799207;  
 RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,  
 RA Eisenberg D., Wall R.;  
 RT "Gene segments encoding transmembrane carboxyl termini of  
 immunoglobulin gamma chains";  
 RT Cell 26:19-27(1981).  
 RN [4]  
 RP SEQUENCE OF 1-44 FROM N.A.  
 RX MEDLINE=82222190; PubMed=6283537;  
 RA Yanawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;  
 RT "Nucleotide sequences of gene segments encoding membrane domains of  
 immunoglobulin gamma chains";  
 RT Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).  
 CC -1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA  
 SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED  
 GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-  
 BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED  
 IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND  
 SEGMENT OF MU CHAINS.  
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 DR EMBL; V00793; CAA24172.1; -;  
 DR EMBL; V00793; CAA24173.1; -;  
 DR EMBL; V00793; CAA24174.1; -;  
 DR PIR; B02159; GIMSM.  
 DR HSP; P01842; 7FAB.  
 DR MGD; MGI:96446; Igh-4.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003597; Ig\_cl.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00407; IGcl; 2.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
 KW Alternative splicing; Transmembrane.  
 FT NON\_TER 1  
 FT DOMAIN 1 97 CH1.  
 FT DOMAIN 98 110 HINGE.  
 FT DOMAIN 111 217 CH2.  
 FT DOMAIN 218 324 CH3.  
 FT DISULFID 27 82  
 FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 138 198  
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 FT TRANSMEM 358 393  
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 Best Local Similarity 62.2%; Pred. No. 2.3e-71;  
 Matches 206; Conservative 55; Mismatches 60; Indels 10; Gaps 4;





RX MEDLINE=81223894; PubMed=6787604;  
RA Olio R., Aufray C., Morchamps C., Rougeon F.;  
RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes  
RT suggests that exons can be exchanged between genes in a multigenic  
RT family.";  
RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).  
RN [4]  
RP MYELOMA PROTEIN MOPC 173.  
RX MEDLINE=74175517; PubMed=4831970;  
RA Bourgois A., Fougereau M., Rocca-Serra J.;  
RT "Determination of the primary structure of a mouse IgG2a  
RT immunoglobulin:amino-acid sequence of the Fc fragment. Implications  
RT for the evolution of immunoglobulin structure and function.";  
RL Eur. J. Biochem. 43:423-435(1974).  
RN [5]  
RP DISULFIDE BONDS.  
RX MEDLINE=73056887; PubMed=4565406;  
RA de Preval C., Fougereau M.;  
RT "Determination of the primary structure of a mouse gamma G2a  
RT immunoglobulin. Identification of the disulfide bridges.";  
RL Eur. J. Biochem. 30:452-462(1972).  
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CC -----  
DR EMBL; V00798; CAA24178.1; -;  
DR PIR; A02152; G2MSA.  
DR HSSP; P01842; 7FAB.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003597; Ig\_cl.  
DR InterPro; IPR003600; Ig\_like.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00410; IG\_like; 1.  
DR SMART; SM00407; IGcl; 2.  
DR PROSITE; PS00290; IG\_MHC; 1.  
DR Immunoglobulin domain; Immunoglobulin C region.  
KW NON\_TER 1  
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).  
FT DISULFID 27 82  
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 144 204  
FT DISULFID 250 308  
FT MOD\_RES 330 330 REMOVED POST-TRANSLATIONALLY.  
SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;  
  
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Best Local Similarity 63.9%; Pred. No. 1e-70;  
Matches 212; Conservative 43; Mismatches 73; Indels 4; Gaps 3;  
  
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Db 1 AKTAPSVYPLAPVCGDTGSGSVTLGCLVKGYFPEPTVLTWNSGSLSCGVHTFPAVLQSD 60  
  
Qy 201 GLYSLSSVTVPPSSSLGTQTYICNVNHHKPSNTKVDKRVPEKSCDKTHTCPP--CPAPEL 258  
Db 61 -LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKEPRG-PTIKPCPCPKCPAPNLL 118  
  
Qy 259 GGPSVFLPPPKDITLMSRPEVTCVVDVYSHEDPEKFNWYDGVVHNKAKTPREQ 318  
Db 119 GGPSVFIFFPKIKDVLMSLPIVTCVVDVYSEDDPQVQISWFVNNVHVHTAQOTQRED 178  
  
Qy 319 YNSTRVVSVTLVLDHNLCKEYKCKVSKNALPAPIETKISKAKGQPREQVYTLPPSR 378  
Db 179 YNSTLRVVSALPIQHDWMSKEFKCKVNNKDLPAPIERTISKPGSVRAPOVYVLPPE 238

Qy 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGPENNYKTTTPPVLDSDGSGFFLYSKLTVDKS 438  
Db 239 EEMTKQVTLTCMTVDFMPEDIIYVETWNTKTELYKNTPEVLDSDGSGFFLYSKLRVEKK 298  
Qy 439 RWQGNVFSQSCVMHEALNHYTOKSLSLSPGK 470  
Db 299 NWVERNSYSCSVVHGLNHHHTKSFSPGK 330  
  
RESULT 14  
GCC\_RAT  
ID GCC\_RAT STANDARD; PRT; 329 AA.  
AC P20762;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig gamma-2C chain C region.  
DE Rattus norvegicus (Rat).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88166903; PubMed=3127222;  
RA Brueggemann M., Delmastro-Galfrè P., Waldmann H., Calabi F.;  
RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant  
RT region cDNA: extensive homology to mouse gamma 3.";  
RL Eur. J. Immunol. 18:317-319(1988).  
CC -----  
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CC -----  
DR EMBL; X07189; CAA30169.1; -;  
DR PIR; S00847; S00847.  
DR HSSP; P01857; 1FC1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003597; Ig\_cl.  
DR InterPro; IPR003600; Ig\_like.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00410; IG\_like; 1.  
DR SMART; SM00407; IGcl; 2.  
DR PROSITE; PS00290; IG\_MHC; 1.  
DR Immunoglobulin domain; Immunoglobulin C region.  
KW NON\_TER 1  
FT DOMAIN 1 97 CH1.  
FT DOMAIN 98 113 HINGE.  
FT DOMAIN 114 222 CH2.  
FT DOMAIN 223 329 CH3.  
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).  
FT DISULFID 27 82  
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 143 203  
FT DISULFID 249 307  
SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;  
  
Query Match 44.8%; Score 1127.5; DB 1; Length 329;  
Best Local Similarity 62.8%; Pred. No. 1.3e-70;  
Matches 209; Conservative 51; Mismatches 66; Indels 7; Gaps 3;  
  
Qy 141 ASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 200  
Db 1 ARTTAPSVYPLVPGSGTSGSLVTLGCLVKGYFPEPTVTKWNSGALSSGVHTFPAVLQ-S 59  
  
Qy 201 GLYSLSSVTVPPSSSLGTQTYICNVNHHKPSNTKVDKRVPEKSCDKTHTCPP--CPAPEL 257  
Db 60 GLYTLSSSVTVPPSSWSSTVTCSVAHPATKSNLIKRIEPR---RPKRPPTDICSDDN 116

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QY 258 LGGPSVFLPPPKDITMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREE 317
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Db 117 LGRPSVFIFPPPKDITLTPKTVVVDVSEEDPDQFSWFDNRVFTAQTPHEE 176
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 318 QYNSTRYRVSVLTVDHODWLNKGYCKVSNKALPAPIETISKAKGQPREPOVYTLPPS 377
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 177 QLNGTRFVSTLHIOHQDWMGSKGFEKCKVNNKDLPSIEKTIKPRGKARTPOVYTI 236
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 378 REBMTKNVSLTCLVKGFPSPDIAVWESNGQPNENYKTTTPVLDSDGSFFLYSKLTVDK 437
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Db 237 REQMSKNSVLTCTWTSFTPASISVSWERNGELEDQIKNTLPVLDSDSESYFLSKUSVDT 296
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Db 297 DSMRMGDIPTCSVVHEALHNHHTQKNLSRSPGK 329
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RESULT 15
GCAB_MOUSE STANDARD; PRT; 335 AA.
AC P01864:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2A chain C region, B allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
  IgG2a and IgG2b alleles of the mouse."
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN [2]
RP SEQUENCE.
RX MEDLINE=8203777; PubMed=6794027;
RA Dognin M.J., Lauwereys M., Strosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
  chain Fc regions of Ig1a and Ig1b allotypic forms."
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -!- MISCELLANEOUS; THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
  FROM BALB/C MICE, AT 15% OF THE POSITIONS.
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DR EMBL; J00479; -; NOT_ANNOTATED_CDS.
DR PIR; A02153; G2MSAB.
DR HSP; P01857; IFCL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; Ig_c1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER
SQ SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;
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Query Match 44.8%; Score 1126.5; DB 1; Length 335;  
Best Local Similarity 61.6%; Pred. No. 1.6e-70;

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Db 1 AKTTAFSVPLVPVCGGTTGSSVTLGCLVKGYPPEPVTLTNWSSGSLSSGVTTFPALLO-S 59
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 201 GLYSLSVVTVSPSSSLGTQTYICNVNHNKPSNTKVDKRVPEK-----SCDKTHTCPPCPA 254
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 GLYTLSSSVTVTSNTWPSQTITCNVAHPASSTKVDKKIEPRVPIITQNPCCPPHQRVPPCAA 119
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 255 PELLGGPSVFLPPPKDITMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 314
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Db 120 PDLGGPSVFIFPPKIKDVLMISSLPMVTCVVVDVSEDDPDQIISWFWNNVEVHTAQTOT 179
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 315 REEOYNSTRYRVSVLTVDHODWLNKGYCKVSNKALPAPIETISKAKGQPREPOVYTL 374
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 180 HREDYNSTRYRVSVLTVDHODWLNKGYCKVSNKALPAPIETISKAKGQPREPOVYTL 239
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 375 PPSREEMTKNQVSLTCLVKGFPSPDIAVWESNGQPNENYKTTTPVLDSDGSFFLYSKLT 434
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 240 PPPAEEMTKKEFSLTCTMITGFLPAETIAVDWTSGRTEQYKNTATVLDSDGSYFMYSKLR 299
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 435 VDKSRHQGQNVFSCSVHHEALHNHYTKQSLSPGK 470
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 300 VOKSTWERSLFAFACSVVHEVLTNNHLLTKTISRSLGK 335
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Job time: 689 sec
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OM protein - protein search, using sw model

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(without alignments)  
433.386 Million cell updates/sec

Title: US-09-499-662-147  
Perfect score: 2517  
Sequence: 1 MWSCHILFLVATATGVHSQ.....MHEALHNHYTQKSLSPGK 470

Scoring table:  
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Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_nhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1636.5	65.0	473	11 Q9D8L4	Q9d8l4 mus musculus
2	1625.5	64.6	463	11 Q99LC4	Q99lc4 mus musculus
3	1585.5	63.0	473	11 Q99L25	Q99l25 mus musculus
4	1559	61.9	468	11 Q99L31	Q99l31 mus musculus
5	1436.5	57.1	437	11 Q99L31	Q99l31 mus musculus
6	1423.5	56.6	473	11 Q99L31	Q99l31 mus musculus
7	1263.5	50.2	337	6 Q95M34	Q95m34 equus caball
8	1257	49.9	701	4 Q96P08	Q96pq8 homo sapien
9	983	39.1	278	11 Q921K1	Q921k1 mus musculus
10	930.5	37.0	614	4 Q96GA6	Q96ga6 homo sapien
11	887.5	35.3	481	11 Q99LW3	Q99lw3 mus musculus
12	862	34.2	500	4 Q9BRV0	Q9brv0 homo sapien
13	833.5	33.1	481	11 Q99LW1	Q99lw1 mus musculus
14	817	32.5	488	11 Q99LW1	Q99lw1 mus musculus
15	815.5	32.4	597	4 Q96BB9	Q96bb9 homo sapien
16	807	32.1	496	4 Q96DK0	Q96dk0 homo sapien

#### ALIGNMENTS

RESULT 1

Q9D8L4 ID Q9D8L4 PRELIMINARY; PRT; 473 AA.  
AC Q9D8L4;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE 181006009RIK PROTEIN.  
GN IGH-1 OR 181006009RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,  
RA Saito T., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Kadota K., Okada T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,  
RT Hayashizaki Y.;  
RL "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 403:685-690(2001).  
DR EMBL; AK007918; BAB25349.1; -.  
HSSP; P01842; 7FAB.

17 765.5 30.4 597 4 Q9BU10 Q9bu10 homo sapien  
18 761.5 30.3 597 4 Q9BQB8 Q9bqb8 homo sapien  
19 755.5 30.0 618 4 Q96AA6 Q96aa6 homo sapien  
20 755 30.0 484 11 Q99LA6 Q99la6 mus musculus  
21 737 29.3 494 4 Q96K68 Q96k68 homo sapien  
22 735 29.2 613 4 Q96EY0 Q96ey0 homo sapien  
23 727.5 28.9 487 11 Q99RA4 Q99ra4 mus musculus  
24 721.5 28.7 479 11 Q91WP5 Q91wp5 mus musculus  
25 703 27.9 486 11 Q91Z07 Q91z07 mus musculus  
26 692.5 27.5 480 11 Q91XE1 Q91xe1 mus musculus  
27 659 26.2 482 11 Q91X92 Q91x92 mus musculus  
28 655 26.0 479 11 Q99M22 Q99m22 mus musculus  
29 644 25.6 496 4 Q96KX8 Q96kx8 homo sapien  
30 605 24.0 426 11 Q9DCD9 Q9dcd9 mus musculus  
31 580.5 23.1 416 4 Q9NPP6 Q9npp6 homo sapien  
32 539.5 21.4 143 11 Q91V67 Q91v67 mus musculus  
33 527.5 21.0 143 11 Q924P9 Q924p9 mus musculus  
34 525 20.9 150 4 Q9V298 Q9v298 homo sapien  
35 514 20.4 142 11 Q924Q2 Q924q2 mus musculus  
36 511 20.3 157 4 Q95978 Q95978 homo sapien  
37 510.5 20.3 145 11 Q924R3 Q924r3 mus musculus  
38 499.5 19.8 159 4 Q96QSO Q96qso homo sapien  
39 495.5 19.7 143 11 Q924Q5 Q924q5 mus musculus  
40 494 19.6 146 11 Q924R8 Q924r8 mus musculus  
41 493 19.6 144 11 Q924P5 Q924p5 mus musculus  
42 492.5 19.6 145 11 Q924Q7 Q924q7 mus musculus  
43 488.5 19.4 145 11 Q924R4 Q924r4 mus musculus  
44 486.5 19.3 143 11 Q924Q0 Q924q0 mus musculus  
45 486 19.3 140 11 Q924P8 Q924p8 mus musculus



DR SMART; SM00407; IGcl; 3.  
 DR SMART; SM00406; IGv; 1.  
 DR SMART; SM00410; IG\_Like; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 63.0%; Score 1585.5; DB 11; Length 473;  
 Best Local Similarity 63.4%; Pred. No. 1.le-124;  
 Matches 301; Conservative 61; Mismatches 106; Indels 7; Gaps 5;

Qy 1 MWSCIIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSKCAGSYTFTSYWQVVRQAP 60  
 Db 1 MWSWVFLFLSVTGVHSQVQLVQSGDAELVKPGASVKISCKVSGTFTDTHFWVKQRP 60  
 Qy 61 GQLEWMEGIDPSDSTYNKFKGKATLTVDSTSTAYMELSSRSDEDTAVVYCARNRD 120  
 Db 61 EGLEWIGWIDEDGETYAPFQDKATITADTSSNTAYLQLSSLTSEDTAIYICARNLL 120  
 Qy 121 --YNN--WYDFWVGQTLTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVS 177  
 Db 61 EGLEWIGWYIPRDGSTRYNEKFGKATLTADKSSSTAYMQLNSLTSEDSAVCFCSRGSS 120  
 Qy 121 --YNN--WYDFWVGQTLTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVS 177  
 Db 121 IYGGGLYFYFYWGQGTITVSSAKTTAPSVYPLAPVCGDTGSSVTILGCLVKGYFPEPV 180  
 Qy 178 TVSNWSGALTSGVHTFPAVLQSD-LYTLSSSVTVTSSWPSQISITCNVAHPASSTKVDK 237  
 Db 181 TLTNWSSLSGSHVTFPAVLQSD-LYTLSSSVTVTSSWPSQISITCNVAHPASSTKVDK 239  
 Qy 238 VEPKSCDTHRCPP--CPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPE 295  
 Db 240 IEPGR-PTIKPCPCCKCAPNLGGPSVFIFFPKIKDVLMLSLSPMVTGVVDVSEDDPD 298  
 Qy 296 VKFNWYDGVVHNAKTPREQYNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPI 355  
 Db 299 VQISWVFNVEVLTAAQTOTREDYNSLTRVVSALPIQHDWMSGKEFKCKVNNKALPAPI 358  
 Qy 356 EKTISKAKGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYK 415  
 Db 359 ERTISKAGSRAPQVYVLPPEEEMTKQVTLTCMTDFMPEDIVYVSWTNGKTELNYK 418  
 Qy 416 TTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTKSLSLSPGK 470  
 Db 419 NTEPVLDSDGSFYFMYSKLVEKKNVVERNSYSCSVVHEGLHNHHTTKFSRTPGK 473

RESULT 4  
 Q99L31  
 ID Q99L31 PRELIMINARY; PRT; 468 AA.  
 AC Q99L31  
 DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE SIMILAR TO RIKEN CDNA 1810060009 GENE.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC003878; AA003878.1; -.  
 DR HSSP; P01842; 7FAB.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR003597; Ig.cl.  
 DR InterPro; IPR003600; Ig.like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 4.  
 DR SMART; SM00409; IGcl; 3.  
 DR SMART; SM00407; IGcl; 3.  
 DR SMART; SM00406; IGv; 1.  
 DR SMART; SM00410; IG\_Like; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.

SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match 61.9%; Score 1559; DB 11; Length 468;  
 Best Local Similarity 62.7%; Pred. No. 1.8e-122;  
 Matches 296; Conservative 62; Mismatches 108; Indels 6; Gaps 4;

Qy 1 MWSCIIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSKCAGSYTFTSYWQVVRQAP 60  
 Db 1 MKCSWVIFFLMAVIGVNSEVQLQSGAEVLRPGASVKLSCTASGNFKIDSLMHWVKQRP 60  
 Qy 61 GQLEWMEGIDPSDSTYNKFKGKATLTVDSTSTAYMELSSRSDEDTAVVYCARNRD 120  
 Db 61 EGLEWIGWIDEDGETYAPFQDKATITADTSSNTAYLQLSSLTSEDTAIYICARNLL 120  
 Qy 121 YNNWYDFWVGQTLTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVS 180  
 Db 121 YGG--YDYWGQGTITVSSAKTTAPSVYPLAPVCGDTGSSVTILGCLVKGYFPEPTLT 178  
 Qy 181 WNSGALTSGVHTFPAVLQSD-LYTLSSSVTVTSSWPSQISITCNVAHPASSTKVDK 240  
 Db 179 WNSGSLSGSHVTFPAVLQSD-LYTLSSSVTVTSSWPSQISITCNVAHPASSTKVDK 237  
 Qy 241 KSCDTHRCPP--CPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVK 298  
 Db 238 RG-PTIKPCPCCKCAPNLGGPSVFIFFPKIKDVLMLSLSPMVTGVVDVSEDDPDVQI 296  
 Qy 299 NNYDGVVHNAKTPREQYNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPI 358  
 Db 297 SHFNWVFNVEVLTAAQTOTREDYNSLTRVVSALPIQHDWMSGKEFKCKVNNKALPAPI 356  
 Qy 359 ISKAKGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYK 418  
 Db 357 ISKPGSRAPQVYVLPPEEEMTKQVTLTCMTDFMPEDIVYVSWTNGKTELNYK 416  
 Qy 419 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTKSLSLSPGK 470  
 Db 417 PVLDSDGSFYFMYSKLVEKKNVVERNSYSCSVVHEGLHNHHTTKFSRTPGK 468

RESULT 5  
 Q99L14  
 ID Q99L14 PRELIMINARY; PRT; 437 AA.  
 AC Q99L14  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wilde K.G.; Yu X.; Ekramoddoullah A.K.M.; Misra S.;  
 RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal  
 RT antibody (Mab 7, its light and heavy chains) and construction of a  
 RT single chain antibody (scFv).";  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF152372; AA040243.1; -.  
 DR HSSP; P01842; 7FAB.  
 DR InterPro; IPR003600; Ig\_Like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig; 4.  
 DR SMART; SM00406; IGv; 1.  
 DR SMART; SM00409; IGcl; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 FT NON\_TER 1  
 FT NON\_TER 437  
 SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match 57.1%; Score 1436.5; DB 11; Length 437;  
Best Local Similarity 59.3%; Pred. No. 3e-112;  
Matches 268; Conservative 71; Mismatches 96; Indels 17; Gaps 7;

QY 21 VOLVQSAEAKKPGASVKKSGAGYFTTSYMWQVRAQFQGLEWGEIDPDSYNNYN 80  
DB 1 VOLQESGGGLVKPGSLKLSAASGFTFSYAMSWVQRTPEKRLWEVASF-SGGIIYYT 59  
QY 81 QKFGKATLVDTSTAYVWELSLRSEDYAVYICARNRDYSNNWYFDVWGQGLTVTVSS 140  
DB 60 DSVKGRITTYIKDNRNLSLQMSLSRSEDYAVYICARG-DYS-----AYWGPGLTVTVSA 113  
QY 141 ASTKGPSVFLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSVHTFPVAVLQSS 200  
DB 114 AKTTPPSVPLAPGSAATNSMTVLGCLVKGYRPEPVTVWNSGSLSSGVTHTFPVAVLQSD 173  
QY 201 GLYSLSWTVVPSLSLGTQYICNVNHPKSNTPKVDKRVKPSKDKHTHTCP--CPAPELL 258  
DB 174 -LTVLSSVTVPSWTPSEPTVCNVAHPASSTKVKKIVPRDCG---CKPCICTVPEV- 227  
QY 259 GGPVFLFPKPKDITLMSRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREQ 318  
DB 228 --SSVTFEPKPKDVLITLTPKVCVVDISKDDPEVQSFVWVDVVEVHTAQTPREQ 285  
QY 319 YNSTYRVSVTLVHODWLNKGYCKVSNKALPAPIEKTISKAKGQRPQVYTLPPSR 378  
DB 286 FNSTFSVSELPIMHODWLNKGYCKVSNKALPAPIEKTISKTKGPKAPQVYTLPPPK 345  
QY 379 EEMTKNOVSLTCLVKGYRPSDIAVEENSGQPNKYKTPVLDSDGSLFLYSLKLTVDKS 438  
DB 346 EQWAKDKVSLTCLVDFPEPDIIVQWNGQPAENYKNTQPIMDTSGSVFYVSKLVNQRS 405  
QY 439 RWQGNVFCVSMHEALHNHYTKSLSPGK 470  
DB 406 NWEAGNTFTCSVLHGLEHNNHTEKNLSHSPGK 437

RESULT 6  
Q91205 ID Q91205 PRELIMINARY; PRT; 473 AA.  
AC Q91205  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DE HYPOTHETICAL 51.9 KDA PROTEIN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC010327; AH010327.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 56.6%; Score 1423.5; DB 11; Length 473;  
Best Local Similarity 57.1%; Pred. No. 4.2e-111;  
Matches 270; Conservative 74; Mismatches 114; Indels 15; Gaps 5;

QY 7 ILFLVATATGVHSQVLQVSGAELKPGASVKKSGAGYFTTSYMWQVRAQFQGLEW 66  
DB 7 LVLVLILKGVQCEVQLVSGGLVKGPGSRKLSCAASGFTFSDYGNHWHVRAQPEKLEW 66  
QY 67 MGEIDPSDSTYNNQKFGKATLVDTSTAYMELSLRSEDYAVYICARNRDYSNNWY 126  
DB 67 VAVINSGSTIYVADRVKGRFTISRDNAKNTLFLQMTLSRSEDYAVYICAREL----WL 121  
QY 127 --FDVWGQGLTVTVSSASTKGPSVFLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSG 184  
DB 122 RRIDYWGQGTITVSSAKTTPPSVPLAPGCGDTTSGSVTLGCLVKGYPESVTVTWSG 181

QY 185 ALTSGVHTFPVAVLQSSGLYSLSWTVVPSLSLGTQYICNVNHPKSNTPKVDKRVKPSK 244  
DB 182 SLSSVHTFPVAVLQ-SGLYTWSSSVTVPSWTSQVTCVVAHPASSTVVDKLEPSGPI 240  
QY 245 KT-HTCPCP-----CPAPELLGGPSVFLFPKPKDITLMSRTPEVTCVVDVSHEDPEVK 297  
DB 241 STINPCPCCKECHKCAPNLEGGPSVFIFFPNIKDLVMSLTLPKVTGVVDVSEDDPDVQ 300  
QY 298 FNVYVDGVEVHNKTKPREQYNSTYRVSVTLVHODWLNKGYCKVSNKALPAPIEK 357  
DB 301 ISFVNVNVEVHTAQTHREDYNTIRVSALPIQHODWMSGKEFKCKVNNKDLPSPIER 360  
QY 358 TISKAKGQRPQVYTLPPSREEMTKNOVSLTCLVKGYRPSDIAVEENSGQPNKYKTT 417  
DB 361 TISKIKGLVAPQVYTLPPPAEQLSRKDVSLTCLVGVGNPGDISVENTSNGHTENYKDT 420  
QY 418 PPVLDSDGSLFLYSLKLTVDKSRQGNVFCVSMHEALHNHYTKSLSPGK 470  
DB 421 APVLDSDGSLFYISKLDIKTSKEKTDSCNVRHEGLKNYLLKTTISRSPGK 473

RESULT 7  
Q95M34 ID Q95M34 PRELIMINARY; PRT; 337 AA.  
AC Q95M34  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE IMMUNOGLOBULIN GAMMA 1 HEAVY CHAIN CONSTANT REGION  
DE (FRAGMENT).  
GN IGHCL.  
OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_Taxid=9796;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wagner B.;  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98383416; PubMed=9717671;  
RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,  
RA Leibold W., Radbruch A.;  
RT "Organization of the equine immunoglobulin heavy chain constant region  
genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";  
RT Immunobiology 199;105-119(1998).  
DR EMBL; AJ300675; CAC44624.1; -.  
FT NON\_TER  
SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;

Query Match 50.2%; Score 1263.5; DB 6; Length 337;  
Best Local Similarity 68.9%; Pred. No. 6.9e-98;  
Matches 233; Conservative 44; Mismatches 52; Indels 9; Gaps 3;

QY 141 ASTKGPSVFLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSVHTFPVAVLQSS 200  
DB 1 ASTAPKRVFALAPCGCTTSDSTVALGCLVSGYFPEPVKVSWSGSLTSVHTFPVAVLQSS 60  
QY 201 GLYSLSWTVVPSLSLGTQYICNVNHPKSNTPKVDKRVKPEP-----KSCDKTHTCPCPA 254  
DB 61 GFYSLSWTVVPAWTSWTSETYICNVVHAASNFVKVDKRIEIPDNHQVKVCDMS-KCPKCPA 119  
QY 255 PELLGGSVFLFPKPKDITLMSRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKP 314  
DB 120 PELLGGSVFIFFPNPKDITLMSRTPEVTCVVDVSHEDPEVKFNWYMDGVEVHTATRP 179  
QY 315 REEQYNSTYRVSVTLVHODWLNKGYCKVSNKALPAPIEKTISKAKGQRPQVYTL 374  
DB 180 KEQFNSTYRVSVTLVHODWLNKGYCKVSNKALPAPIEKTITKGRSQEPQVYVL 239



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Qy 375 PPSREMTKNOVSLTCLVKGFPYSDIAVWESNGQP--ENNYKTPPVLDSDGSFFLYSK 432
Db 240 APHDELSKSVSTCLVKDFYPPPEINEMQSGNQPLETEYKSTTQAQODSDGSFYLYSK 299
Qy 433 LTVDKSRWQGNVFSVMSHEALHNHYTKSLSLSPGK 470
Db 300 LSVDRNRWQGGTTFTCGVMHEALHNHYTKQVSNRPGK 337

RESULT 8
Q96PQ8 ID Q96PQ8 PRELIMINARY; PRT; 701 AA.
AC Q96PQ8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.;
RT "targeting tissue factor on tumor vascular endothelial cells and tumor
RL cells for immunotherapy in mouse models of prostatic cancer.";
DR Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
DR EMBL: AF272774; AAK58686.1; -.
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;

Query Match 49.9%; Score 1257; DB 4; Length 701;
Best Local Similarity 99.1%; Pred. No. 6.9e-97;
Matches 230; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 239 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTHLISRPTVTCVVVDVSHEDPEVKF 298
Db 470 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTHLISRPTVTCVVVDVSHEDPEVKF 529
Qy 299 NWYVDGVEVHNAKTKPREEQYNTRYVSVLTVLHQDLNGKEYCKVSNKALPAPIEKT 358
Db 530 NWYVDGVEVHNAKTKPREEQYNTRYVSVLTVLHQDLNGKEYCKVSNKALPAPIEKT 589
Qy 359 ISKAKGQPREPQVYTLPPSRREMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 418
Db 590 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTP 649
Qy 419 PVLDSGSGFFLYSKLTVDKSRWQGNVFSVMSHEALHNHYTKSLSLSPGK 470
Db 650 PVLDSGSGFFLYSKLTVDKSRWQGNVFSVMSHEALHNHYTKSLSLSPGK 701

RESULT 9
Q921K1 ID Q921K1 PRELIMINARY; PRT; 278 AA.
AC Q921K1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE UNKNOWN (PROTEIN FOR MGC:18977).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RS SEQUENCE FROM N.A.
RX Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC012207; AAK12207.1; -.
SQ SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;
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Query Match 39.1%; Score 983; DB 11; Length 278;
Best Local Similarity 67.1%; Pred. No. 1.8e-74;
Matches 186; Conservative 33; Mismatches 50; Indels 8; Gaps 3;

Qy 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQVVRQAP 60
Db 1 MGWNCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWKORR 60
Qy 61 GQGLEWMEIDPSDSTNYNOKFKGKATLTDVTSTSTAYMELSSLRSEDTAVYYCARNRD 120
Db 61 GQGLEWIGNINPNSGCTNYNEKFNKATLAVDKSSSTVYMQLSLTSSEDAVYYCTRGV 120
Qy 121 YSNWYFDVWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVVS 180
Db 121 Y-DDVYFDVWGAGTTVTSSAKTTAPSVYPLAPVCGGTGSSVTLGCLVKGYFPEPTILT 179
Qy 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHRKPSNTKYDKRVEP 240
Db 180 WNSGSLSGVHTFPALLQ-SGLYTLSSSVTVTSNTPWPSQTITCNVAHPASSTKYDKKIEP 238
Qy 241 K-----SCKDTHTCPPCPAPPELLGGPSVFLFPPPKP 271
Db 239 RVPITONPCPLKECPCAAPDLLGGPSVFIFPPPSR 275

RESULT 10
Q96GA6 ID Q96GA6 PRELIMINARY; PRT; 614 AA.
AC Q96GA6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE UNKNOWN (PROTEIN FOR MGC:15420).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RX TISSUE=PRIMARY B-CELLS FROM TONSILS;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC009851; AAK09851.1; -.
SQ SEQUENCE 614 AA; 67921 MW; 55EF36E77AA9BBB CRC64;

Query Match 37.0%; Score 930.5; DB 4; Length 614;
Best Local Similarity 36.7%; Pred. No. 1.4e-69;
Matches 212; Conservative 84; Mismatches 166; Indels 115; Gaps 17;

Qy 1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQVVRQAP 60
Db 1 MDWTWRIILFLVAAATDAYSQMLVQSGAEVKKPGASVKVSCKASGYTFTSYLHWVRQAP 60
Qy 61 GQGLEWMEIDPSDSTNYNOKFKGKATLTDVTSTSTAYMELSSLRSEDTAVYYCARNRD 120
Db 61 GQALEWGWITPFNGNTNYAQKQFQDRVTITRDSMNTAYMELSSLRSEDTAYYCARG-- 118
Qy 121 YSNW--YFDVWGQGLTVTVSSASTKGPSVFPLAPSSKSTSG-GTAALGCLVKDYFPEPV 177
Db 119 YSSMDDADFIWQGTQVTVTVSSGASAPTLFPLVSCENSPSDTSSVAVGCLAQDLPSI 178
Qy 178 TVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVTVTPVPSSSL--GTQTY-ICNVNHRKPSN- 231
Db 179 TFSMKYKNSDISSTRGFPVLR-GGKYAATSOVLLPSKDVMOGQDEHVCKVQHPGNK 237
Qy 232 -----TKVDRKVEPKS-----CDKTHTCP----- 250
Db 238 EKNVPLPVIAELPPKVSFVFPVRDGFNGPRKRKLCICATGFSRQIOVSWLREGKQVGS 297
Qy 251 -----PCPAPELLGGPS----- 262
Db 298 GVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRLGLTFQONASSMCVPD 357
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Qy	395	FYPSPDIAVESNQ--PENNYKTPPVLD-SDG--SFFLYSKLTVDKRWQQGNVFSCS	449
Dd	402	FSPKDLVLRQLQSGLPREKYLTWASRQPSSQGTTFVAVTSILRVAAEDKKGDTFSCM	461
Qy	450	VMHEALHNHYTKSLSLSPCK	470
Dd	462	VGHEALPLAFTQTETIDRLAGK	482
RESULT 13			
Q91WT1	ID	Q91WT1 PRELIMINARY;	PRT; 481 AA.
AC	Q91WL1		
DT	01-DEC-2001	(TEMBLrel. 19, Created)	
DF	01-DEC-2001	(TEMBLrel. 19, Last sequence update)	
DT	01-DEC-2001	(TEMBLrel. 19, Last annotation update)	
DE	HYPOTHETICAL 52.1 KDA PROTEIN.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
ON	NCB1_TaxId=10090;		
RX	[1]	SEQUENCE FROM N.A.	
RC	TISSUE=COLON;		
RA	Strausberg R.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; BC013490; AAH13490.1; -;		
KQ	Hypothetical protein.		
SW	SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;		

Query Match	33.18;	Score	833.5;	DB	11;	Length	481;
Best Local Similarity	40.24;	Pred.	No. 1.4e-61;				
Matches	194;	Conservative	73;	Mismatches	184;	Indels	31;
Gaps	15;						
Qy	1	MGWSCIIILFVATATGVHSSOVQLVQSGAEVKKPKASVKVSKASGYFTSYWMOHWQCAP	60				
Db	1	MGWRWIFLLUSGAVOCQVQLQSGPELVKPKASVKISKASGYFTSYIIHWKQRP	60				
Qy	61	GGGLEWAGEIDPDSYTNYNQKFKGKATLTVDTSTJATMELSSLRSDTAVVYCARNRD	120				
Db	61	GQGLVWIGWIYPGDNTKYNEKFKGKTLTADKSSSTAYMFLSSLTSEDSAVFYCTR---	117				
Qy	121	YSNNWYEDVWGQGLTVTVSSASTKGPVFPAPASKSTSGGTAALGCLVKDYFPE-PVTV	179				
Db	118	-GGGAEDYWGQGLTVTVSSPAPREPTIPLT-EPQALSSDPVIGLIIHDYFPFGTMNV	175				
Qy	180	SNWSGALTSGVHTTTPAVLQSSGLYSLGSVTVTPSSSLGT-QTYICNVNHHKSNTKVDKRV	238				
Db	176	TWGSKGDDITVNEPPLAASGRVTMSQLTFLPAVEGEGESVSKCSQVH-DSNPVQELNV	234				
Qy	239	EPKSCDKTHTCPPCPAPPELLGGSVFVFPFKPKDRLISRPTVEVTVVVDVSHEDPE-VK	297				
Db	235	NCPGICSPPTTPPPSCQ---PSLSLQRPALD-LLLGSDASITCTLNL- RDPEGAV	287				
Qy	298	FNWTVDGEVINAKTKPREQYNT---YRVVSVLTVLHQDLWGKEYKCKVSKNALPAP	354				
Db	288	FTW-----EPSTGDAVQKKAVQSCGYSYSSVLLPGCAERNWSGASGFVTHPESDT-	341				
Qy	355	IEKTIKAKGQRPPEQVVTLPSPREMTKNO-VSLTCLVKGFYPSDTLAVESNQO---P	410				
Db	342	LTGIIAKVTYVTFPPQVHLLPPSEELALNELSVLTCILVRAFNPKEVLRVRLHNGEELSP	401				
Qy	411	ENNYKTTTPPVLDSDG--SFFLYSKLTVDKSRWQOQNVFSCSMHEALHNHVTQKSLSP	468				
Db	402	ESYLVFPELKEPGEGATYLTYSVLVRSAEIWKOGDQYSCWVGHEALPMNFTQKIDELS	461				
Qy	469	GK	470				
Db	462	GK	463				

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RESULT 14
Q91WRI ID Q91WRI PRELIMINARY; PRT; 488 AA.
AC Q91WRI;
DT 01-DEC-2001 (TtEMBLrel. 19, Created)
DT 01-DEC-2001 (TtEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TtEMBLrel. 19, Last annotation update)
DE DE HYPOTHETICAL 53.0 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013539; AH13539.1; -
KW Hypothetical protein.
SQ SEQUENCE 488 AA; 52964 MW; FL2068460B400B9D CRC64;

Query Match 32.5%; Score 817; DB 11; Length 488;
Best Local Similarity 39.2%; Pred. No. 3.4e-60;
Matches 191; Conservative 85; Mismatches 177; Indels 34; Gaps

Qy 1 MGNSCIILFLVATATGVSQVQLVQSGAEVKKPKGASVKYKSCAKSGYTFTSYNMOWYRQAP 60
Db 1 MGNNWIFELLSGTAGIYSEVQLQSGPELVKPGASVKLSCKASGYTITDYVYVNWYKQSH 60

Qy 61 GQGLEWGEIDPSDSTYNQKFKGKATLVTDVSTSTAYMELSSLRSDETAYVYICARNRD 120
Db 61 GKSLEWGDINPYNGGTSYNQKFKGKATLVTDKSSSIAYMQLNNLTSDDSAVYICARGPV 120

Qy 121 YSNWNYF----DWVGQGLTVTVSSASTKGSVFPLAPSSKSTSGCTAALGCLVKDYFPE 175
Db 121 YYS--YFSYDRGDYWGQGLTVTVSAEPAREPTIYPLT-PPQALSSDPVIIGLIHDYFPS 177

Qy 176 -PVTVSNNGALTSGVHTFFAVILQSGSLYSLSSVWTVVPSSSLGT-QTYICNVNHNKPSNFK 233
Db 178 GTMNVTWGKSGKDITTVNFFPALASGGRYTMSSQLTLPAVECPGEGSVKCSVQH-DSNPV 236

Qy 234 VDKRVPKSCDKHTCCPPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVYVVDVSHED 293
Db 237 QELNVNCGICSPPTTPPPSPSCQ----PSLSLGRPALED-LLLGSDASITCTLNLGL--RD 289

Qy 294 PE-VKFNWYVDGEVHNAKTKPREQYNSTP---YRVVSVLTVLHDQNLNGKEYVKCKVSNK 349
Db 290 PEGAVFTW-----EPSTGKDAVKAVQNGCGCYSSVSLPFGCAERWNGSGASPKCVTHP 344

Qy 350 ALPAIEKTIKAKGQPREPQVTLPPSRREMTKQ-VSLTCLVKGFPYPSDIAVESNG 408
Db 345 ESDR-LNGTIKTVNTFPQVHLLPPPSSEALNELVSLTCLVRAFNKPEVLVRLHGN 403

Qy 409 Q---PENNYKTPVLVDSGDG--SEFFLYSKLTVDKSRWQNGQVETSCSMHEALHNHYTQKS 463
Db 404 EELSPESYLFEPLKEGEGATTYLVTSVLRVSAEINWKQGDQYSCMWGHEALPMNFTQKT 463

Qy 464 LSLSPGK 470
Db 464 IDRLSGK 470

RESULT 15
Q96BB9 ID Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9;
DT 01-DEC-2001 (TtEMBLrel. 19, Created)
DT 01-DEC-2001 (TtEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TtEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 65.0 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 15:15:40 ; Search time 230.21 Seconds  
(without alignments)  
226.770 Million cell updates/sec

Title: US-09-499-662-157  
Perfect score: 2518  
Sequence: 1 MWSCIIILFLVATATGVHSQ.....MHEALNHHTQKSLSPQK 470

Scoring table:  
BLOSUM62DX  
Gapop 10.0 , Capext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_032802:\*  
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2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT:\*  
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22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2518	100.0	470	21	Humanised HFE7A de
2	2498	99.2	470	19	Anti-Fas humanised
3	2498	99.2	470	21	Humanised anti-Fas
4	2498	99.2	470	21	Humanised HFE7A de
5	2498	99.2	470	21	Humanised anti-Fas
6	2497	99.2	470	21	Humanised anti-Fas
7	2495	99.1	470	21	Humanised anti-Fas
8	2485	98.7	470	19	Anti-Fas humanised
9	2485	98.7	470	21	Humanised anti-Fas
10	2485	98.7	470	21	Humanised HFE7A de
11	2363.5	93.9	731	22	Humanised HMFG-1 h

12	2363.5	93.9	741	22	AAM52159
13	2358.5	93.7	729	22	AAM52158
14	2358.5	93.7	739	22	Humanised HMFG-1 h
15	2352.5	93.4	730	22	AAM52161
16	2352.5	93.4	740	22	Humanised HMFG-1 h
17	2291.5	91.0	465	22	Humanised HMFG-1 h
18	2289	90.9	652	19	Humanised 323/A3 (
19	2286.5	90.8	464	22	Heavy chain of hma
20	2274	90.3	470	21	Humanised 323/A3 (
21	2269	90.1	476	20	A dimeric anti-CD2
22	2264	89.9	466	22	Monoclonal antibody
23	2259.5	89.7	481	13	Chimeric 2403 IgG
24	2238	88.9	472	20	Sequence of anti-bo
25	2238	88.9	476	14	Antibody D heavy c
26	2230	88.6	449	14	Completely humani
27	2230	88.6	449	19	Amino acid sequenc
28	2219.5	88.1	583	22	Ganglioside GM2 an
29	2210.5	87.8	452	20	Recombinant immuno
30	2210.5	87.8	452	21	Humanised anti-IL-
31	2210.5	87.8	452	21	Humanised anti-IL-
32	2207.5	87.7	467	22	Human immune syste
33	2201.5	87.4	452	19	Anti-IL-8 humanise
34	2193	87.1	474	22	Human novel protei
35	2192.5	87.1	473	22	Human type antihum
36	2190	87.0	472	20	Chimeric mouse/hum
37	2189.5	87.0	473	22	Human type antihum
38	2184.5	86.8	473	22	Human type antihum
39	2183.5	86.7	475	22	Amino acid sequenc
40	2177.5	86.5	473	22	Human type antihum
41	2172	86.3	468	20	D9D10 heavy chain
42	2172	86.3	711	20	MoAb11 fusion pro
43	2171	86.2	592	22	Amino acid sequenc
44	2168	86.1	595	20	Anti-5T4 single ch
45	2161	85.8	470	13	Reshaped CAMPATH-1

ALIGNMENTS

RESULT 1

AAW90936

ID AAW90936 standard; Protein; 470 AA.

AC AAW90936;

DT 08-AUG-2000 (first entry)

DE Humanised HFE7A designed heavy chain HHH type protein.

XX Fas; antibody: human; anti-inflammatory; anti-anemic; antidiabetic;  
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;  
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
KW nephrotropic; antifertility; neuroprotective; antiarteriosclerotic;  
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
KW Sjogren's syndrome; rheumatoid arthritis; graft versus host disease;  
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

XX Synthetic.

XX EP990663-A2.

PD 05-APR-2000.

XX 29-SEP-1999; 99EP-0307711.

PR 30-SEP-1998; 98JP-0276881.

PR 30-SEP-1998; 98JP-0276882.

PA (SANY ) SANKYO CO LTD.

Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
 WPI: 2000-258930/23.  
 N-PSDB; AAL11655.  
 New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems -  
 Claim 2: Page 188-189; 263pp; English.  
 This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral, immunomodulatory, dermatological, immunosuppressive, thymomimetic, antirheumatic, nephrotropic, antiinfertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody HFE7A heavy chain construct HHH type which is described in the method of the invention.  
 Sequence 470 AA:

Query Match 100.0%; Score 2518; DB 21; Length 470;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-144;  
 Matches 470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 361 kagqgpreqvvtlppsreemtknqvslclvkgfypsdiavewesngqpennkttppv 420  
 QY 421 LQSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHHYTKQSLSPGK 470  
 Db 421 LQSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHHYTKQSLSPGK 470  
 RESULT 2  
 AAW83037  
 ID AAW83037 standard; Protein; 470 AA.  
 XX  
 AC AAW83037;  
 XX 15-MAR-1999 (first entry)  
 DE Anti-Fas humanised antibody HFE7A heavy chain.  
 XX  
 KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;  
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;  
 KW systemic lupus erythematosus; graft versus host disease;  
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;  
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;  
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;  
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;  
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;  
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;  
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;  
 KW transplant rejection; therapy.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /label= Sig\_peptide  
 FT Protein 20..470  
 FT /label= Mat\_protein  
 FT Region 20..140  
 FT /label= Variable  
 FT Region 141..464  
 FT /label= Constant  
 FT Region 50..54  
 FT /label= CDR\_H1  
 FT /note= "claim 9"  
 FT Region 69..84  
 FT /label= CDR\_H2  
 FT /note= "claim 9"  
 FT Region 118..129  
 FT /label= CDR\_H3  
 FT /note= "claim 9"  
 XX AU9859701-A.  
 PD 08-OCT-1998.  
 XX 30-MAR-1998; 98AU-0059701.  
 PF 08-OCT-1997; 97JP-0276064.  
 PR 01-APR-1997; 97JP-0082953.  
 PR 25-JUN-1997; 97JP-0169088.  
 XX (SANY ) SANKYO CO LTD.  
 XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;  
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;  
 XX WPI: 1998-543440/47.  
 DR N-PSDB; AAV70080.  
 XX New antibodies and proteins bind conserved epitope of Fas antigen -  
 PT used to evaluate drugs in animal models and to treat Fas-associated  
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,  
 PT myocarditis, hepatitis and AIDS

```
XX Claim 22; Page 225-227; 292pp; English.
XX This is the amino acid sequence of the HV type humanised heavy
CC chain of murine anti-human Fas monoclonal antibody HFE7A. It
CC includes humanising R44G and A76T amino acid substitutions that are
CC are conserved in the human IgG heavy chain. Host Escherichia coli
CC pGHPDHV3 SANK 70298 harbors plasmid pGHPDHV3 carrying a fusion
CC fragment of the humanised HV type HFE7A heavy chain and DNA
CC encoding human IgG1 constant region (see AAV70080), and is deposited
CC as FERM BP-6273 (claimed). The invention provides methods for
CC producing humanised antibodies by culturing host cells. Humanised
CC versions of HFE7A (see AAN83031-37), like native HFE7A, are capable
CC of inducing apoptosis in abnormal cells expressing Fas, and of
CC inhibiting Fas-induced apoptosis in normal cells. The humanised
CC antibodies are used to evaluate, in animal models, treatments of
CC diseases that involve Fas/Fas ligand interactions, and also to
CC treat such diseases, including autoimmune disease (e.g. systemic
CC lupus erythematosus, Hashimoto's disease, graft versus host disease,
CC Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,
CC Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,
CC autoimmune haemolytic anaemia, sterility, myasthenia gravis,
CC multiple scl rosis, Basedow's disease, thrombopenia purpura and
CC insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
XX
SQ Sequence 470 AA;
Query Match 99.2%; Score 2498; DB 19; Length 470;
Best Local Similarity 98.9%; Pred. No. 2.3e-143;
Matches 465; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MGWSCIIILFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVRQAP 60
Db 1 MGWSCIIILFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVRQAP 60
Qy 61 GQGLEWMGEIDPSDSTYNQKFKGRVITRDSTSTAYMELSLRSEDSTAVYICARNRD 120
Db 61 GQGLEWMGEIDPSDSTYNQKFKGKATLTVDSTSTAYMELSLRSEDSTAVYICARNRD 120
Qy 121 YSNWNYFDVWGEGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
Db 121 YSNWNYFDVWGEGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
Qy 121 YSNWNYFDVWGEGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
Db 121 YSNWNYFDVWGEGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
Qy 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVYTPSSSLGTQTYICNVNHNKPSNTKVDKRVPE 240
Db 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVYTPSSSLGTQTYICNVNHNKPSNTKVDKRVPE 240
Qy 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVYTPSSSLGTQTYICNVNHNKPSNTKVDKRVPE 240
Db 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVYTPSSSLGTQTYICNVNHNKPSNTKVDKRVPE 240
Qy 241 KSCDKTHTCPPCPAPELGGPSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNW 300
Db 241 KSCDKTHTCPPCPAPELGGPSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNW 300
Qy 301 YVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
Db 301 YVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
Qy 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
Db 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
Qy 421 LDSGSEFFLYSKLTVDKSRWQQGQNVFSCSVNHEALHNHYTOKSLSLSPGK 470
Db 421 LDSGSEFFLYSKLTVDKSRWQQGQNVFSCSVNHEALHNHYTOKSLSLSPGK 470
RESULT 3
AAB14779
ID AAB14779 standard; Protein; 470 AA.
XX
AC AAB14779;
XX
```

```
DT 24-NOV-2000 (first entry)
DE Humanised anti-Fas antibody heavy chain, SEQ ID NO:117.
XX
XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
KW murine; humanised antibody; complementarity determining region; CDR;
KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancyelophthisis;
KW hepatitis; AIDS; graft rejection; heavy chain.
XX
OS Chimeric - Mus musculus.
OS Chimeric - Homo sapiens.
XX
XX JP2000169393-A.
XX 20-JUN-2000.
XX
XX 30-SEP-1999; 99JP-0278301.
XX
XX 30-SEP-1998; 98JP-0276883.
XX (SANY ) SANKYO CO LTD.
XX
XX WPI; 2000-485645/43.
XX N-PSDB; AAA72184.
XX
XX Preventive or treating agent for the diseases caused by an abnormality
PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
PT anti-Fas antibody -
XX
XX Claim 21; Page 108-109; 139pp; Japanese.
XX
XX The invention relates to compositions for the prevention or treatment
CC or diseases caused by an abnormality in the Fas/Fas ligand system
CC containing an anti-Fas antibody as the active component. The anti-Fas
CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
CC or a humanised version of HFE7A containing identical CDRs
CC (complementarity determining regions) to antibody HFE7A. Via its
CC interaction with Fas, the antibody of the invention acts as a modulator
CC of apoptosis. The compositions of the invention may therefore be used
CC the treatment or prevention of conditions such as autoimmune diseases,
CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
CC and organ graft rejection. Sequences AAB14775-B14776 and AAB14779
CC represent the heavy chains (or fragments thereof) of various humanised
CC HFE7A-derived anti-Fas antibodies.
XX
SQ Sequence 470 AA;
Query Match 99.2%; Score 2498; DB 21; Length 470;
Best Local Similarity 98.9%; Pred. No. 2.3e-143;
Matches 465; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MGWSCIIILFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVRQAP 60
Db 1 MGWSCIIILFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVRQAP 60
Qy 61 GQGLEWMGEIDPSDSTYNQKFKGRVITRDSTSTAYMELSLRSEDSTAVYICARNRD 120
Db 61 GQGLEWMGEIDPSDSTYNQKFKGKATLTVDSTSTAYMELSLRSEDSTAVYICARNRD 120
Qy 121 YSNWNYFDVWGEGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
Db 121 YSNWNYFDVWGEGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
Qy 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVYTPSSSLGTQTYICNVNHNKPSNTKVDKRVPE 240
Db 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVYTPSSSLGTQTYICNVNHNKPSNTKVDKRVPE 240
Qy 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVYTPSSSLGTQTYICNVNHNKPSNTKVDKRVPE 240
Db 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVYTPSSSLGTQTYICNVNHNKPSNTKVDKRVPE 240
Qy 241 KSCDKTHTCPPCPAPELGGPSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNW 300
Db 241 KSCDKTHTCPPCPAPELGGPSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNW 300
```







CC apoptosis in cells with a normal system, by inhibiting binding between  
CC Fas and its ligand. The products of the invention have anti-inflammatory,  
CC anti-anemic, anti-diabetic, anti-allergic, anti-arthritis, antiviral,  
CC immunomodulatory, dermatological, immunosuppressive, thymimetic,  
CC anti-rheumatic, nephrotropic, anti-fertility, neuroprotective,  
CC anti-arteriosclerotic, cardiant and hepatropic activity. (I) induce  
CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
CC inhibition of ligand binding. (I) are used to treat and/or prevent  
CC diseases associated with the Fas/Fas ligand system, especially systemic  
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
CC cells. They bind to both human and murine Fas, so can be evaluated in  
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
CC the native ligand, do not induce liver disease, and have reduced risk of  
CC inducing a human anti-murine antibody response. This sequence represents  
CC a humanised anti-Fas antibody heavy chain construct designated Heu 2  
CC which is described in the method of the invention.

XX  
SQ Sequence 470 AA;

Query Match 99.2%; Score 2497; DB 21; Length 470;  
Best Local Similarity 98.9%; Pred. No. 2.6e-143;  
Matches 465; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGWSCIILFVATATGVHQSQVQLVQSGAEVKKPGASVKYCKRSGSYFTSYWQWVROAP 60  
DB 1 mgwscililfvatatgvhqsqvlvsgaevkkgpgasvkysckasgyftfsywmqwkqap 60  
QY 61 GQGLEWMEIDPSDSTYNQKFGKVTITRTSTSTAYMELSSRSEDVAVYYCARNRD 120  
DB 61 gqglewmeidpsdsytnynqkfgkatitvdtststaymelslrsedtavyyccarnrd 120  
QY 121 YSNWYFDVWGSGTLVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVVS 180  
DB 121 ysnwfydvwggtlvtvssastkgpsvflapsskstsggtaalgclvkdyfpeptvvs 180  
QY 181 WNSGALTSVGHVFPVQLQSGSLYSLSSVYVTPVSSSLGTQTYICNVNHKPSNTKVDKRVP 240  
DB 181 wnsгалtsvghvfpavlqsgslslssvvtvpvssslgtqtyicnvnhkpsntkvdkrvp 240  
QY 241 KSCDTHTCPCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVYVDSHEDPEVKFNW 300  
DB 241 kscdthtcpcpcapellggpsvflfppkpkdtlmisrtpevtcvvyvdsvedpevkfnw 300  
QY 301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVTLQDWLNKGKEYCKVSKNALKAPTEKTIS 360  
DB 301 yvdgvevhnaaktpreeqynstyrvvsvltvtlqdwlngkeyckvsknalkapiekttis 360  
QY 361 KAKGQPREPQVYTLPPSRREMTKNQVSLTCLVKGFVPSDIAVEWESNGQPENNYKTPPV 420  
DB 361 kagqprepqvylppsrreemtknqvsltcclvkgyfypsdiavewesngqpennnykttppv 420  
QY 421 LDSGDSFFLYSKLTVDKSRWQQGNFVSCSVMHAEALHNHYTKQSLSPGK 470  
DB 421 ldsdgsfflyskltvdksrwqqgnvfscsvmhaealhnhytkqslslspgk 470

RESULT 7

AAW90933  
ID AAW90933 standard; Protein; 470 AA.

XX AAW90933;

XX 08-AUG-2000 (first entry)

XX

DE Humanised anti-Fas designed heavy chain Heu 1 protein.  
XX Fas; antibody; human; anti-inflammatory; anti-anemic; anti-diabetic;  
XX anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;  
XX dermatological; immunosuppressive; thymimetic; anti-rheumatic; anti-Fas;  
XX nephrotropic; anti-fertility; neuroprotective; anti-arteriosclerotic;  
XX Hashimoto disease; rheumatoid arthritis; systemic lupus erythematosus;  
XX Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;  
XX Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
XX multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
XX insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
XX cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
OS Synthetic.  
XX EP990663-A2.  
XX 05-APR-2000.  
XX 29-SEP-1999; 99EP-0307711.  
XX 30-SEP-1998; 98JP-0276881.  
XX 30-SEP-1998; 98JP-0276882.  
XX (SANY ) SANKYO CO LTD.  
XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
XX WPI; 2000-258930/23.  
XX N-PSDB; AAA11644.  
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
XX inflammatory or autoimmune disease, induces apoptosis selectively in  
XX cells with abnormal Fas-Fas ligand systems -  
XX Claim 2; Page 169-170; 263pp; English.

XX This invention describes a novel humanized anti-Fas antibody-like  
XX molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
XX ligand system, by binding to Fas on the cell surface, and prevents  
XX apoptosis in cells with a normal system, by inhibiting binding between  
XX Fas and its ligand. The products of the invention have anti-inflammatory,  
XX anti-anemic, anti-diabetic, anti-allergic, anti-arthritis, antiviral,  
XX immunomodulatory, dermatological, immunosuppressive, thymimetic,  
XX anti-rheumatic, nephrotropic, anti-fertility, neuroprotective,  
XX anti-arteriosclerotic, cardiant and hepatropic activity. (I) induce  
XX apoptosis by binding to cell surface Fas or inhibit it by competitive  
XX inhibition of ligand binding. (I) are used to treat and/or prevent  
XX diseases associated with the Fas/Fas ligand system, especially systemic  
XX lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
XX versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
XX anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
XX disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
XX multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
XX dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
XX cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
XX (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
XX inhibit apoptosis in normal cells but selectively induce it in abnormal  
XX cells. They bind to both human and murine Fas, so can be evaluated in  
XX murine disease models. (I) act on the active site of Fas, i.e. they mimic  
XX the native ligand, do not induce liver disease, and have reduced risk of  
XX inducing a human anti-murine antibody response. This sequence represents  
XX a humanised anti-Fas antibody heavy chain construct designated Heu 1  
XX which is described in the method of the invention.

SQ Sequence 470 AA;

Query Match 99.1%; Score 2495; DB 21; Length 470;  
Best Local Similarity 98.7%; Pred. No. 3.5e-143;  
Matches 464; Conservative 4; Mismatches 2; Indels 0; Gaps 0;



QY 241 KSCDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300  
Db 241 kscdkthtccpccpapelggpsvflfpkpdkdtlmsrtpevtcvvvdvshedpevkfnw 300  
QY 301 YDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKTIS 360  
Db 301 ydgvgevhnaktkpreeqynstyrvvsvltvlhqdmlngkeyckvsnkalpapiektis 360  
QY 361 KAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420  
Db 361 kagqgprepqvyltppsrreemtknqvsltcclvkgyfypsdiavewesngqpennnykttppv 420  
QY 421 LDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470  
Db 421 ldsdgsfflyskltvdksrwqgnvfscsvmhealhnhytqkslsispgk 470

RESULT 9  
AAB14776  
ID AAB14776 standard; Protein; 470 AA.  
XX  
AC AAB14776;  
XX  
DT 24-NOV-2000 (first entry)  
XX  
DE Humanised anti-Fas antibody heavy chain, SEQ ID NO:89.  
XX  
KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;  
KW murine; humanised antibody; complementarity determining region; CDR;  
KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;  
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;  
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;  
KW hepatitis; AIDS; graft rejection; heavy chain.  
XX  
OS Chimeric - Mus musculus.  
OS Chimeric - Homo sapiens.  
XX  
PN JP2000169393-A.  
XX  
PD 20-JUN-2000.  
XX  
PF 30-SEP-1999; 99JP-0278301.  
XX  
PR 30-SEP-1998; 98JP-0276883.  
XX  
PA (SANY ) SANKYO CO LTD.  
XX  
DR WPI; 2000-485645/43.  
DR N-PSDB; AAA72159.  
XX  
PT Preventive or treating agent for the diseases caused by an abnormality  
PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains  
PT anti-Fas antibody -  
XX  
PS Claim 21; Page 95-96; 139pp; Japanese.  
XX  
CC The invention relates to compositions for the prevention or treatment  
CC of diseases caused by an abnormality in the Fas/Fas ligand system  
CC containing an anti-Fas antibody as the active component. The anti-Fas  
CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,  
CC or a humanised version of HFE7A containing identical CDRs  
CC (complementarity determining regions) to antibody HFE7A. Via its  
CC interaction with Fas, the antibody of the invention acts as a modulator  
CC of apoptosis. The compositions of the invention may therefore be used in  
CC the treatment or prevention of conditions such as autoimmune diseases,  
CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,  
CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS  
CC and organ graft rejection. Sequences AAB14775-B14776 and AAB14779  
CC represent the heavy chains (or fragments thereof) of various humanised  
CC HFE7A-derived anti-Fas antibodies.  
XX  
SQ Sequence 470 AA;

Query Match 98.7%; Score 2485; DB 21; Length 470;  
Best Local Similarity 98.5%; Pred. No. 1.4e-142;  
Matches 463; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MGWSCIIILFLVATATGVHSQVLVQSGAEVKKPGASVKVSCKASGVTFTSYWQMQRQAP 60  
Db 1 mgwsciiilflvatatgvhsqvlvqsgaevkkpgasvkvsckasgytftsywmqmrqap 60  
QY 61 GQGLEWMEIDPSDSTNNYKQKGRVITRDTSTSTAYMELSLRSEDVAVYCARND 120  
Db 61 gqrlewmgeidpsdstnnynqkfgkatltvdtstastaymelslrsedvavycarnrd 120  
QY 121 YSNWYFDVWGEGTLTVSSASTKGPSVFPLAPSSKSTSGTAALGCLVKDYPEPEPTVS 180  
Db 121 ysnwyfdvwgegtltvssastkgpsvfplapsskstsgttaalgclvkdyppeptvs 180  
QY 181 WNSGALTSGVHTFPAVLQSGGLYSLSSVTPVPSSTSGTQYICNVNHPKSTNTKDKRVEP 240  
Db 181 wnsгалtsgvhtfpavllqsgglyslssvtpvpsstsgtqyicnvnhkpsntkdkrvrep 240  
QY 241 KSCDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300  
Db 241 kscdkthtccpccpapelggpsvflfpkpdkdtlmsrtpevtcvvvdvshedpevkfnw 300  
QY 301 YDGVGVHNAKTKPREEQYNSTYRVVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKTIS 360  
Db 301 ydgvgevhnaktkpreeqynstyrvvsvltvlhqdmlngkeyckvsnkalpapiektis 360  
QY 361 KAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420  
Db 361 kagqgprepqvyltppsrreemtknqvsltcclvkgyfypsdiavewesngqpennnykttppv 420  
QY 421 LDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470  
Db 421 ldsdgsfflyskltvdksrwqgnvfscsvmhealhnhytqkslsispgk 470

RESULT 10  
AAW90926  
ID AAW90926 standard; Protein; 470 AA.  
XX  
AC AAW90926;  
XX  
DT 08-AUG-2000 (first entry)  
XX  
DE Humanised HFE7A designed heavy chain protein.  
XX  
KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;  
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;  
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;  
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;  
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;  
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;  
KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;  
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;  
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;  
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;  
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.  
XX  
OS Synthetic.  
XX  
PN EP990663-A2.  
XX  
PD 05-APR-2000.  
XX  
PF 29-SEP-1999; 99EP-0307711.  
XX  
PR 30-SEP-1998; 98JP-0276881.  
PR 30-SEP-1998; 98JP-0276882.  
XX  
PA (SANY ) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;  
PI WPI; 2000-258930/23.  
DR N-PSDB; AAA11597.  
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.  
PT inflammatory or autoimmune disease, induces apoptosis selectively in  
PT cells with abnormal Fas-Fas ligand systems -  
XX Example reference 15; Page 134-136; 263pp; English.  
XX This invention describes a novel humanized anti-Fas antibody-like  
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas  
CC ligand system, by binding to Fas on the cell surface, and prevents  
CC apoptosis in cells with a normal system, by inhibiting binding between  
CC Fas and its ligand. The products of the invention have anti-inflammatory,  
CC anti-anemic, antididiabetic, anti-allergic, anti-arthritis, antiviral,  
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,  
CC antirheumatic, nephrotropic, antifertility, neuroprotective,  
CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce  
CC apoptosis by binding to cell surface Fas or inhibit it by competitive  
CC inhibition of ligand binding. (I) are used to treat and/or prevent  
CC diseases associated with the Fas/Fas ligand system, especially systemic  
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft  
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic  
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's  
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin  
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,  
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral  
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively  
CC inhibit apoptosis in normal cells but selectively induce it in abnormal  
CC cells. They bind to both human and murine Fas, so can be evaluated in  
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic  
CC the native ligand, do not induce liver disease, and have reduced risk of  
CC inducing a human anti-murine antibody response. This sequence represents  
CC a humanised anti-Fas antibody HFE7A designed heavy chain which is used in  
CC the method described in the invention.  
XX SQ Sequence 470 AA;

Query Match 98.7%; Score 2485; DB 21; Length 470;  
Best Local Similarity 98.5%; Pred. No. 1.4e-142;  
Matches 463; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MGWSCIILFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCKASGYFTSYMMQWVRQAP 60  
DB 1 mgwsciilflvatatgvhsqvlvqsgaevkpgasvkvsckasgyftsymmqwvkqap 60  
QY 61 GQGLEWMGEIDPDSYNYNOKFKGRVTITRTDTSTAYMELSLRSEDATVYYCARNRD 120  
DB 61 gqglewmgeidpdsytnynokfgrvttitrtdstaymelslrsedatvyycarnrd 120  
QY 121 YSNWNYFDVWGEGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180  
DB 121 ysnwnyfdvwmgegltlvtvssastkgpsvfplapsskstsggtaalgclvkdypfepvtvs 180  
QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVWTVPSSSLGTQYICNVNHNKPSNTKVDKRVPE 240  
DB 181 wnsгалтsgvhtfpavllqssglyslssvwtvpssslgtqyicnvnhnkpsntkvdkrvpe 240  
QY 241 KSCDKHTCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVYDVSHEDPEVKFNW 300  
DB 241 kscdkhtccpcpapelggpsvflfppkpkdtlmisrtpevtcvvdyshedpevkfnw 300  
QY 301 YVDGVEVHNARTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360  
DB 301 yvdgvevhnartkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektis 360  
QY 361 KAGQPREPQVYTLPPSREEMTKNQVSLTCLIVKGFPYSDIAVEWESNGQPENNYKTTTPPV 420  
DB 361 kagqprepqvylppspreemtknqvsltclivkgfpydsiavewesngqpennykttppv 420

DB 361 kagqprepqvylppspreemtknqvsltclivkgfpydsiavewesngqpennykttppv 420  
QY 421 LDSGSEFLYSLKLVDRKSRWQGNVFCVSMHEALHNHYTQKSLSPGK 470  
DB 421 ldsqgsfllyskltvdrksrwqgnvfscvsmhealhnhytqkslspsgk 470  
RESULT 11  
AAM52156  
ID AAM52156 standard; Protein; 731 AA.  
XX AC AAM52156;  
XX DT 05-FEB-2002 (first entry)  
XX DE Humanised HMFG-1 heavy chain/DNase I fusion protein 1.  
XX KW Humanised monoclonal antibody; polymorphic epithelial mucin; PBML;  
XX KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX PN WO200174905-A1.  
XX PD 11-OCT-2001.  
XX PF 26-MAR-2001; 2001WO-GB01324.  
XX PR 03-APR-2000; 2000GB-0008049.  
XX PR 02-OCT-2000; 2000US-237159P.  
XX PA (ANTI-) ANTISOMA RES LTD.  
XX PI Young RJ;  
XX DR WPI; 2001-662969/76.  
XX PT Novel compound used to treat cancer has target cell-specific portion  
PT comprising humanised monoclonal antibody having specificity for  
PT polymorphic epithelial mucin, and cytotoxic portion having  
PT endonucleolytic activity -  
XX Claim 20; Figure 7; 176pp; English.  
XX CC The invention relates to a compound which comprises a target  
CC cell-specific portion, comprising an humanised monoclonal antibody,  
CC having specificity for polymorphic epithelial mucin (PEM) or its antigen  
CC binding fragment and a cytotoxic portion having endonucleolytic activity,  
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The  
CC compound has cytostatic activity useful for treating cancer and acting as  
CC a potential inducer of apoptosis.  
SQ Sequence 731 AA;

Query Match 93.9%; Score 2363.5; DB 22; Length 731;  
Best Local Similarity 93.6%; Pred. No. 5.1e-135;  
Matches 440; Conservative 19; Mismatches 8; Indels 3; Gaps 1;  
QY 1 MGWSCIILFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCKASGYFTSYMMQWVRQAP 60  
DB 1 mgwsciilflvatatgvhsqvlvqsgaevkpgasvkvsckasgyftsymwvwrqap 60  
QY 61 GQGLEWMGEIDPDSYNYNOKFKGRVTITRTDTSTAYMELSLRSEDATVYYCARNRD 120  
DB 61 gqglewmgeidpdsytnynokfgrvttitrtdstaymelslrsedatvyycarnrd 120  
QY 121 YSNWNYFDVWGEGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180  
DB 121 ysnwnyfdvwmgegltlvtvssastkgpsvfplapsskstsggtaalgclvkdypfepvtvs 177  
QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVWTVPSSSLGTQYICNVNHNKPSNTKVDKRVPE 240  
DB 181 wnsгалтsgvhtfpavllqssglyslssvwtvpssslgtqyicnvnhnkpsntkvdkrvpe 240

|||||  
Db 178 wnsгалtsгvhtfpavllqsglyslssvvtvpsslgtqtyicnvnhkpstkvdkkvep 237  
QY 241 KSCDKTHTCPPCPAPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300  
Db 238 kscdkthtccpcpapellgppsflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw 297  
QY 301 YVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360  
Db 298 yvdgvevhnaktprreeqynstyrvvsvltvlhqdwlngkeyckvsnkalpapiektis 357  
QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420  
Db 358 kkgqprepqvyltppsrdeitknqslclvkgfypsdiavewesngqpennnyktppv 417  
QY 421 LQSDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTKQSLSPGK 470  
Db 418 ldsdgsfflyskltvdksrwqgnvfscvmhealhnnhtqkslsispkg 467

RESULT 12  
AAM52159  
ID AAM52159 standard; Protein; 741 AA.  
XX  
AC AAM52159;  
XX  
DT 05-FEB-2002 (first entry)  
XX  
DE Humanised HMFG-1 heavy chain/DNase I fusion protein 4.  
XX  
KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;  
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200174905-A1.  
XX  
PD 11-OCT-2001.  
XX  
PF 26-MAR-2001; 2001WO-GB01324.  
XX  
PR 03-APR-2000; 2000GB-0008049.  
PR 02-OCT-2000; 2000US-237159P.  
XX  
PA (ANTI-) ANTISOMA RES LTD.  
XX  
PI Young RJ;  
XX  
DR WPI; 2001-662969/76.  
XX  
Novel compound used to treat cancer has target cell-specific portion comprising humanised monoclonal antibody having specificity for polymorphic epithelial mucin, and cytotoxic portion having endonucleolytic activity -  
XX  
PS Claim 20; Figure 10; 176pp; English.  
XX  
CC The invention relates to a compound which comprises a target cell-specific portion, comprising an humanised monoclonal antibody, having specificity for polymorphic epithelial mucin (PEM) or its antigen binding fragment and a cytotoxic portion having endonucleolytic activity, exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The compound has cytostatic activity useful for treating cancer and acting as a potential inducer of apoptosis.  
XX  
SQ Sequence 741 AA;

Query Match 93.9%; Score 2363.5; DB 22; Length 741;  
Best Local Similarity 93.6%; Pred. No. 5,1e-135;  
Matches 440; Conservative 19; Mismatches 8; Indels 3; Gaps 1;

QY 1 MGKSCILFLVATATGVHSQVLQSGAEYKVGASVKVSKASGYTFTSYWQWVRQAP 60  
Db 1 mgwscililflvatatgvhsqvlqsgaeavkvgasvkscasgytfsaywiewrqp 60  
QY 61 GQGLEWMGEIDPSDSTNYNQKFKGRVTIPRDTSTAYMELSSLSRSEDPAVYYCARNRD 120  
Db 61 gqglewmgeillpgsnnsrynekfkgrvttrdtstntaymelslrsedtavyycarsy 120  
QY 121 YSNWYFDVWGECLTVTVSSASTKGPSPVPLAPSSKSTSGTAAIGCLVKDYPEPEVTVS 180  
Db 121 fa---wfywgggtclvtvssastkgspsvplapsskstsggtaalgclvkdyppev 177  
QY 181 WNSGALTSGVHTFPAPVLLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRV 240  
Db 178 wnsгалtsгvhtfpavllqsglyslssvvtvpsslgtqtyicnvnhkpstkvdkkvep 237  
QY 241 KSCDKTHTCPPCPAPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300  
Db 238 kscdkthtccpcpapellgppsflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw 297  
QY 301 YVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360  
Db 298 yvdgvevhnaktprreeqynstyrvvsvltvlhqdwlngkeyckvsnkalpapiektis 357  
QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420  
Db 358 kkgqprepqvyltppsrdeitknqslclvkgfypsdiavewesngqpennnyktppv 417  
QY 421 LQSDGSFFLYSKLTVDKSRWQQGNVSCVMHEALHNNHYTKQSLSPGK 470  
Db 418 ldsdgsfflyskltvdksrwqgnvfscvmhealhnnhtqkslsispkg 467

RESULT 13  
AAM52158  
ID AAM52158 standard; Protein; 729 AA.  
XX  
AC AAM52158;  
XX  
DT 05-FEB-2002 (first entry)  
XX  
DE Humanised HMFG-1 heavy chain/DNase I fusion protein 3.  
XX  
KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;  
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200174905-A1.  
XX  
PD 11-OCT-2001.  
XX  
PF 26-MAR-2001; 2001WO-GB01324.  
XX  
PR 03-APR-2000; 2000GB-0008049.  
PR 02-OCT-2000; 2000US-237159P.  
XX  
PA (ANTI-) ANTISOMA RES LTD.  
XX  
PI Young RJ;  
XX  
DR WPI; 2001-662969/76.  
XX  
Novel compound used to treat cancer has target cell-specific portion comprising humanised monoclonal antibody having specificity for polymorphic epithelial mucin, and cytotoxic portion having endonucleolytic activity -  
XX  
PS Claim 20; Figure 9; 176pp; English.  
XX  
CC The invention relates to a compound which comprises a target cell-specific portion, comprising an humanised monoclonal antibody, comprising a target

CC having specificity for polymorphic epithelial mucin (PEM) or its antigen  
CC binding fragment and a cytotoxic portion having endonucleolytic activity,  
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The  
CC compound has cytostatic activity useful for treating cancer and acting as  
CC a potential inducer of apoptosis.  
XX  
SQ Sequence 729 AA;

Query Match 93.7%; Score 2358.5; DB 22; Length 729;  
Best Local Similarity 93.6%; Pred. No. 1e-134;  
Matches 439; Conservative 19; Mismatches 8; Indels 3; Gaps 1;  
Qy 1 MGWSCIIILFLVATATGVHSQVQLVOSGAEVKKPGASVKVCKASGYTFTSYMMQWVRQAP 60  
Db 1 mgwsciiilflvatatgvhsqvlvqsgaevkpgasvkvsckasgytftsaywiewvrqap 60  
Qy 61 GQGLEWGEIDPSDYNYNOKFKGRVTITRDTSSTAYMELSSLRSEDATVYYICARNRD 120  
Db 61 gqglewgeidpsdysynynokfgrvtitrdtsstaymelslrsedatvyyicarsyd 120  
Qy 121 YSNWNYFDVWEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180  
Db 121 fa---wfaywgggtlvtvssastkgpsvfplapsskstsggtaalgclvkdypfepptvs 177  
Qy 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRV 240  
Db 178 wnsгалтsgvhtfpavlgssglyslssvtpssslgtqtyicnvnhnpstnkvdkkv 237  
Qy 241 KSCDKHTCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300  
Db 238 kscdkhtccpcpapellggpsvflfppkpkdtlmisrtpevtcgvvdvshedpevkfnw 297  
Qy 301 YVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 360  
Db 298 yvdgvevhnatkpreeqynstyrvvsvltvlhqdwlngkeyckvsnkalpapiektis 357  
Qy 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 420  
Db 358 kakgqprepqvtytlppsreemtqnqvsitclvkgfypsdiavewesngqpennyktp 417  
Qy 421 LDSGGSFFLYSKLTVDKSRWQGNVFCFSVMHEALHNHYTQKSLSLSPG 469  
Db 418 ldsdgsfflyskltvdksrwqgnvfscsvmhealhnhytdqkslsisp 466

## RESULT 14

AAM52161  
ID AAM52161 standard; Protein; 739 AA.

XX AC AAM52161;

XX XX 05-FEB-2002 (first entry)

XX DE Humanised HMF-1 heavy chain/DNase I fusion protein 6.

XX XX Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;  
KW KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.  
XX XX Homo sapiens.

OS OS Synthetic.

PN PN WO200174905-A1.

XX XX 11-OCT-2001.

XX XX 26-MAR-2001; 2001WO-GB01324.

XX XX 03-APR-2000; 2000GB-0008049.

PR PR 02-OCT-2000; 2000US-237159P.

XX XX (ANTI-) ANTISOMA RES LTD.

XX XX

PI Young RJ;

XX DR WPI; 2001-662969/76.

XX XX Novel compound used to treat cancer has target cell-specific portion  
PT comprising humanised monoclonal antibody having specificity for  
PT polymorphic epithelial mucin, and cytotoxic portion having  
PT endonucleolytic activity -  
XX  
XX PS Claim 20; Figure 12; 176pp; English.

XX CC The invention relates to a compound which comprises a target  
CC cell-specific portion, comprising an humanised monoclonal antibody,  
CC having specificity for polymorphic epithelial mucin (PEM) or its antigen  
CC binding fragment and a cytotoxic portion having endonucleolytic activity,  
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The  
CC compound has cytostatic activity useful for treating cancer and acting as  
CC a potential inducer of apoptosis.  
XX  
SQ Sequence 739 AA;

Query Match 93.7%; Score 2358.5; DB 22; Length 739;  
Best Local Similarity 93.6%; Pred. No. 1e-134;  
Matches 439; Conservative 19; Mismatches 8; Indels 3; Gaps 1;  
Qy 1 MGWSCIIILFLVATATGVHSQVQLVOSGAEVKKPGASVKVCKASGYTFTSYMMQWVRQAP 60  
Db 1 mgwsciiilflvatatgvhsqvlvqsgaevkpgasvkvsckasgytftsaywiewvrqap 60  
Qy 61 GQGLEWGEIDPSDYNYNOKFKGRVTITRDTSSTAYMELSSLRSEDATVYYICARNRD 120  
Db 61 gqglewgeidpsdysynynokfgrvtitrdtsstaymelslrsedatvyyicarsyd 120  
Qy 121 YSNWNYFDVWEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180  
Db 121 fa---wfaywgggtlvtvssastkgpsvfplapsskstsggtaalgclvkdypfepptvs 177  
Qy 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRV 240  
Db 178 wnsгалтsgvhtfpavlgssglyslssvtpssslgtqtyicnvnhnpstnkvdkkv 237  
Qy 241 KSCDKHTCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300  
Db 238 kscdkhtccpcpapellggpsvflfppkpkdtlmisrtpevtcgvvdvshedpevkfnw 297  
Qy 301 YVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 360  
Db 298 yvdgvevhnatkpreeqynstyrvvsvltvlhqdwlngkeyckvsnkalpapiektis 357  
Qy 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 420  
Db 358 kakgqprepqvtytlppsreemtqnqvsitclvkgfypsdiavewesngqpennyktp 417  
Qy 421 LDSGGSFFLYSKLTVDKSRWQGNVFCFSVMHEALHNHYTQKSLSLSPG 469  
Db 418 ldsdgsfflyskltvdksrwqgnvfscsvmhealhnhytdqkslsisp 466

## RESULT 15

AAM52157

ID AAM52157 standard; Protein; 730 AA.

XX XX AAM52157;

XX AC AAM52157;

DT DT 05-FEB-2002 (first entry)

XX XX Humanised HMF-1 heavy chain/DNase I fusion protein 2.

XX DE Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;

XX KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.

XX XX Homo sapiens.

OS OS





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Db 1 MDWTWFLFVAAATGVQSQMVQVQGAEVKKPGSSVTVSCSKASGCTFNSYALISWVRQAP 60  
QY 61 GQLEWNGEIDPSDSTNTNQKFKGRVTITRTSTSTAYMELSSLRSEDSTAVYICARNR- 119  
Db 61 GQLEWNGGIPLFGTPTYSQFQGRVTITADKSTSTAHMELTSLRSEDSTAVYICATDRY 120  
QY 120 ----DYSNNWFDVWNGEGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 174  
Db 121 RQANFDRARVGFDPWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 180  
QY 175 EPTVSWNSGALTSVGHVHTFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHNKPSNTKV 234  
Db 181 EPTVSWNSGALTSVGHVHTFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHNKPSNTKV 240  
QY 235 DKRVEPKCDKTHCPCPCAPPELLGSPSVFLPPKPKDTLMISRTPEVTVVVDVSHEDP 294  
Db 241 DKRVEPKCDKTHCPCPCAPPELLGSPSVFLPPKPKDTLMISRTPEVTVVVDVSHEDP 300  
QY 295 EVKFNMYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAP 354  
Db 301 EVKFNMYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360  
QY 355 IEKTIKAKGQPREPOVYITLPSREMTKNQVSLICLVKGFYPSDIAVWESNGQPENNY 414  
Db 361 IEKTIKAKGQPREPOVYITLPSREMTKNQVSLICLVKGFYPSDIAVWESNGQPENNY 420  
QY 415 KITPPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 470  
Db 421 KITPPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 476

RESULT 2

US-08-458-516-13  
; Sequence 13, Application US/08458516  
; Patent No. 5777085  
; GENERAL INFORMATION:  
; APPLICANT: Co. Man Sung  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Humanized Antibodies Reactive with  
; TITLE OF INVENTION: GPIIb/IIIa  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: US/08/458,516  
; PRIOR APPLICATION DATA:  
; CLASSIFICATION: 424  
; APPLICATION NUMBER: US 08/059,159  
; FILING DATE: 03-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-37-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 449 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

; MOLECULE TYPE: protein  
US-08-458-516-13  
Query Match 88.6%; Score 2230; DB 1; Length 449;  
Best Local Similarity 93.1%; Pred. No. 2.2e-162;  
Matches 420; Conservative 14; Mismatches 15; Indels 2; Gaps 2;  
QY 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQVROAPGQLEWNGEIDPSDSTVNY 79  
Db 1 QVQLVQSGAEVKKPGASVKVSCKASGYAFTNYLIEWRQAPGQGLEWIGVYIPGSGGTNY 60  
QY 80 NQKFKGRVTITRTSTSTAYMELSSLRSEDSTAVYICARNRDYNNNYFDVWNGEGLTVTVS 139  
Db 61 NEKFKGRVLTVDSEINTAYMELSSLRSEDSTAVYFCAR-RDGNYGW-FAYWGGQTLTVTS 118  
QY 140 SASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPPEPTVTSWNSGALTSVGHVTFPAVLQS 199  
Db 119 SASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPPEPTVTSWNSGALTSVGHVTFPAVLQS 178  
QY 200 SGLYSLSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKRVKPKSCDKTHCPCPCAPPELLG 259  
Db 179 SGLYSLSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKRVKPKSCDKTHCPCPCAPPELLG 238  
QY 260 GPSVFLFPPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQY 319  
Db 239 GPSVFLFPPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQY 298  
QY 320 NSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPOVYITLPSRE 379  
Db 299 NSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPOVYITLPSRE 358  
QY 380 EMTKQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSR 439  
Db 359 ELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSR 418  
QY 440 WQGNVFCSCVMHEALHNHYTKQSLSLSPGK 470  
Db 419 WQGNVFCSCVMHEALHNHYTKQSLSLSPGK 449

RESULT 3

US-09-027-449-71  
; Sequence 71, Application US/09027449  
; Patent No. 6025158  
; GENERAL INFORMATION:  
; APPLICANT: Gonzalez, Tania R.  
; APPLICANT: Leong, Steven R.  
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and  
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/027,449  
; FILING DATE: 20-Feb-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/074,330  
; FILING DATE: 22-Jan-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/038,664

FILING DATE: 21-Feb-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Love, Richard B.  
 REGISTRATION NUMBER: 34,  
 REFERENCE/DOCKET NUMBER:  
 TELECOMMUNICATION INFORMATION  
 TELEPHONE: 650/225-5530  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 7  
 SEQUENCE CHARACTERISTICS  
 LENGTH: 452 amino acids  
 TYPE: Amino acid  
 TOPOLOGY: Linear  
 US-09-027-449-71

Query Match 87.8%; Score 2210.5; DB 3; Length 452;  
Best Local Similarity 90.3%; Pred. No. 6.9e-161;  
Matches 408; Conservative 27; Mismatches 16; Indels 1; Gaps 1;

[illegible]

```

RESULT      4
US-09-026-985-71
; Sequence 71, Application US/09026985
; Patent No. 6133426
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Po
; TITLE OF INVENTION: Humanized Anti-IL-8
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
;

```

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,985
; FILING DATE: 20-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-026-985-71

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Query Match	87.8%;	Score 2210.5;	DB 4;	Length 452;
Best Local Similarity	90.3%;	Pred. No. 6.9e-161;		
Matches	408;	Conservative 27;	Mismatches 16;	Indels 1;
Gaps				
QY	20	QVQLVQSGAEVKKPGASVKYSCKASGYTFTSYMQWVRQAPGCGLEWMEGIDPSDSYNY	79	
Db	1	EVQLVQSGGGLVPGGSLRLISCAASGYFSFSHYMHVWRQAPGKLEWVGVIDPSNGETTY	60	
QY	80	NQKFKGRTVITRTSTSTAYMELSSLSRSEDATVYYCAR-NRDYSNNWYFDVMWEGTFLTV	138	
Db	61	NQKFKGRTILSRNSKNKNTALQNNLSLRSEDATVYYCARGDYRNGDWDFDVMQGGLTVT	120	
QY	139	SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ	198	
Db	121	SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ	180	
QY	199	SSGLYSLSSVVTVPSSSLGTQITICNVNHHKPSNTKYDKRVEPKSCDKTHTCCPCAPPELL	258	
Db	181	SSGLYSLSSVVTVPSSSLGTQITICNVNHHKPSNTKYDKRVEPKSCDKTHTCCPCAPELL	240	
QY	259	GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNAAKTKPREEQ	318	
Db	241	GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNAAKTKPREEQ	300	
QY	319	YNSTYRVVSVLTVTHQDWLNGKEYCKVSKNALPAPEKTIKAKGPQREPQVYTIPLPSR	378	
Db	301	YNSTYRVVSVLTVTHQDWLNGKEYCKVSKNALPAPEKTIKAKGPQREPQVYTIPLPSR	360	
QY	379	EEMTKNOVSLTCLVKGFYPDSIDIAVWESNGQPENNYKTTTPPVLDSDGSFFLYSKLVYDKS	438	
Db	361	EEMTKNOVSLTCLVKGFYPDSIDIAVWESNGQPENNYKTTTPPVLDSDGSFFLYSKLVYDKS	420	
QY	439	RWQGNVFCFSVMHEALHNHYTQKSLSLSPGK	470	
Db	421	RWQGNVFCFSVMHEALHNHYTQKSLSLSPGK	452	

```

RESULT      5
US-09-049-672A-8
; Sequence 8, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN TUMOR SYSTEM ASSOCIATED PROTEIN

```



Patent No. 6350860  
GENERAL INFORMATION:  
APPLICANT: Buysse, Marie-Ange  
ATTORNEY: Sablon, Erwin  
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,  
FILE REFERENCE: INNS:015  
CURRENT APPLICATION NUMBER: US/09/485,737B  
CURRENT FILING DATE: 2000-02-14  
PRIOR APPLICATION NUMBER: PCT/EP 98/05165  
PRIOR FILING DATE: 1998-08-14  
PRIOR APPLICATION NUMBER: EPO 98870139.7  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: EPO 97870122.5  
PRIOR FILING DATE: 1997-08-18  
NUMBER OF SEQ ID NOS: 104  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 90  
LENGTH: 711  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: SYNTHETIC  
US-09-485-737B-90

Query Match 86.3%; Score 2172; DB 4; Length 711;  
Best Local Similarity 88.0%; Pred. No. 1.1e-157;  
Matches 409; Conservative 20; Mismatches 32; Indels 4; Gaps 1;  
Qy 6 ILFLVATGTVHVSQVQLVQSGAEVKKPGASVKVSCKASGTTFTSYNMQWVRQAPGQGLE 65  
Db 7 IFSELLSASVILQVQLVQSGSELKPKGASVKISCKASGYTFDTYGMNWKQAPGQGLK 66  
Qy 66 WMGEIDPSDSTNTYNNQKFKGRVTTTRDTSTSTAYMELSLRSEDATVYVCARNRDYSNNW 125  
Db 67 WMGWINYTGESTVDDFKGRFVSLDTSVSAAYLQISLKAEDTATYFCARRGFYA--- 123  
Qy 126 YFDVWGEGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGA 185  
Db 124 -MDYWGQGTITVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGA 182  
Qy 186 LTSVHTFPVAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVKRRVEPKSCDK 245  
Db 183 LTSVHTFPVAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVKRRVEPKSCDK 242  
Qy 246 THTCPAPPELLGGPSVFLPAPPKDTLMISRTPEVTCVVDVSHEDPEVKENMYVDGV 305  
Db 243 THTCPAPPELLGGPSVFLPAPPKDTLMISRTPEVTCVVDVSHEDPEVKENMYVDGV 302  
Qy 306 EVHNKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 365  
Db 303 EVHNKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 362  
Qy 366 PREQVYTLPPSREMTKNQVSLTCLVKGFTPSDIAVWESNGOPENNYKTTTPPVLDSDG 425  
Db 363 PREQVYTLPPSREMTKNQVSLTCLVKGFTPSDIAVWESNGOPENNYKTTTPPVLDSDG 422  
Qy 426 SFFLYSKLTVDKSRWQOQNVFSCSVNHEALHNHYTQKSLSLSPGK 470  
Db 423 SFFLYSKLTVDKSRWQOQNVFSCSVNHEALHNHYTQKSLSLSPGK 467

RESULT 8  
US-08-793-450-8  
Sequence 8, Application US/08793450  
Patent No. 6312690  
GENERAL INFORMATION:  
APPLICANT: EDELMAN, LENA  
APPLICANT: MARGARITTE, CHRISTEL  
APPLICANT: KACZOREK, MICHEL  
APPLICANT: CHARABIH, HASSAN  
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D

TITLE OF INVENTION:  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P.C.  
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/793,450  
FILING DATE: 03-MAR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 94/10566  
FILING DATE: 02-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 660-118-0 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 472 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-793-450-8

Query Match 85.2%; Score 2146; DB 4; Length 472;  
Best Local Similarity 85.3%; Pred. No. 6e-156;  
Matches 405; Conservative 25; Mismatches 37; Indels 8; Gaps 3;  
Qy 1 MGWSCIILFLVATGTVHVSQVQLVQSGAEVKKPGASVKVSCKASGTTFTSYNMQWVRQAP 60  
Db 1 MGWSCIILFLVATGTVHVSQVQLVQSGAEVKKPGASVKVSCKASGTTFTSYNMQWVRQAP 60  
Qy 61 CGGLEWMEIDPSDSTNTYNNQKFKGRVTTTRDTSTSTAYMELSLRSEDATVYVCARNRD 120  
Db 61 GKGLEWIGEINHSGS-TNYPNLSKSRVTISVDTSKNPSLNSVTAADTAVYCARAPE 119  
Qy 121 YSNW-----YFDVWGEGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPE 175  
Db 120 Y--KWKYHGDWFDPMGQGTITVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPE 177  
Qy 176 PVTYSWNSGALTSGVHTFPVAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVD 235  
Db 178 PVTYSWNSGALTSGVHTFPVAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVD 237  
Qy 236 KRVEPKSCDKTHTCPAPPELLGGPSVFLPAPPKDTLMISRTPEVTCVVDVSHEDPE 295  
Db 238 KKAEPKSCDKTQTCPCAPPELLGGPSVFLPAPPKDTLMISRTPEVTCVVDVSHEDPE 297  
Qy 296 VKFNMYVDGVEVHNKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 355  
Db 298 VKFNMYVDGVEVHNKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 357  
Qy 356 EKTISKAKGQPREQVYTLPPSREMTKNQVSLTCLVKGFTPSDIAVWESNGOPENNYK 415  
Db 358 EKTISKAKGQPREQVYTLPPSREMTKNQVSLTCLVKGFTPSDIAVWESNGOPENNYK 417  
Qy 416 TTPPVLDSDGSFFLYSKLTVDKSRWQOQNVFSCSVNHEALHNHYTQKSLSLSPGK 470  
Db 418 TTPPVLDSDGSFFLYSKLTVDKSRWQOQNVFSCSVNHEALHNHYTQKSLSLSPGK 472

```

301 EQYNSTYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 360
377 SREEMTKNQSLSLTKLVKGYPSPDIAVWEWSNGOPENNYKTTTPVLDSDGSEFFLYSLKTV 436
361 SREEMTKNQSLSLTKLVKGYPSPDIAVWEWSNGOPENNYKTTTPVLDSDGSEFFLYSLKTV 420
437 KSRWQGNVFSQSVMEALHNHYTQKSLSLSPGK 470
421 KSRWQGNVFSQSVMEALHNHYTQKSLSLSPGK 454

RESULT 10
US-08-437-642B-22
; Sequence 22, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 08/146206
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 07/15272
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-9881
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-22

Query Match 85.1%; Score 2142.5; DB 2; Length 454;
Best Local Similarity 88.3%; Pred. No. 1.le-155;
Matches 401; Conservative 20; Mismatches 30; Indels 3; Gaps 1;

QY 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVRQAPGGLEWMGIEDPSDYTN 79
DB 1 QVQLQSGPELVKPGASVKISCKTSGYTFETMHWKQSHGKSLIEWIGFNPKNKGSSH 60
QY 80 NQKFKGRVTITRDITSTAYMELSLRSDEDTAVYYCARNRDYSNNW---YFDVWGEGLTV 136
DB 61 NQREWDKATLAVDKSTSTAYMELSLRSDESGIYYICARWGLNYGFDVYFDVWAGATTV 120
QY 137 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSVNSGALTSGVHTFPAV 196
DB 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSVNSGALTSGVHTFPAV 180
QY 197 LOSSGLYSLSSVTVTPSSSLGQTICNVNHRKPSNTKVDKRVKPSCKDTHRCPCPAPPE 256
DB 181 LOSSGLYSLSSVTVTPSSSLGQTICNVNHRKPSNTKVDKRVKPSCKDTHRCPCPAPPE 240
QY 257 LLGSPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 316
DB 241 LLGSPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 300
QY 317 EQYNSTYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 376
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Db 61 NORFMDKATLAVDKSTSTAYMELSLRSDSGIYYICARWRLNYGDFVRYFDVWGAGTTV 120  
Qy 137 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFPAV 196  
Db 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFPAV 180  
Qy 197 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKRVPEKSCDKTHTCCPPCPAPE 256  
Db 181 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKRVPEKSCDKTHTCCPPCPAPE 240  
Qy 257 LLGSPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVVEVHNAKTKPRE 316  
Db 241 LLGSPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVVEVHNAKTKPRE 300  
Qy 317 EOYNSTYRVSVSLTVLHODWLNKREYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 376  
Db 301 EOYNSTYRVSVSLTVLHODWLNKREYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 360  
Qy 377 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVD 436  
Db 361 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVD 420  
Qy 437 KSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 470  
Db 421 KSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 454

## RESULT 11

PCT-US93-07832-22

; Sequence 22, Application PC/TUS9307832

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; TITLE OF INVENTION: Immunoglobulin Variants

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/07832

; FILING DATE: 19930820

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/715272

; FILING DATE: 14-JUN-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/05126

; FILING DATE: 15-JUN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/934373

; FILING DATE: 21-AUG-1992

; ATTORNEY/AGENT INFORMATION:

; NAME:

; REGISTRATION NUMBER:

; REFERENCE/DOCKET NUMBER: 709P2PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE:

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 454 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

PCT-US93-07832-22

Query Match 85.1%; Score 2142.5; DB 5; Length 454;  
Best Local Similarity 88.3%; Pred. No. 1.1e-155;  
Matches 401; Conservative 20; Mismatches 30; Indels 3; Gaps 1;

Qy 20 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYMMQWRQAPQGGLWGEIDPSDSTYNY 79  
Db 1 QVQLQQSGPELVKPGASVKISCKTSGYFTTEYTHMWMKQSHGKSLIEWIGGFNPKNGGSSH 60  
Qy 80 NQKFKGRVTITRDTSTAYMELSLRSDSTAYVYICARNRDYSNNW---YFDVWCEGTLV 136  
Db 61 NORFMDKATLAVDKSTSTAYMELSLRSDSGIYYICARWRLNYGDFVRYFDVWGAGTTV 120  
Qy 137 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFPAV 196  
Db 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFPAV 180  
Qy 197 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKRVPEKSCDKTHTCCPPCPAPE 256  
Db 181 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKRVPEKSCDKTHTCCPPCPAPE 240  
Qy 257 LLGSPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVVEVHNAKTKPRE 316  
Db 241 LLGSPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVVEVHNAKTKPRE 300  
Qy 317 EOYNSTYRVSVSLTVLHODWLNKREYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 376  
Db 301 EOYNSTYRVSVSLTVLHODWLNKREYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 360  
Qy 377 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVD 436  
Db 361 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVD 420  
Qy 437 KSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 470  
Db 421 KSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 454

## RESULT 12

US-08-887-352B-14

; Sequence 14, Application US/08887352B

; Patent No. 5994511

; GENERAL INFORMATION:

; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe

; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of

; TITLE OF INVENTION: Improving Polypeptides

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/887,352B

; FILING DATE: 03-Jul-1997

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Svoboda, Craig G.

; REGISTRATION NUMBER: 39,044

; REFERENCE/DOCKET NUMBER: P1123

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-1489

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 14:

US-08-466-151-65  
Sequence 65, Application US/08466151  
Patent No. 6037453  
GENERAL INFORMATION:  
APPLICANT: Jardieu, Paula M.  
APPLICANT: Presta, Leonard G.  
TITLE OF INVENTION: Immunoglobulin Variants  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESS: Genentech, Inc.  
STREET: 1 DNA way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disks  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,151  
FILING DATE:  
CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-466-151-65

Query Match 85.08; Score 2141; DB 3; Length 451;
Best Local Similarity 88.3%; Pred. No. 1.4e-155;
Matches 399; Conservative 23; Mismatches 28; Indels 2; Gaps 2;

Qy 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YMQWVRRQAPGGQLEWMGIEDPSDSTN 78
Db 1 EVQLVESGGGLVQPGGSLRLSCAIVSYISITSGYSNNWIRQAPGKLEWVASI-TYDGSN 59

Qy 79 YNQKFKGRVTTTRDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGEGTLTV 138
Db 60 YNPVSKGRITTSRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTV 119

Qy 139 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 198
Db 120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 179

Qy 199 SSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNPKVDKRVKPKSCDKTHTCPCPAPELL 258
Db 180 SSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNPKVDKRVKPKSCDKTHTCPCPAPELL 239

Qy 259 GGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 318
Db 240 GGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 299

Qy 319 YNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 378
Db 300 YNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 359

Qy 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 438
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 419

Qy 439 RWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
Db 420 RWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451

RESULT 15
US-09-109-207C-14
; Sequence 14, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide

; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109.207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAEL1
US-09-109-207C-14

Query Match 85.08; Score 2141; DB 4; Length 451;
Best Local Similarity 88.3%; Pred. No. 1.4e-155;
Matches 399; Conservative 23; Mismatches 28; Indels 2; Gaps 2;

Qy 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YMQWVRRQAPGGQLEWMGIEDPSDSTN 78
Db 1 EVQLVESGGGLVQPGGSLRLSCAIVSYISITSGYSNNWIRQAPGKLEWVASI-TYDGSN 59

Qy 79 YNQKFKGRVTTTRDTSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGEGTLTV 138
Db 60 YNPVSKGRITTSRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTV 119

Qy 139 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 198
Db 120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 179

Qy 199 SSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNPKVDKRVKPKSCDKTHTCPCPAPELL 258
Db 180 SSGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNPKVDKRVKPKSCDKTHTCPCPAPELL 239

Qy 259 GGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 318
Db 240 GGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 299

Qy 319 YNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 378
Db 300 YNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 359

Qy 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 438
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 419

Qy 439 RWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
Db 420 RWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451

Search completed: August 14, 2002, 15:17:09
Job time: 692 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:19:02 ; Search time 108.64 Seconds  
(without alignments)  
415.703 Million cell updates/sec

Title: US-09-499-662-157  
Perfect score: 2518  
Sequence: 1 MGWSCIIILFVATATGVHSHQ.....MHEALHNYHTOKSLSLSPGK 470  
Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues  
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR.71.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1758	69.8	330	1 GHU	Ig gamma-1 chain C
2	1639.5	65.1	377	2 A23511	Ig gamma-3 chain C
3	1637.5	65.0	377	2 A60764	Ig gamma-3 chain C
4	1610	63.9	326	1 G2HU	Ig gamma-2 chain C
5	1599.5	63.5	327	1 G4HU	Ig gamma-4 chain C
6	1591.5	63.2	459	2 S37483	Ig gamma-2a chain
7	1535	61.0	474	1 G2MS11	Ig gamma-2b chain
8	1525	60.6	446	2 S40295	Ig gamma-2a chain
9	1485	59.0	470	2 S22080	Ig heavy chain pre
10	1482.5	58.9	475	2 S01321	Ig gamma-2b chain
11	1481	58.8	472	2 S31459	Ig gamma-1 chain -
12	1443	57.3	374	2 S69339	Ig heavy chain v r
13	1440.5	57.2	444	2 PC4436	monoclonal antibod
14	1267	50.3	328	2 I47159	Ig gamma 2a chain
15	1261	50.1	328	2 I47160	Ig gamma 2b chain
16	1253	49.8	255	4 S31866	Ig gamma-1 chain C
17	1245	49.4	234	2 PT0207	Ig gamma chain C r
18	1235	49.0	328	2 I47158	Ig gamma 1 chain C
19	1231.5	48.9	323	1 GHRB	Ig gamma chain C r
20	1231	48.9	328	2 I47161	Ig gamma 3 chain C
21	1210.5	48.1	329	1 G2GP	Ig gamma-2 chain C
22	1165.5	46.3	308	2 C30554	Ig heavy chain C r
23	1157	45.9	289	1 G3HUW1	Ig gamma-3 heavy c
24	1155	45.9	326	2 PS0017	Ig gamma-1 chain C
25	1150	45.7	329	1 G3MSC	Ig gamma-3 chain C
26	1145	45.5	324	1 GLWS	Ig gamma-1 chain C
27	1144.5	45.5	333	2 PS0018	Ig gamma-2b chain C
28	1140	45.3	393	1 G1MSM	Ig gamma-1 chain C
29	1139	45.2	398	1 G3MSM	Ig gamma-3 chain C

RESULT 1  
GHU

Ig gamma-1 chain C region - human  
C;Species: Homo sapiens (man)

C;Date: 31-Jan-1981 #sequence\_revision 18-Aug-1982 #text\_change 16-Jul-1999  
C;Accession: A93433; S36861; S3887; B90563; A90564; B91668; A91723; A02146  
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.  
Nucleic Acids Res. 10, 4071-4079, 1982

A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A;Reference number: A93433; MUID:82274238

A;Accession: A93433

A;Molecule type: DNA

A;Residues: 1-330 <ELL>

A;Cross-references: EMBL:Z17370

A;Note: this sequence has the Gln(17) allotypic marker, 97-Lys, and the Gln(1) marker  
A;Note: Lys-330 is removed after translation  
R;Harris, L.J.

submitted to the EMBL Data Library, October 1992

A;Reference number: S33904

A;Accession: S36861

A;Molecule type: DNA

A;Residues: 2-330 <HAR>

A;Cross-references: EMBL:Z17370

R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.  
Cell 29, 671-679, 1982

A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of  
A;Reference number: S33887; MUID:83001943

A;Accession: S33887

A;Molecule type: DNA

A;Residues: 88-113;235-330 <TAK>

A;Cross-references: EMBL:Z17370

R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman  
Biochemistry 9, 3161-3170, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq  
A;Reference number: A90563; MUID:71064024

A;Contents: myeloma protein Eu

A;Accession: B90563

A;Molecule type: protein

A;Residues: 1-96,'R',98-135 <CUN>

A;Note: this sequence has the Gln(3) marker, 97-Arg

R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.  
Biochemistry 9, 3171-3181, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se

A;Reference number: A90564; MUID:71064025

A;Contents: Eu

A;Accession: A90564

A;Molecule type: protein

A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',;  
A;Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met

R;Fonstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein N1

igen Primaerstruktur.  
A:Reference number: A91668; MUID:77070269  
A:Contents: myeloma protein Nie  
A:Accession: B91668  
A:Molecule type: protein  
A:Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27  
A:Note: this sequence has the Gm(17) and Gm(1) markers  
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
A:Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOI  
A:Reference number: A91723; MUID:83289131  
A:Contents: myeloma protein KOL; disulfide bonds  
A:Accession: A91723  
A:Molecule type: protein  
A:Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH  
A:Note: this sequence has the Gm(3) and Gm(non-1) markers  
R:Call, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid  
A:Reference number: A90565; MUID:71064027  
A:Contents: annotation; disulfide bonds  
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976  
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob  
enbromide cleavage products, and the disulfide bridges.  
A:Reference number: A91667; MUID:77070267  
A:Contents: annotation; disulfide bonds  
C:Genetics:  
A:Gene: GDB:IGHG1  
A:Cross-references: GDB:120085; OMTM:147100  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1; 114/1; 224/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:137-206/Domain: immunoglobulin homology <IM2>  
F:27-310/Domain: immunoglobulin homology <IM3>  
F:27-83,144-204,250-308/Disulfide bonds: #status experimental  
F:103/Disulfide bonds: interchain (to light chain) #status experimental  
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 69.8%; Score 1758; DB 1; Length 330;  
Best Local Similarity 99.1%; Pred. No. 1.5e-93;  
Matches 327; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSNWSGALTSGVHTFPAVLQSS 200  
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSNWSGALTSGVHTFPAVLQSS 60

QY 201 GLYSLSSVVTVPSSSLGTQYICNVNHPKNTKVDKRVK 320  
Db 61 GLYSLSSVVTVPSSSLGTQYICNVNHPKNTKVDKRVK 120

QY 239 -----EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKPKDT 273  
Db 121 DTPPPCPAPPELLGGPSVFLFPPPKPKDT 180

QY 274 LMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 333  
Db 181 LMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 240

QY 334 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVK 393  
Db 241 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVK 300

QY 394 GYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMHE 453  
Db 301 GYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMHE 360

QY 454 ALHNHYTQKSLSLSPGK 470  
Db 361 ALHNHYTQKSLSLSPGK 377

RESULT 3  
A50764  
Ig gamma-3 chain C region, form LAT - human  
C:Species: Homo sapiens (man)  
C:Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 16-Jul-1999  
C:Accession: A50764  
R:Huck, S.; Lefranc, G.; Lefranc, M.P.  
Immunogenetics 30, 250-257, 1989  
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 conv  
A:Reference number: A50764; MUID:90007613  
A:Accession: A50764  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-377 <HUC>  
C:Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 65.0%; Score 1637.5; DB 2; Length 377;  
Best Local Similarity 82.8%; Pred. No. 1.3e-86;  
Matches 312; Conservative 7; Mismatches 11; Indels 47; Gaps 1;

Qy 141 ASTKGPSVFPLAPSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200  
Dy 1 ASTKGPSVFPLAPCSRSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
Qy 201 GLYSLSVVTVTPSSSLGTQTYICNVNHPKSNKTKVDKRV----- 238  
Dy 61 GLYSLSVVTVTPSSSLGTQTYICNVNHPKSNKTKVDKRVELKTPGLDTHTCPCRPPEPKSC 120  
Qy 239 -----EPKSCDKTHTCPCPAPPELLGGPSVFLFPPPKKDT 273  
Dy 121 DTPPCPCPCPKSCDTPPCPCPEPKSCDTPPCPCPEPKSGVFLFPPPKKDT 180  
Qy 274 LMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNNAKTKPREEQYNSTYRVWSVLTVLH 333  
Dy 181 LMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNNAKTKPREEQYNSTYRVWSVLTVLH 240  
Qy 334 ODWLNGKEYKCKVSNKALPAPIETKISKAKQPREPVYITPPSRREEMTKNOVSLTCLVK 393  
Dy 241 ODWLNGKEYKCKVSNKALPAPIETKISKAKQPREPVYITPPSRREEMTKNOVSLTCLVK 300  
Qy 394 GFYPDSDAVENESGQPENNYKTPPVLDSDGSFFLYSLKLVNDRKRWQGQGVFSCVMHE 453  
Dy 301 GFYPDSDAVENESGQPENNNTTPPVLDSDGSFFLYSLRFLVDRKRWQEGNVFSCVMHE 360  
Qy 454 ALHNHYTQKSLSLSPGK 470  
Dy 361 ALHNRYTQKSLSLSPGK 377

RESULT 4

G2HU  
Ig gamma-2 chain C region - human  
C;Species: Homo sapiens (man)  
C;Date: 30-Apr-1981 #sequence\_revision 13-Jun-1983 #text\_change 21-Jul-2000  
C;Accession: A93906; A92809; A93132; A02148  
R;Ellison, J.; Hood, L.  
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982  
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con  
A;Reference number: A93906; MUID:82137621  
A;Accession: A93906  
A;Molecule type: DNA  
A;Residues: 1-326 <ELL>  
A;Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056  
A;Note: Lys-326 is probably removed posttranslationally  
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.  
J. Immunol. 125, 1048-1054, 1980  
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f  
A;Reference number: A92809; MUID:81007873  
A;Contents: myeloma protein Til  
A;Accession: A92809  
A;Molecule type: protein  
A;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>  
A;Note: Trp-156 is at or near the complement-binding site  
R;Connell, G.E.; Parr, D.M.; Hofmann, T.  
Can. J. Biochem. 57, 758-767, 1979  
A;Title: The amino acid sequences of the three heavy chain constant region domains of a  
A;Reference number: A90752; MUID:80001357  
A;Contents: myeloma protein Zie  
A;Accession: A90752  
A;Molecule type: protein  
A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-  
A;Note: this sequence has since been revised  
R;Hofmann, T.; Parr, D.M.  
Mol. Immunol. 16, 923-925, 1979  
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g

A;Reference number: A93132; MUID:80114419  
A;Contents: Zie  
A;Accession: A93132  
A;Molecule type: protein  
A;Residues: 238-275 <HOF>  
R;Hofmann, T.; Parr, D.M.  
submitted to the Atlas, March 1980  
A;Reference number: A94591  
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268  
A;Note: the revised sequence differs from that shown in having 60-Ala and in the ami  
ned  
R;Milstein, C.; Frangione, B.  
Biochem. J. 121, 217-225, 1971  
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.  
A;Reference number: A90253; MUID:72033500  
A;Contents: annotation; myeloma protein Sa, disulfide bonds  
R;Frangione, B.; Milstein, C.; Pink, J.R.L.  
Nature 221, 145-148, 1969  
A;Title: Structural studies of immunoglobulin G.  
A;Reference number: A93157; MUID:69064124  
A;Contents: annotation; Sa, disulfide bonds  
C;Genetics:  
A;Gene: GDB:IGHG2  
A;Cross-references: GDB:119338; OMIM:147110  
A;Map position: 14q32.33-14q32.33  
A;Complex: An immunoglobulin heterotetramer subunit consists of two identical light i  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IM1>  
F;133-202/Domain: immunoglobulin homology <IM2>  
F;239-306/Domain: immunoglobulin homology <IM3>  
F;14/Disulfide bonds: interchain (to light chain) #status experimental  
F;27-83,140-200,246-304/Disulfide bonds: #status experimental  
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 63.9%; Score 1610; DB 1; Length 326;  
Best Local Similarity 91.8%; Pred. No. 4.1e-85;  
Matches 303; Conservative 10; Mismatches 13; Indels 4; Gaps 2;  
Qy 141 ASTKGPSVFPLAPSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200  
Dy 1 ASTKGPSVFPLAPCSRSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
Qy 201 GLYSLSVVTVTPSSSLGTQTYICNVNHPKSNKTKVDKRVKPKSCDKTHTCPCPAPPELLGG 260  
Dy 61 GLYSLSVVTVTPSSSLGTQTYICNVNHPKSNKTKVDKRVKPKSCDKTHTCPCPAPPELLGG 116  
Qy 261 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNNAKTKPREEQYN 320  
Dy 117 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNNAKTKPREEQYN 176  
Qy 321 STYRVVSVLTVHQDWLNGKEYKCKVSNKALPAPIETKISKAKQPREPVYITPPSRREE 380  
Dy 177 STYRVVSVLTVHQDWLNGKEYKCKVSNKALPAPIETKISKAKQPREPVYITPPSRREE 236  
Qy 381 MTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSLKLVNDRKRW 440  
Dy 237 MTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSLKLVNDRKRW 296  
Qy 441 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470  
Dy 297 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 326

RESULT 5

G4HU  
Ig gamma-4 chain C region - human  
C;Species: Homo sapiens (man)  
C;Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 16-Jul-1999  
C;Accession: A90933; A90249; A02150

R:Ellison, J.; Buxbaum, J.; Hood, L.  
DNA 1, 11-18, 1981  
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.  
A:Reference number: A90933; MUID:83157104  
A:Accession: A90933  
A:Molecule type: DNA  
A:Residues: 1-327 <ELL>  
A:Note: the sequence was determined from the germline gene  
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.  
Biochem. J. 117, 33-47, 1970  
A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant  
A:Reference number: A90249; MUID:70207360  
A:Accession: A90249  
A:Molecule type: protein  
A:Residues: 1-30; 81-326 <PIN>  
C:Genetics:  
A:Gene: GDB:IGHC4  
A:Cross-references: GDB:119340; OMIM:147130  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1; 111/1; 221/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)  
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
main disulfide bonds. Interchain (to light chain) #status experimental  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:99-110/Region: hinge  
F:134-203/Domain: immunoglobulin homology <IM2>  
F:240-307/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83, 141-201, 247-305/Disulfide bonds: #status predicted  
F:106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 63.5%; Score 1599.5; DB 1; Length 327;  
Best Local Similarity 91.8%; Pred. No. 1.6e-84;  
Matches 303; Conservative 9; Mismatches 15; Indels 3; Gaps 1;  
QY 141 ASTKGSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSVHTFPFAVLQSS 200  
Db 1 ASTKGSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVYSWNSGALTSVHTFPFAVLQSS 60  
QY 201 GLYSLSVTVPSSSLGCTQYICNVNHPKSNKTKVDRKPEKCDKTHTCPPCAPPELLGG 260  
Db 61 GLYSLSVTVPSSSLGCTQYICNVNHPKSNKTKVDRKPEKCDKTHTCPPCAPPELLGG 117  
QY 261 PSVLEPPPKPKDLMISRPEPTCVVVDVSHDEPEYKENWYVDGVVHNKTKPREEQYN 320  
Db 118 PSVLEPPPKPKDLMISRPEPTCVVVDVSHDEPEYQFNWYVDGVVHNKTKPREEQFN 177  
QY 321 STYRVSVLTVLHQDLNGKEYCKYKSNKALPAPIEKTISKAKGQPREPVYTLPPSREE 380  
Db 178 STYRVSVLTVLHQDLNGKEYCKYKSNKGLPSSIEKTIKAKGQPREPVYTLPPSQEE 237  
QY 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYKLTVDKSRW 440  
Db 238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYKLTVDKSRW 297  
QY 441 OQGNVFSCSVMEALHNHYTOKSLSPGK 470  
Db 298 OQGNVFSCSVMEALHNHYTOKSLSPGK 327

RESULT 6  
S37483  
Ig gamma-2a chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
A:Accession: S37483  
R:Ducancel, F.F.D.  
submitted to the EMBL Data Library, February 1993  
A:Reference number: S37483  
A:Accession: S37483

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-469 <DUC>  
A:Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 63.2%; Score 1591.5; DB 2; Length 469;  
Best Local Similarity 63.3%; Pred. No. 7e-84;  
Matches 299; Conservative 63; Mismatches 105; Indels 5; Gaps 4;  
QY 1 MGWSWIFLLSCTAGVHCQIQIQSSPELVKPGASVKISCKASGYTFTDYINWVKQP 60  
Db 1 MGWSWIFLLSCTAGVHCQIQIQSSPELVKPGASVKISCKASGYTFTDYINWVKQP 60  
QY 61 GQGLEWGEIDPSDSTNTNPKFGRVTTTRDTSTSTAYMELSLRSEDATVYICARNRD 120  
Db 61 GQGLKVGWIIYIPASGNTKYENFKGATLTVDTSSTAYMQLSLSLTSEDATVYFCARAMG 120  
QY 121 YSNMWFDVWGEGLTVTVSSASTKGPSVPLAPSSKSTSGTAAALGCLVKDYFPEPVTVS 180  
Db 121 -ATATLLDTWGGQTTLTVSAAKTATPSVPLAPVCGDFTGSSVTLGCLVKGYFPEPVTLT 179  
QY 181 WNSGALTSVHTFPFAVLQSSGLYSLSVTVPSSSLGCTQYICNVNHPKSNKTKVDRKPE 240  
Db 180 WNSGSLSSGVTTPFAVLQSD-LYTLSSSVTVTSSTWPSQSIITCNVAHPASSTKVDKKIEP 238  
QY 241 KSCDKTHTCPP--CPAPELGGPSVFLFPPPKDTHMISRTPEVTCVVDVSHDEPEVKF 298  
Db 239 RG-PTTKPCPPCKPAPNLLGGPSVFIFPPKIKDVLMLISLSPVITCVVDVSEDDPDVQI 297  
QY 299 NWYVDGVVHNKTKPREEQYNSTYRVSVLTVLHQDLNGKEYCKYKSNKALPAPIEKT 358  
Db 298 SNFVNNVEVHTAGTQTHREDYNSTLRVVSALPIHQDWMKSEKFKCKVNNKDLPAPIERT 357  
QY 359 ISKAKGQPREPVYTLPPSREEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 418  
Db 358 ISKPKGSVAPQVYVLPPEEEMTKKQVLTLCMTVDFMPEDIYVEWTNNGKTELNYKNT 417  
QY 419 PVLDSGSEFLYKLTVDKSRWQGNVFCSCVMHEALHNHYTOKSLSPGK 470  
Db 418 PVLDSGSEFLYKLTVDKSRWVFNERNYSVCSVVEGLHNHHTTKFSRTPGK 469

RESULT 7  
G2MS11  
Ig gamma-2b chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Mar-1980 #sequence\_revision 01-Dec-2000 #text\_change 01-Dec-2000  
C:Accession: S25057; A26235; A26232; A26233; A53598  
R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.  
submitted to the EMBL Data Library, July 1992  
A:Description: Production of a tobacco mosaic virus (TMV) inactivating neotop specifi  
A:Reference number: S25057  
A:Accession: S25057  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-474 <FIS>  
A:Cross-references: EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827  
R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.  
Nature 283, 786-789, 1980  
A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned fr  
A:Reference number: A02157; MUID:80120716  
A:Contents: a allele  
A:Accession: A02157  
A:Molecule type: DNA  
A:Residues: 138-161, 'L', 163-189, 'Fp', 193-474 <YAM>  
A:Cross-references: GB:J00461  
A:Note: the sequence was determined from the germline gene  
R:Fucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.  
Science 206, 1299-1303, 1979



A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b heavy chain  
A:Reference number: A26235; MUID:80081501  
A:Contents: MPC 11  
A:Accession: A26235  
A:Molecule type: mRNA  
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU1>  
A:Note: Lys-474 is probably removed posttranslationally  
R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.  
Science 206, 1303-1306, 1979  
A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglobulin heavy chain  
A:Reference number: A26232; MUID:80081502  
A:Accession: A26232  
A:Molecule type: DNA  
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU2>  
R:Ollo, R.; Rougeon, F.  
Nature 296, 761-763, 1982  
A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma2b heavy chain  
A:Reference number: A26233; MUID:82173203  
A:Contents: b allele  
A:Accession: A26233  
A:Molecule type: DNA  
A:Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLL>  
A:Cross-references: GB:J00461  
R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi, J. Biol. Chem. 269, 12345-12350, 1994  
A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.  
A:Reference number: A53598; MUID:94216359  
A:Accession: A53598  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 234-251 <KIM>  
A:Comment: The a allele sequence is shown.  
C:Genetics:  
A:Introns: 138/1: 236/1: 258/1: 368/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) and two heavy (lambda) chains. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin  
F:157-222/Domain: immunoglobulin homology <IM1>  
F:236-257/Region: hinge  
F:281-350/Domain: immunoglobulin homology <IM2>  
F:387-454/Domain: immunoglobulin homology <IM3>  
F:152/Disulfide bonds: interchain (to light chain) #status predicted  
F:164-220,288-348,394-452/Disulfide bonds: #status predicted  
F:247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted  
F:324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 61.0%; Score 1535; DB 1: Length 474;  
Best Local Similarity 60.4%; Pred. No. 1.2e-80;  
Matches 288; Conservative 70; Mismatches 109; Indels 10; Gaps 3;

Qy 1 MGWSCIILFLVATATGHSOVQVQSGAEVKKPGASVKASGYTFTSYVMQVROAP 60  
Db 1 MWSHIFLFLSGTAGVHSEVQVQSGELVNPGRASVKMSKASGYTFTSYVMHVKQKP 60

Qy 61 GQGLWMEIDFSDSYTYNOKFKGRVTITRDTSTAYMELSSRLSSEDATVYYCARNRD 120  
Db 61 GQGLWEGYINPNKDGTFNEKFKATLTSKSSNTAYMELSSLTSEDSAVYYCARDYD 120

Qy 121 YSNWYFDWEGTLLTVSSASTKGPSPFPPLAPSSKSTSGGTAALGCLVKDYFPPPVTVS 180  
Db 121 YD--WFAYWQGTLLTVSAAKTTPSVYPLAPGCGDTGSSVTSGCLVKGYFPESVTVT 177

Qy 181 WNSGALTSQVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNNVHNPSTKVDKRYEP 240  
Db 178 WNSGSLSSVHTFPAVLQSSGLYTMSSSVTPSPSTWPSQVTCVAHPASSTVDKKLEP 237

Qy 241 KSCDKT-ITCPP-----CPAPELGPGSVFLFPKPKDITMSRTPEVTVCVVDVSHED 293  
Db 238 SGPISTINPCPKCKECHKCPAPNLGSGSVFIFPNIKDVLMSITPKVTCVVDVSEDD 297

Qy 294 PEVKFNWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHODWLNGKEYCKVSNKALPA 353

Db 298 PDVQISWFEVNNVEVHTAQQTQTHREDYNSTIRVSVTLPIQHDWMSGKEFKCKVNNKDLPS 357  
Qy 354 PLEKTISSAKGQPREPQVYTLPPSREEMTKNOVSTCLVKGYFSPVDIAVWEWSNGQPENN 413  
Db 358 PIERTISIKIGLVRAPOVYILPPPAEQUSLRKDVSLTCLVVGPNPGDISVWETSNGHTEEN 417  
Qy 414 YKTTPEVLDSGGSFFLYSKLTVKDRWQOGNVFSGSMHEALHNHYTKSLSLSPCK 470  
Db 418 YKDTAPVLDSGGSYFIYSKLNKTKSKWEKTSFSCNVRHEGLKNYLYLKKTISRSPCK 474

RESULT 8  
S40295  
Ig gamma-2a chain (mAb735) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 16-Jul-1999  
C:Accession: S40295  
R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C., submitted to the EMBL Data Library, January 1993  
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 again  
A:Reference number: S40295  
A:Accession: S40295  
A:Molecule type: protein  
A:Residues: 1-446 <KLE>  
C:Genetics:  
A:Map position: 12  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglyutamic acid  
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>  
F:1-117/Domain: V-D-J region <VDJ>  
F:118-446/Domain: C region <CHR>  
F:118-214/Domain: C1 region <CH1>  
F:215-230/Region: hinge  
F:231-340/Domain: C2 region <CH2>  
F:341-446/Domain: C3 region <CH3>  
F:360-427/Domain: immunoglobulin homology <IM>  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:22-96,144-199,261,367-425/Disulfide bonds: #status predicted  
F:132/Disulfide bonds: interchain (to light chain) #status predicted  
F:224,227,229/Disulfide bonds: interchain #status predicted  
F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 60.6%; Score 1525; DB 2: Length 446;  
Best Local Similarity 63.3%; Pred. No. 4.2e-80;  
Matches 286; Conservative 62; Mismatches 96; Indels 8; Gaps 4;

Qy 20 QVOLVQSGAEVKKPGASVKASGYTFTSYVMQVROAPGQGLWMEIDFSDSYTYN 79  
Db 1 QTLOQSGPELVPRPGASVKISCKASYTFTDYIIHWKQRPGEGLWIGVYPGSGNTRY 60

Qy 80 NOKFKGRVTITRDTSTAYMELSSRLSSEDATVYYCARNRDYNNWYFDWEGTLLTVS 139  
Db 61 NEKFKGKATLVDTSSSTAYMQLSSLTSEDSAVYFCARGGKFA----MDYWGQGTSTVTS 116

Qy 140 SASTKGPSPFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 199  
Db 117 SAKTTAPSVYPLAPVCGDTGSSVTLGCLVKGYFPEPTVLTWNSGSLSSGVHTFPAVLQ 176

Qy 200 SGLYSLSSVTVTPSSSLGTQTYICNNVHNPSTKVDKRYEPKSCDKTHTCPP--CPAPEL 257  
Db 177 D-LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKTIEPRG-PTIKCPCKCKCPAPNL 234

Qy 258 LGGPSVFLFPKPKDITMSRTPEVTVCVVDVSHEDPEVKFNWYVDGVEVHNAKTPREE 317  
Db 235 LGGPSVFIIPPPIKDKVLMISLSLSPMTVCVVDVSEDDPDVQISWFEVNNVEVHTAQQTQTHRE 294

Qy 318 QYNSTYRVVSVLTVLHODWLNGKEYCKVSNKALPAPIERTISIKAKGQPREPQVYTLPPS 377  
Db 295 DYNSTLRVVSALPIQHDWMSGKEFKCKVNNKDLPAPIERTISIKPKGSYRAQVYVLP 354

Qy 378 REEMTKNOVSLTCLVKGYFSPVDIAVWEWSNGQPENNYKTTPTPVLDSDGSFFLYSKLTVDK 437

Db 355 EEMTKKQVLTCTMVTDFMPEDIVETWNGKTELNYKTEPVLDSDGSYFMSKLRVEK 414  
Qy 438 SRWOGNVFSCSYMHAEALHNHYTKSLSPG 469  
Db 415 KNWVERNSYSCSVVHEGLHNHHTKFSRTPG 446

RESULT 9  
S22080  
Ig heavy chain precursor (B/MT 4A.17.H5.A5) - bovine  
N:Alternate names: Ig gamma-1 chain C region (clone 8.10)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S22080; S06610; A31303  
R:Sanders, P.G.  
submitted to the EMBL Data Library, November 1991  
A:Reference number: S22080  
A:Accession: S22080  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-470 <SAN>  
A:Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440  
R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.  
Mol. Immunol. 26, 841-850, 1989  
A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma 1  
A:Reference number: S06610; MUID:90097956  
A:Accession: S06610  
A:Molecule type: DNA  
A:Residues: 142-470 <SYM>  
A:Cross-references: EMBL:X16701  
A:Note: the sequence was determined from the germline gene  
C:Genetics:  
A:Gene: Ig CH gamma-1  
A:Introns: 98/1; 111/1; 221/1  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein  
F:161-225/Domain: immunoglobulin homology <IMM>  
F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 59.0%; Score 1485; DB 2; Length 470;  
Best Local Similarity 60.6%; Pred. No. 8.5e-78;  
Matches 286; Conservative 63; Mismatches 113; Indels 10; Gaps 7;

Qy 3 WSCIILFLVATATGVHSGVQLVQSGAEVKKPGASVKASKASYTFTSYMMQVVRQAPG 62  
Db 5 WT--LLFLVSLAPIGVLSQVLRSGSLVKKPSQTLSTCTVSGFSSYALTWVRQAPGK 62  
Qy 63 GLEWMGEIDPDSYTYNQKFKGRVTITRDTSTAYMELSLRSEDATVYYCARNR--D 120  
Db 63 ALEWVGGI--TSGGTYTYPALKSRSLTITKENSQSLSVSSYTPEDTATYYCARSTYGE 121  
Qy 121 YSNWTFDVMGEGTLTVSSASTKGFSPVPLAPSSKSTSGGTAALGLVKKDYDPEPVTVS 180  
Db 122 VGDGAIADAMGQGLLTVSSASTAPKVPYPLSSCCGDKSSSTYTLGCLVSSYMPPEVTVT 181  
Qy 181 WNSGALTSGVHTFPVAVLQSSGLYSLSVWTVPSLSLGTQTYICNVNHPKNTKVDKRVPE 240  
Db 182 WNSGALKSGVHTFPVAVLQSSGLYSLSVWTVPGSTSG-QFTTCNVAPASSTKVDKRAVDP 240  
Qy 241 KSCDKTHTCCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300  
Db 241 -TC-KPSPDCDCPPPELPGGPSVFIFPPKPKDTLTISGTEPVTCVVVDVGHDDPEVKFSW 298  
Qy 301 YVDGVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 360  
Db 299 FVDDVEVNTATTKPREEQNFSTYRVVYSAIRIQHQTQDTGCKEKKVHNEGLPAPIVRTIS 358  
Qy 361 KAKGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTT 418  
Db 359 RTKGPAREQVYVLAAPQBELSKSTVSLTCMWTSFYPDYIAVEWQRNGQPESEDKTGTTP 418

Qy 419 PVLDSDGSFFLYSKLTVDKSRWQGNVFCSCYMHAEALHNHYTKSLSPGK 470  
Db 419 PQLDADSSYFLYSLKLRVDRNSWQEGDYTCVVMHEALHNHYTKSTKSACK 470

RESULT 10  
S01321  
Ig gamma-2b chain precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 23-Jul-1999  
C:Accession: S01321  
R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Pliers, W.  
Eur. J. Biochem. 176, 287-295, 1988  
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed  
A:Reference number: S01320; MUID:88329081  
A:Accession: S01321  
A:Molecule type: mRNA  
A:Residues: 1-475 <DEL>  
A:Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781  
A:Note: this sequence was determined from the differentiated gene  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>  
F:159-223/Domain: immunoglobulin homology <IMM>

Query Match 58.9%; Score 1482.5; DB 2; Length 475;  
Best Local Similarity 59.5%; Pred. No. 1.2e-77;  
Matches 284; Conservative 69; Mismatches 115; Indels 9; Gaps 4;

Qy 1 MGWSCIILFLVATATGVHSGVQLVQSGAEVKKPGASVKASKASYTFTSYMMQVVRQAP 60  
Db 1 MEWIFLFLILSGTAGVQSQVQLQSGAELAPGASVKLSCKASGYTLTSYGISWVQRT 60  
Qy 61 GQLEWGEIDPDSYTYNQKFKGRVTITRDTSTAYMELSLRSEDATVYYCARNR 120  
Db 61 GQLEWGEITGYPGSGNSYFNEKFKGATLVDKSSSTAYLHLSLTSSEDSAVYFCAGPRQ 120  
Qy 121 YSNWTFDVMGEGTLTVSSASTKGFSPVPLAPSSKSTSGGTAALGLVKKDYDPEPVTVS 180  
Db 121 V-GLLPGYWGQGLTVLTASAATTPPSVYPLACGGDTGSSVTGLGCLVKGYPFESVTVT 179  
Qy 181 WNSGALTSGVHTFPVAVLQSSGLYSLSVWTVPSLSLGTQTYICNVNHPKNTKVDKRVPE 240  
Db 180 WNSGSLSSSVHTFPALLQ-SGLYTMSSSVTPSPSTWPSQVTCVSAHPASSTTVDDKLEP 238  
Qy 241 KSCDKT-HTCPCP-----CPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED 293  
Db 239 SGPTSTINPCPCCKECHKCPAPNLEGGPSVFIFPPNPKDVLMLSLTPKVCVVDVSEDD 298  
Qy 294 PEVKFNWYVDGVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPA 353  
Db 299 PDVQISWFMVNNVEVLTAQTQTHREDYNSTIRVVSALDIQHDWMSGKEFKCKVNNKDLPA 358  
Qy 354 PIEKTSKAKGQPREQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENN 413  
Db 359 PIERTSKIKGIYRAQVYTLSPPEQLSRKDVSLTCLAVGFSPEDISVEWTSNGHTEEN 418  
Qy 414 YKTTTPVLSDSGFFLYSKLTVDKSRWQGNVFCSCYMHAEALHNHYTKSLSPGK 470  
Db 419 YKDTAPVLSDGSYFYIYSLKNMKTSEKWEKTDSPSCNVRHEGLKNYLLKTKTISRSPGK 475

RESULT 11  
S31459  
Ig gamma-1 chain - sheep (fragment)  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 16-Jul-1999  
C:Accession: S31459  
R:Patri, S.; Nau, F.  
submitted to the EMBL Data Library, December 1992  
A:Reference number: S31459



Qy	196	VLQSSGLYSLSVVVTPSSSLGTQTYICNVNHHKPSNTKYDKRVRPEKSCDKTHTCP--CP	255
Db	176	VLQSD-LYTLSSSTVPSSTWSPSTVTCNVNHHKPSNTKYDKRVRPEKSCDKTHTCPDGC---CKPCICT	230
Qy	254	APELLGSPSVFLPPPKDKDTLMISRPEVTCVVVDYSHEDPEVKENNYVDGVEVINAKTK	313
Db	231	VPEV---SSVFIPPPKDKDVLTLTPKVKTCVVVDISKDDPEVQFSWFVDDVEVHTAQIQ	287
Qy	314	PREEQYNSTRVYSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYT	373
Db	288	PREEQFNSTRYSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRKPAQVYT	347
Qy	374	LPPSRBEWTKNOVSLTCLVKGFYPSDIAEVESNGQPENNYKTTPPVLDSDGSFFLYSKL	433
Db	348	IPPKQEMAKDKVSLTCMTIDFPEDITVEMQWNGQPAENYKNTQPIMDTDGSYFYVYSKL	407
Qy	434	TVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPCK	470
Db	408	NVQKSNWEAGNTFCSVLHGLEHNNHTEKLSLSPCK	444
RESULT 14			
I47159			
Ig gamma 2a chain constant region - pig (fragment)			
C:Species: Sus scrofa domestica (domestic pig)			
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000			
C:Accession: I47159			
R:Kacskovics, I.; Sun, J.; Butler, J. E.			
J. Immunol. 153, 3565-3573, 1994			
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequence			
A:Reference number: I47158; MUID:95015845			
A:Accession: I47159			
A>Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: mRNA			
A:Residues: 1-328 <KAC>			
A:Cross-references: EMBL:U03779; NID:g433123; PID:AAA52217.1; PID:g433124			
C:Genetics:			
A:Gene: IGG2a			
C:Superfamily: immunoglobulin C region; immunoglobulin homology			
F:133-202/Domain: immunoglobulin homology <IMM>			
Query Match 50.3%; Score 1267; DB 2; Length 328;			
Best Local Similarity 69.9%; Pred No. 1.6e-65;			
Matches 232; Conservative 42; Mismatches 52; Indels 6; Gaps			
Qy	141	ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVWSNKGALTSGVHTFPAVLQSS	200
Db	1	APKTAPSVYPLAPCSRDTSPGNVALGCLASSYFPEPTVTWNSGALSSGVHTFPSVLQPS	60
Qy	201	GLYSLSLVTVTPSSSLGTQTYICNVNHHKPSNTKYDKRVRPEKSCDKTHTCPCPAPELLGG	260
Db	61	GLYSLSMWTVTPASSLSKSKSYTCNVNHPATTTKYDKRVGTTKTKPCPCIPACESP---g	116
Qy	261	PSVLFPPPKDKDTLMISRPEVTCVVVDYSHEDPEVKENNYVDGVEVINAKTKPREEQYN	320
Db	117	PSVFIPPPKDKDTLMISRTPQVTCVVVDYSQENPEVQFSWYDGVEVHTAQTRPKEEQFN	176
Qy	321	STRVYSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSRRE	380
Db	177	STRVYSLVLP IQHODWLNGKEFKCKVNNKDLPAPIRIISKAKGTREPPQVYTLPPHAE	236
Qy	381	MTKNQVSLTCLVKGFYPSDIAEVESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKS	438
Db	237	LSRSKVSITCLVIGFPPDIDVEMQWNGQPEEGNVRTPTPOQDVDTGTYFYLSKFSVDKA	296
Qy	439	RWQGNVFCSCVMHEALHNHYTKQSLSLSPCK	470
Db	297	SWOGGGIFQCAVMHEALHNHYTKQSLSPCK	328

RESULT  
I47160  
15

1

Ig gamma 2b chain constant region - pig (fragment)  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
 C:Accession: I47160  
 E:Kacs Kovics, I.; Sun, J.; Butler, J.E.  
 J. Immunol. 153, 3563-3573, 1994  
 A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of  
 A:Reference number: I47158; MUID:95015845  
 A:Accession: I47160  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-328 <KAC>  
 A:Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126  
 C:Genetics:  
 A:Gene: IgG2b  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 E:I33-202/Domain: immunoglobulin homology <IMM>

	Query Match	50.1%	Score 1261;	DB 2;	Length 328;
	Best Local Similarity	69.6%	Pred. No. 3.6e-65;		
	Matches 231;	Conservative 41;	Mismatches 54;	Indels 6;	Gaps 2;
Qy	141	ASTGKPSVFPIAPSKSTSGGTAALGCLVKDYFPEPVTYVNSNGALTSGVHTFPAVLQSS	200		
Db	1	APKTAFLVPLAPGRDTSQGNVALGCLASSYFPEPVTYVNSGALTSGVHTFPSVLQPS	60		
Qy	201	GLYSLSVVTVPPSSLSGQTQYICNVNHNKPSNTKVDKRYEPKSCDKTHTCPAPPELLGG	260		
Db	61	GLYSLSVVTVPPSSLSKSTCNVHNHPTATTKVDKRVGTGKTKPCPCIPACESP---G	116		
Qy	261	PSVFLFPKPKDITLMISRTPEVTCCVVDVSHEDPEVKFNWYDGVGEVHNAKTKPREQYN	320		
Db	117	PSVFIFFPKPKDITLMISRTPTQVVDVDSQENPEVQFSWYDGVGEVHTAQTRPKREQFN	176		
Qy	321	STYRVWSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTIISAKAGQPREPQVYTLPPSREE	380		
Db	177	STYRVWSVLPTQHDWLNGKEFKCKVNNKNDLPAPITRIISAKAGQTRPEPQVYTLPPHAE	236		
Qy	381	MTKNQVSLTCLVKGFPSPDIAYEVESNQ--PENNYKTPPVLDSGFFLYSKLTVDKS	438		
Db	237	LSRSKVSITCLVIGFYPPDIDVEHQRNQPPPEGNRYRTPPQQDVGDTYFLYSKFSVDKA	296		
Qy	439	RWQGNVFCSCVMHEALHNHYTKQSLSLSPGK	470		
Db	297	SWGGGIGFOCAVMHEALHNHYTKQSLSKTPGK	328		

Search completed: August 14, 2002, 15:19:03  
Job time: 691 sec



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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:23:16 ; Search time 53.64 Seconds  
(without alignments)  
339.265 Million cell updates/sec

Title: US-09-499-662-157

Perfect score: 2518

Sequence: 1 MGWSCILFLVATATGVHSQ.....MHEALHNHYTQKSLSPGK 470

Scoring table:  
BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1758	69.8	330	1 GCL_HUMAN	P01857 homo sapien
2	1610	63.9	326	1 GCL_HUMAN	P01859 homo sapien
3	1599.5	63.5	327	1 GCL_HUMAN	P01861 homo sapien
4	1231.5	48.9	323	1 GC_RABIT	P01870 oryctolagus
5	1210.5	48.1	329	1 GC2_CAVPO	P01862 cavia porce
6	1162	46.1	290	1 GCL_HUMAN	P01860 homo sapien
7	1155	45.9	326	1 GCL_RAT	P02759 rattus norv
8	1150	45.7	329	1 GCL_MOUSE	P22436 mus musculu
9	1145	45.5	324	1 GCL_MOUSE	P01868 mus musculu
10	1144.5	45.5	333	1 GCB_RAT	P20761 rattus norv
11	1140	45.3	393	1 GCL_MOUSE	P01869 mus musculu
12	1139	45.2	398	1 GCB_MOUSE	P03987 mus musculu
13	1129	44.8	330	1 GCAA_MOUSE	P01863 mus musculu
14	1127.5	44.8	329	1 GCC_RAT	P20762 rattus norv
15	1126.5	44.7	335	1 GCB_MOUSE	P01864 mus musculu
16	1124	44.6	399	1 GCB_MOUSE	P01865 mus musculu
17	1115	44.3	322	1 GCA_RAT	P20760 rattus norv
18	1085	43.1	336	1 GCB_MOUSE	P01866 mus musculu
19	1080	42.9	405	1 GCB_MOUSE	P01867 mus musculu
20	540.5	21.5	139	1 HV07_MOUSE	P01751 mus musculu
21	509	20.2	117	1 HV06_MOUSE	P01750 mus musculu
22	506.5	20.1	137	1 HV11_MOUSE	P01755 mus musculu
23	502	19.9	138	1 HV48_MOUSE	P03980 mus musculu
24	497	19.7	117	1 HV05_MOUSE	P01749 mus musculu
25	495	19.7	117	1 HV1G_HUMAN	P23083 homo sapien
26	492	19.5	140	1 HV02_MOUSE	P01746 mus musculu
27	486.5	19.3	429	1 EPC_RAT	P01855 rattus norv
28	486	19.3	428	1 EPC_HUMAN	P01854 homo sapien
29	485	19.3	117	1 HV09_MOUSE	P01753 mus musculu
30	484	19.2	117	1 HV1B_HUMAN	P01743 homo sapien
31	480	19.1	117	1 HV04_MOUSE	P01748 mus musculu
32	471	18.7	421	1 EPC_MOUSE	P06336 mus musculu
33	469	18.6	117	1 HV49_MOUSE	P06328 mus musculu

ALIGNMENTS

RESULT 1

ID	GCL_HUMAN	STANDARD;	PRT;	330 AA.
AC	P01857;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	ig gamma-1 chain C region.			
GN	IGHG1.			
OS	Homo sapiens (Human).			P01744 homo sapien
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			P01754 mus musculu
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			P01759 mus musculu
OX	NCBI_TaxID=9606;			P01871 homo sapien
RN	[1]			P01872 mus musculu
RP	SEQUENCE FROM N.A.			P06329 mus musculu
RX	MEDLINE=82274236; PubMed=6287432;			P01756 mus musculu
RA	Ellison J.W., Berson B.J., Hood L.E.;			P01755 mus musculu
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene."			P03988 oryctolagus
RL	Nucleic Acids Res. 10:4071-4079(1982).			P01873 mus musculu
RN	[2]			P01747 mus musculu
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			P04221 oryctolagus
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RT	Waxdal M.J., Edelman G.M.;			
RL	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."			
RN	Biochemistry 9:3161-3170(1970).			
RP	SEQUENCE OF 136-329 (EU).			
RX	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RT	Edelman G.M.;			
RL	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."			
RN	Biochemistry 9:3171-3181(1970).			
RP	SEQUENCE (MYELOMA PROTEIN NIE).			
RX	MEDLINE=77070269; PubMed=826475;			
RA	Ponstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).			
RN	[5]			
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RX	MEDLINE=83289131; PubMed=6884994;			
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RT	"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."			
RN	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).			
RP	[6]			
RX	DISULFIDE BONDS.			
RA	MEDLINE=71064027; PubMed=4923144;			
RT	Gall W.E., Edelman G.M.;			
	"The covalent structure of a human gamma G-immunoglobulin. X.			

RT Intrachain disulfide bonds.";  
RL Biochemistry 9:3188-3196(1970).  
RN [7]  
RP DISULFIDE BONDS.  
RX MEDLINE=77070267; PubMed=1002129;  
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal  
RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and  
RT characterization of the protein, the L- and H-chains, the  
RT cyanogen bromide cleavage products, and the disulfide bridges.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
RN [8]  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
RX MEDLINE=81208100; PubMed=7236608;  
RA Deisenhofer J.;  
RT "Crystallographic refinement and atomic models of a human Fc fragment  
RT and its complex with fragment B of protein A from Staphylococcus  
RT aureus at 2.9- and 2.8-A resolution.";  
RL Biochemistry 20:2361-2370(1981).  
CC -1- MISCELLANEOUS: NIE HAS THE G1M(17) ALLOTYPIC MARKER, 97-K, & THE  
CC G1M(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE G1M(3)  
CC MARKER & THE G1M (NON-1) MARKERS.  
CC -1- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF  
CC 35,116,198,269 & 272.  
CC -1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES  
CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES  
CC 268-272.  
CC -1- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF  
CC RESIDUES 198,267&272.  
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DR EMBL; J00228; AAC82527.1; ALT\_INIT.  
DR PIR; A02146; GHU.  
DR PDB; 1FC1; 15-JUL-92.  
DR PDB; 1FC2; 15-JUL-92.  
DR MIM; 147100; -.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003600; Ig\_Like.  
DR Pfam; PF00047; ig; 3.  
DR SMART; SM00410; Ig\_Like; 1.  
DR SMART; SM00407; Igcl; 2.  
DR PROSITE; PS00290; IG\_MHC; 2.  
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
KW 3D-structure.  
FT NON\_TER 1 1  
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FT DOMAIN 99 110 HINGE.  
FT DOMAIN 111 223 CH2.  
FT DOMAIN 224 330 CH3.  
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FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).  
FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).  
FT DISULFID 144 204  
FT DISULFID 250 308  
FT CARBOHYD 180 180  
FT MOD\_RES 330 330  
FT VARIANT 97 97  
FT VARIANT 239 239  
FT VARIANT 241 241  
FT STRAND 123 126  
FT HELIX 130 134

FT TURN 136 137  
FT STRAND 141 148  
FT STRAND 158 162  
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FT HELIX 238 240  
FT TURN 241 242  
FT STRAND 245 256  
FT STRAND 260 266  
FT TURN 267 268  
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FT TURN 283 284  
FT STRAND 287 296  
FT HELIX 297 301  
FT TURN 302 303  
FT STRAND 306 312  
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FT TURN 316 317  
FT STRAND 320 324  
SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;  
  
Query Match 69.8%; Score 1758; DB 1; Length 330;  
Best Local Similarity 99.1%; Pred. No. 1.1e-114;  
Matches 327; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
  
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DB 1 ASTKGSVPPLAPSSKSTSGTAAALCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
  
QY 201 GLYSLSVVTVPSSSLGTQYICNVNHPKSTKVDKRVKPKCDKHTCCPCPAPELLGG 260  
DB 61 GLYSLSVVTVPSSSLGTQYICNVNHPKSTKVDKRVKPKCDKHTCCPCPAPELLGG 120  
  
QY 261 PSVFLEPPPKDFTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNKATKPREQYN 320  
DB 121 PSVFLEPPPKDFTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNKATKPREQYN 180  
  
QY 321 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPSREE 380  
DB 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPSREE 240  
  
QY 381 MTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 440  
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 300  
  
QY 441 QGQNVFSCSVMHREALHNYTKQSLSPGK 470  
DB 301 QGQNVFSCSVMHREALHNYTKQSLSPGK 330  
  
RESULT 2  
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ID GC2\_HUMAN STANDARD; PRT; 326 AA.  
AC P01859;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Ig gamma-2 chain C region.  
GN IGHG2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.



OX NCBI\_TaxID=9606;  
 RP [1]  
 RP SEQUENCE OF 2-326 FROM N.A.  
 RP MEDLINE=82197621; PubMed=6804948;  
 RA Ellison J.W., Hood L.E.;  
 RA "Linkage and sequence homology of two human immunoglobulin gamma  
 heavy chain constant region genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).  
 RP [2]  
 RP SEQUENCE OF 88-115 FROM N.A.  
 RP TISSUE=Fetal liver;  
 RC MEDLINE=83001943; PubMed=6811139;  
 RC Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;  
 RA "Structure of human immunoglobulin gamma genes: implications for  
 evolution of a gene family.";  
 RL Cell 29:671-679(1982).  
 RP [3]  
 RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.  
 RP TISSUE=Fetal liver;  
 RC MEDLINE=84235992; PubMed=6329676;  
 RC Krawinkel U., Rabbitts T.H.;  
 RA "Comparison of the hinge-coding segments in human immunoglobulin gamma  
 heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass  
 genes.";  
 RL EMBO J. 1:403-407(1982).  
 RP [4]  
 RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).  
 RP MEDLINE=81007873; PubMed=6774012;  
 RA Wang A.-C., Tung E., Fudenberg H.H.;  
 RA "The primary structure of a human IgG2 heavy chain: genetic,  
 evolutionary, and functional implications.";  
 RL J. Immunol. 125:1048-1054(1980).  
 RP [5]  
 RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).  
 RP MEDLINE=80001357; PubMed=113060;  
 RA Connell G.E., Parr D.M., Hofmann T.;  
 RA "The amino acid sequences of the three heavy chain constant region  
 domains of a human IgG2 myeloma protein.";  
 RL Can. J. Biochem. 57:758-767(1979).  
 RP [6]  
 RP SEQUENCE OF 238-275 (ZIE).  
 RP MEDLINE=80114419; PubMed=118920;  
 RA Hofmann T., Parr D.M.;  
 RA "A note of the amino acid sequence of residues 381-391 of human  
 immunoglobulins gamma chains.";  
 RL Mol. Immunol. 16:923-925(1979).  
 RP [7]  
 RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).  
 RA Hofmann T., Parr D.M.;  
 RA Submitted (MAR-1980) to the PIR data bank.  
 RP [8]  
 RP SEQUENCE OF 1-121 (DOT).  
 RP MEDLINE=9525298; PubMed=7737190;  
 RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;  
 RA "Characterization of the two unique human anti-flavin monoclonal  
 immunoglobulins.";  
 RL Eur. J. Biochem. 228:886-893(1995).  
 RP [9]  
 RP DISULFIDE BONDS.  
 RP MEDLINE=72033500; PubMed=4940472;  
 RA Milstein C., Frangione B.;  
 RA "Disulphide bridges of the heavy chain of human immunoglobulin G2.";  
 RL Biochem. J. 121:217-225(1971).  
 RP [10]  
 RP DISULFIDE BONDS.  
 RP MEDLINE=69064124; PubMed=5782707;  
 RA Frangione B., Milstein C., Pink J.L.;  
 RA "Structural studies of immunoglobulin G.";  
 RL Nature 221:145-148(1969).  
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 DR EMBL; J00230; AAB59393.1; -;  
 DR PIR; A02148; G2HU.  
 DR HSSP; P01857; 1FC1.  
 DR MIN; 147110; -;  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003597; Ig\_C1.  
 DR InterPro; IPR003600; Ig\_Like.  
 DR Pfam; PF00047; Ig; 3.  
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 DR SMART; SM00407; Igel; 2.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 KW Immunoglobulin domain; Immunoglobulin C region.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 98 CH1.  
 FT DOMAIN 99 110 HINGE.  
 FT DOMAIN 111 219 CH2.  
 FT DOMAIN 220 326 CH3.  
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 27 83  
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 140 200  
 FT DISULFID 246 304  
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 FT MOD\_RES 326 326  
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 FT CONFLICT 109 109 AT OR NEAR THE COMPLEMENT-BINDING SITE.  
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 Query Match 63.9%; Score 1610; DB 1; Length 326;  
 Best Local Similarity 91.8%; Pred. No. 1.9e-104;  
 Matches 303; Conservative 10; Mismatches 13; Indels 4; Gaps 2;  
 Qy 141 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 200  
 Db 1 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
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 Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKPEKSCDKTHTCPCPAPPELLGG 116  
 Qy 261 PSVFLFPPKPKDTLMISRTPEVTCVYVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320  
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 Qy 321 STYRVVSVLTVHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSREE 380  
 Db 177 STFRVYSLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREE 236  
 Qy 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 440  
 Db 237 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 296  
 Qy 441 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470  
 Db 297 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 326  
 RESULT 3  
 ID GC4\_HUMAN STANDARD; PRG; 327 AA.  
 AC P01861;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DR 21-JUL-1986 (Rel. 01, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Ig gamma-4 chain C region.  
GN IGHG4.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83157104; PubMed=6299662;  
RA Ellison J.W., Buxbaum J.N., Hood L.E.;  
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";  
RL DNA 1:11-18(1981).  
RN [2]  
RP SEQUENCE OF 1-30 AND 81-326.  
RX MEDLINE=70207560; PubMed=4192699;  
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;  
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the  
constant region of a gamma 4 chain.";  
RL Biochem. J. 117:33-47(1970).  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; K01316; AAB59394.1; ALT\_INIT.  
DR PIR; A02150; G4HU.  
DR HSSP; P01842; 7FAB.  
DR MIM; 147130; -.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003597; Ig\_C1.  
DR InterPro; IPR003600; Ig\_Like.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00410; Ig\_Like; 1.  
DR SMART; SM00407; IgC1; 2.  
DR PROSITE; PS00290; IG\_MHC; 2.  
KW Immunoglobulin domain; Immunoglobulin C region.  
FT NON\_TER 1  
FT DOMAIN 1 98 CH1.  
FT DOMAIN 99 110 HINGE.  
FT DOMAIN 111 220 CH2.  
FT DOMAIN 221 327 CH3.  
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).  
FT DISULFID 27 83  
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 141 201  
FT DISULFID 247 305  
FT SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;  
  
Query Match 63.5%; Score 1599.5; DB 1; Length 327;  
Best Local Similarity 91.8%; Pred. No. 1e-103;  
Matches 303; Conservative 15; Mismatches 15; Gaps 1;  
  
QY 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200  
DB 1 ASTKGPSVFPLAPSSKSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
QY 201 GLYSLSVVTVPSSSLGTYTCNVNHPKSNTKVDRKRPKCDKTHTCPPCPAPPELLGG 260  
DB 61 GLYSLSVVTVPSSSLGTYTCNVNHPKSNTKVDRKRPKCDKTHTCPPCPAPPELLGG 117  
QY 261 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYN 320  
DB 118 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQFN 177  
QY 321 STYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIETISKAKGQPREPQVYTLPPSREE 380  
DB 118 STYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIETISKAKGQPREPQVYTLPPSREE 380

Db 178 STYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIETISKAKGQPREPQVYTLPPSREE 237  
QY 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRW 440  
Db 238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRW 297  
QY 441 QCGNVPSCSVMHHEALHNHYTQKSLSLSPGK 470  
Db 298 QCGNVPSCSVMHHEALHNHYTQKSLSLSPGK 327  
  
RESULT 4  
GC\_RABIT ID GC\_RABIT STANDARD; PRT; 323 AA.  
AC P01870;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig gamma chain C region.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=84030930; PubMed=6313520;  
RA Bernstein K.E., Alexander C.B., Mage R.G.;  
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant  
F-I haplotype.";  
RL Immunogenetics 18:387-397(1983).  
RN [2]  
RP SEQUENCE OF 1-128.  
RX MEDLINE=76135469; PubMed=1243651;  
RA Pratt D.M., Mole L.E.;  
RT "Sequence studies on the constant region of the Fd sections of rabbit  
immunoglobulin G of different allotype.";  
RL Biochem. J. 151:337-349(1975).  
RN [3]  
RP SEQUENCE OF 88-266 FROM N.A.  
RX MEDLINE=83299917; PubMed=6193512;  
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;  
RT "Heavy chain genes of rabbit IgG: Isolation of a cDNA encoding gamma  
heavy chain and identification of two genomic C gamma genes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).  
RN [4]  
RP SEQUENCE OF 132-161.  
RX MEDLINE=70110015; PubMed=5461106;  
RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;  
RT "Sequence studies of the Fd section of the heavy chain of rabbit  
immunoglobulin G.";  
RL Biochem. J. 116:249-259(1970).  
RN [5]  
RP SEQUENCE OF 129-131 AND 155-322.  
RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;  
RL (In) Killeander J. (eds.);  
RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,  
Stockholm (1967).  
CC -!- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,  
104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15  
MARKERS AND REF.5 THE E15 MARKER.  
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CC -----  
DR EMBL; M16426; AAA31289.1; -.  
DR PIR; A02161; GHRB.  
DR HSSP; P01857; 1FC1.  
DR InterPro; IPR003006; Ig\_MHC.

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DR InterPro; IPR003597; Ig_cl.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 N -> E (IN REF. 2).
FT CONFLICT 71 71 V -> VPV (IN REF. 2).
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 173 173 N -> D (IN REF. 5).
FT CONFLICT 187 187 Q -> E (IN REF. 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 Q -> E (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 N -> D (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> D (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).
FT CONFLICT 284 284 N -> S (IN REF. 5).
SQ SEQUENCE 323 AA; 35404 MW; 69E8AAl18D579A8B CRC64;

Query Match 48.9%; Score 1231.5; DB 1; Length 323;
Best Local Similarity 70.0%; Pred. No. 2.8e-78;
Matches 229; Conservative 34; Mismatches 57; Indels 7; Gaps 2;

QY 144 KGPSVEPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLY 203
DB 4 KAPSVFELAPCCGTPSSFTVLGKGLYLPETVTVWNSGTLNGLVTFPSVQSSGLY 63

QY 204 SLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVKPEKSCDKTHPCPCAPELILGGPSV 263
DB 64 SLSSVSVTSSS---QPTVCNVHPATNTKYDKTVAPSTCSK----PTCPPPELLGGPSV 116

QY 264 FLFPKPDKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYNSTY 323
DB 117 FIFPPKPKDTLMISRTPEVTCVVDVSDQDPEVQFTWYINNEQVTRAPPLRQEQFNSTI 176

QY 324 RVSVTLVTHDNLGKGVCKVSKNKPALPAIEKTIKAKGPQREPOVYTLPPSREMTK 383
DB 177 RVSVTLVTHDNLGKGVCKVSKNKPALPAIEKTIKAKGPQREPOVYTLPPSREMTK 236

QY 384 NOVSLTCLVKGYFSPDIAVESNGSQPNKYKTPPVLDSDGSFEFLYSKLTVKDSRMQQG 443
DB 237 RVSLSLTCLVKGYFSPDIAVESNGSQPNKYKTPPVLDSDGSFEFLYSKLTVKDSRMQQG 296

QY 444 NVFSCSVNHEALHNHYTQKSLSLSPGK 470
DB 297 DVFTCSVNHEALHNHYTQKSLSLSPGK 323

RESULT 5
GC2_CAVPO STANDARD; PRT; 329 AA.
ID GC2_CAVPO
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
OX NCBI_TaxId=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
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RA Birshstein B.K., Hussain Q.Z., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT half-cystine joining heavy and light chains.";
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT and hinge region cyanogen bromide fragments.";
RL Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4804-4811(1974).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:26-31(1971).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC 13 INBRED GUINEA PIGS.
DR PIR; A02151; G2GP.
DR HSP; P01772; 2EB4.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003597; IG_cl.
DR InterPro; IPR003600; IG_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202 N-LINKED (GLCNAC. . .).
FT CARBOHYD 178 178
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 48.1%; Score 1210.5; DB 1; Length 329;
Best Local Similarity 69.8%; Pred. No. 8.1e-77;
Matches 233; Conservative 30; Mismatches 62; Indels 9; Gaps 4;

QY 140 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 199
DB 1 SARTTAPSVFPLAASCVDTSGMTGLGKLVGYPPEPTVKVNSGALTSGVHTFPAVLQ- 59

QY 200 SGLYSLSVSVVTPSSSLGTQTYICNVNHNKPSNTKVDKRVKPEKSCDKTH--TCPPCAPDEL 257
DB 60 SGLYSLSVSVVTPSSSLGTQTYICNVNHNKPSNTKVDKRVKPEKSCDKTH--TCPPCAPDEL 115

QY 258 LGGPSVFLFPKPDKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREE 317
DB 116 LGGPSVFLFPKPDKDTLMISRTPEVTCVVDVSDQDPEVQFTWYINNEQVTRAPPLRVE 175
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Db 179 ISKTGQPREPOVYTLPPSREMTKNOVSLTCLVKGFPSPDIADVWESSGQPENNYNTTP 238
Qy 419 PVLSDSGSFFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTOKSLSLSPCK 470
Db 239 PMLSDSGSFFLYSLKLTVDKSRWQGNIFCSCVMHEALHNHYTOKSLSLSPCK 290

RESULT 7
GCI_RAT STANDARD; PRT; 326 AA.
AC P20759;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR: PS0017; PS0017.
DR HSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Igcl; 2.
DR PROSITE; PS00290; Ig_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1
FT DOMAIN 1 97 CHI.
FT DOMAIN 98 112 HINGE.
FT DOMAIN 113 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match 45.9%; Score 1155; DB 1; Length 326;
Best Local Similarity 63.4%; Pred. No. 5.5e-73;
Matches 211; Conservative 52; Mismatches 60; Indels 10; Gaps 4;

Qy 141 ASTKGPSVEPLAPSSKSTSGTALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200
Db 1 AETAPSYIPLAPGATLKSNNVTGLCLVKGYFPEPTVTWNSGALTSGVHTFPAVLQ-S 59

Qy 201 GLYSLSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKRVKPSCKDKTHTCP-PCAPPELLG 260
Db 60 GLYLTSSVTVPSSTWPSQVTCNVNHNKPSNTKVDKRVKPSCKDKTHTCP-PCAPPELLG 113

Qy 261 ---PSVFLFPPKPKDMLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVNHNKTKPRE 317
Db 114 SEVSVFIFPPKPKDMLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVNHNKTKPRE 173

Qy 318 QYNSTYRVVSVLTVLDHDLNKGKYEKCVSNKALPAPIETISKAKGPREPQVITLPPS 377
Db 174 QFNSTFRSVSELPITLDHDLNNGRTFRCKVTSAAPFSPSIEKTIKPEGRQTQVPHYVTSPT 233

Qy 378 REEMTKNOVSLTCLVKGFPSPDIADVWESSGQPENNYNTTPPVLSDSGSFFLYSLKLTVDK 437
Db 234 KEEMTKNOVSLTCLVKGFPSPDIADVWESSGQPENNYNTTPPVLSDSGSFFLYSLKLTVDK 293

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Qy 438 SRWQGNVFCSCVMHEALHNHYTOKSLSLSPCK 470
Db 294 EKWQGNFTFTCSVLHGLNHNHTEKSLSHSPCK 326

RESULT 8
GCI_MOUSE STANDARD; PRT; 329 AA.
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A.; Word C.J.; Rimm D.; Der-Balan G.P.; Martinez H.M.;
RA Tucker P.W.; Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
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CC -----
CC EMBL; J00451; -; NOT_ANNOTATED_CDS.
CC PIR: B02156; G3MSC.
CC HSP; P01857; 1FC1.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003597; Ig_cl.
CC InterPro; IPR003600; Ig_like.
CC Pfam; PF00047; Ig; 3.
CC SMART; SM00410; Ig_Like; 1.
CC SMART; SM00407; Igcl; 2.
CC PROSITE; PS00290; Ig_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1
FT DOMAIN 1 97 CHI.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 45.7%; Score 1150; DB 1; Length 329;
Best Local Similarity 65.0%; Pred. No. 1.2e-72;
Matches 215; Conservative 44; Mismatches 68; Indels 4; Gaps 3;

Qy 142 STKGPSVEPLAPSSKSTSGTALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 201
Db 1 TTTAPSYIPLVPGSDTSGSSVTGLCLVKGYFPEPTVKNYNGALSSGVRTVSSVLO-SG 59

Qy 202 LYSLSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKRVKPSCKDKTHTCP-PCAPPELLG 259
Db 60 FYSLSLVTVPSSTWPSQVTCNVNHNKPSNTKVDKRVKPSCKDKTHTCP-PCAPPELLG 118

Qy 260 GPSVFLFPPKPKDMLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVNHNKTKPREQY 319
Db 119 GPSVFLFPPKPKDMLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVNHNKTKPREQY 178

Qy 320 NSTYRVVSVLTVLDHDLNKGKYEKCVSNKALPAPIETISKAKGPREPQVITLPPSRE 379
Db 179 NSTYRVVSVLTVLDHDLNKGKYEKCVSNKALPAPIETISKAKGPREPQVITLPPSRE 238

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QY 380 EMTKNQVSLTCLVKGYPSPDIKAVESNQGPNKYKTPPVLDSDGSEFFLYSKLTVDKSR 439  
Db QMSKKVSLTCLVTFNEFSEISVSEWERNGELEDQYKNTPTPILDSODGTFLYSLKLTVDTD 298  
QY 440 WQGNVFCSCVMHEALHNYTKQSLSPGK 470  
Db WQGEIFTCVSVHEALHNYTKQSLSPGK 329

RESULT 9  
GCL\_MOUSE STANDARD; PRT; 324 AA.

AC P01868;  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Ig gamma-1 chain C region.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=80045036; PubMed=115593;  
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,  
RA Takahashi N., Mano Y.;  
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin  
gamma 1 chain gene.";  
RL Cell 18:559-568(1979).  
RN [2]  
RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).  
RX MEDLINE=80202559; PubMed=6769752;  
RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,  
RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;  
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences  
cloned in a bacterial plasmid.";  
RL Gene 9:87-97(1980).  
RN [3]  
RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).  
RX MEDLINE=80012837; PubMed=113776;  
RA Rogers J., Clarke P., Salser W.;  
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin  
heavy chain.";  
RL Nucleic Acids Res. 6:3305-3321(1979).  
RN [4]  
RP SEQUENCE (MYELOMA PROTEIN MOPC 21).  
RX MEDLINE=78242288; PubMed=98524;  
RA Adetugbo K.;  
RT "Evolution of immunoglobulin subclasses. Primary structure of a  
murine myeloma gamma1 chain.";  
RL J. Biol. Chem. 253:6068-6075(1978).  
RN [5]  
RP DISULFIDE BONDS (MOPC 21).  
RX MEDLINE=73008889; PubMed=5073237;  
RA Svasti J., Milstein C.;  
RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";  
RL Biochem. J. 126:837-850(1972).  
RN [6]

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DR EMBL; V00793; CAA24172.1; -  
DR EMBL; V00793; CAA24173.1; -  
DR EMBL; V00793; CAA24174.1; -  
DR EMBL; V00793; CAA24175.1; -  
DR EMBL; V00795; CAA24176.1; -  
DR PIR; A02159; GLMS.  
DR HSSP; P01842; 7FAB.

DR GlycoSuiteDB; P01868; -  
DR MGD; MGI:96446; Igh-4.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003597; Ig\_cl.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00407; IGcl; 2.  
DR PROSITE; PS00290; IG\_MHC; 1.  
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
KW Alternative splicing.

FT NON\_TER 1 1  
FT DOMAIN 1 97 CHL.  
FT DOMAIN 98 110 HINGE.  
FT DOMAIN 111 217 CH2.  
FT DOMAIN 218 324 CH3.  
FT DISULFID 27 82  
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).  
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 138 198  
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).  
FT /FTID=CAR\_000055.

FT DISULFID 244 302 REMOVED POST-TRANSLATIONALLY.  
FT MOD\_RES 324 324 N -> D (IN REF. 3).  
FT CONFLICT 276 276 N -> D (IN REF. 3).  
FT CONFLICT 278 278 N -> D (IN REF. 3).

SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;  
Query Match 45.5%; Score 1145; DB 1; Length 324;  
Best Local Similarity 62.3%; Pred. No. 2.7e-72;  
Matches 207; Conservative 55; Mismatches 60; Indels 10; Gaps 4;

QY 141 ASTKGPSVPLAPSSKTSSTGTAALCLVKDYPEPTVYSWNSGALTSVHTFPVAVLQSS 200  
Db 1 AKTTPSVTPPLAPGSAQAQNSWVTLGCLVKGYPEPTVYSWNSGSSSGVHTFPVAVLQSD 60

QY 201 GLYSLSVTVTPSSSLGTQTYICNVNHPKSNKVKRVEPKSCDKTHCTCPP--CPAPELL 258  
Db 61 -LYTLSSSVTVPSPPRSETVTCNVAHPASSTKVKDKKIVPRDCG---CKPCICTVPEV- 114

QY 259 GGPVFLFPKPKDKTLMISRTPEVTCVVDVSHEDPEVFNWYVDGVEVHNATKPREEQ 318  
Db 115 --SSVEIFPPKPKDVLITITLPKVTCTVVDVSDISKDDPEVQVSWFVDDVEVHTAQTQPREQ 172

QY 319 YNSTYRWSVLTVLHODWLNKEYCKVSNKALPAPIEKTIKAKGQPRPQVYTLPPSR 378  
Db 173 FNSTFSVSELPIHQDWLNGREFKCRVNSAAPAPIEKTIKTKGRPAQVYTIPTPK 232

QY 379 EEMTKNQVSLTCLVKGYPSPDIKAVESNQGPNKYKTPPVLDSDGSEFFLYSKLTVDKS 438  
Db 233 EQMAKDKVSLTCLMITDFFPEDITVEQWNGQPAENYKNTQPIINTNGSVFVSKLVNQS 292

QY 439 RWOQGNVFCSCVMHEALHNYTKQSLSPGK 470  
Db 293 NWEAGNTFTCSVLHGLHNHHTKSLSPGK 324

RESULT 10  
ID GCL\_MOUSE STANDARD; PRT; 333 AA.  
AC P20761;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig gamma-2b chain C region.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89232738; PubMed=3149946;

```
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0018;
DR HSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig-like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG_Like; 1.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
SQ SEQUENCE 333 AA; 3649 MW; 55F8B64D48D460A6 CRC64;

Query Match 45.5%; Score 1144.5; DB 1; Length 333;
Best Local Similarity 63.7%; Pred. No. 3e-72;
Matches 214; Conservative 45; Mismatches 68; Indels 9; Gaps 3;

QY 141 ASYKGPSVFPPLAPSSKTSCTAALGLVDYPPPEVTVSWNSGALSGVHTFPVAVLQSS 200
Db 1 AQTAPSVFPLAPCGDGTSTVTGLGVGYPPPEVTVTWSGALSSDVHTFPVAVLQ-S 59

QY 201 GLXSLSWVVPSSSLGTQYICNVNHPKPSNTKVKDKEPKS-----CDKTHTCPCPA 254
Db 60 GLYLTSSVT--SSTWFSQVITCVNAPASTKVDKKVERRNGIGHKCTCTCHKCPV 117

QY 255 PELGGPSVFLFPKPKDLMISRTPEVTVVVDVSHEDPEVKFNMVYDGVVEVHNAKTKP 314
Db 118 PELGGPSVFLFPKPKDILLISQNAKVTVCVVDVSEEDPVQPSFVNVEVHTAQTP 177

QY 315 REQYNSTYRVSVLTVHDLNGEKYCKVSNKALPAPIEKTIISKAKGPPEPVYTL 374
Db 178 REQYNSTYRVSVLTVHDLNGEKYCKVSNKALPAPIEKTIISKAKGPPEPVYTL 374

QY 375 PPSEEMTKNQVSLTCLVKGFYPSDIAVEESNGQPENNYKTTPPVLDSDGSFFLYSKLT 434
Db 238 GPTEQLTEQTVSLTCLTSGLFNDIGVETSNGLHIEKNYKNTPEVWDSGDSFFMYSKLN 297

QY 435 VDKSRWQGNVFSVSMHEALHNHYTQKSLSLSPGK 470
Db 298 VERSRWDSRAPFCVSVVHEGLNHHHVEKSISSRPFGK 333

RESULT 11
GC1M_MOUSE STANDARD; PRT; 393 AA.
AC P01869;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-1 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.:
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
```

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RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 323-393 FROM N.A.
RX MEDLINE=82197626; PubMed=6804950;
RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
RT "mRNA for surface immunoglobulin gamma chains encodes a highly
conserved transmembrane sequence and a 28-residue intracellular
domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
RN [3]
RP SEQUENCE OF 323-366 FROM N.A.
RX MEDLINE=82115295; PubMed=6799207;
RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA Eisenberg D., Wall R.;
RT "Gene segments encoding transmembrane carboxyl termini of
immunoglobulin gamma chains.";
RL Cell 26:19-27(1981).
RN [4]
RP SEQUENCE OF 1-44 FROM N.A.
RX MEDLINE=82222190; PubMed=6283537;
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
immunoglobulin gamma chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
SEGMENT OF MU CHAINS.
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CC EMBL; V00793; CAA24172.1; -
CC EMBL; V00793; CAA24173.1; -
CC EMBL; V00793; CAA24174.1; -
CC PIR; B02159; GIMSM.
CC HSP; P01842; 7FAB.
CC MGD; MGI:96446; Igh-4.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003597; Ig-cl.
CC Pfam; PF00047; Ig; 3.
CC SMART; SM00407; IGC1; 2.
CC PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing; Transmembrane.
FT NON_TER 1
FT DOMAIN 1 97 CHI.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
FT DISULFID 244 302 POTENTIAL.
FT TRANSEM 340 357 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 358 393
SQ SEQUENCE 393 AA; 43386 MW; 4CC88343B7AICE27 CRC64;

Query Match 45.3%; Score 1140; DB 1; Length 393;
Best Local Similarity 62.2%; Pred. No. 7.6e-72;
Matches 206; Conservative 55; Mismatches 60; Indels 10; Gaps 4;
```





RX MEDLINE=81223894; PubMed=6787604;  
 RA Olio R., Aufiray C., Morchamps C., Rougeon F.;  
 RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes  
 RT suggests that exons can be exchanged between genes in a multigenic  
 RT family";  
 RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).  
 RN [4]  
 RP MYELOMA PROTEIN MOPC 173.  
 RA MEDLINE=74175517; PubMed=4831970;  
 RX Bourgois A., Fougereau M., Rocca-Serra J.;  
 RT "Determination of the primary structure of a mouse IgG2a  
 RT immunoglobulin: amino-acid sequence of the Fc fragment. Implications  
 RT for the evolution of immunoglobulin structure and function.";  
 RL Eur. J. Biochem. 43:423-435(1974).  
 RN [5]  
 RP DISULFIDE BONDS.  
 RA MEDLINE=73056887; PubMed=4565406;  
 RX De Preval C., Fougereau M.;  
 RT "Determination of the primary structure of a mouse gamma G2a  
 RT immunoglobulin. Identification of the disulfide bridges.";  
 RL Eur. J. Biochem. 30:452-462(1972).  
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 CC -----  
 DR EMBL; V00798; CAA24178.1; -;  
 DR PIR; A02152; G2MSA.  
 DR HSSP; P01842; 7FAB.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003600; Ig\_like.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00410; Ig\_like; 1.  
 DR SMART; SM00407; IGcl; 2.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 DR Immunoglobulin domain; Immunoglobulin C region.  
 KW NON\_TER 1 1 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 15 15  
 FT DISULFID 27 82  
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 144 204  
 FT DISULFID 250 308  
 FT MOD\_RES 330 330 REMOVED POST-TRANSLATIONALLY.  
 SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;  
 Query Match 44.8%; Score 1129; DB 1; Length 330;  
 Best Local Similarity 63.9%; Pred. No. 3.5e-71;  
 Matches 212; Conservative 43; Mismatches 73; Indels 4; Gaps 3;  
 Qy 141 ASTKGPSVFLPAPSKSTSGGTAALGCLVKDYFPEPTVWNSGALTSGVHTFPAVLQSD 200  
 Db 1 AKTTAPSVYPLAPVCGDTGSSVTLGCLVKGYFPEPTVLTWNSGSLSGVHTFPAVLQSD 60  
 Qy 201 GLYLSVVTPVPSSSLGTQTYICNVNHNKPSNTKVDKRVKPKSCDKTHTCPP--CPAPEL 258  
 Db 61 -LYTLSSSVTVTSSTWSPQSITCNVAHPASSTKVDKIEPRG-PTIKPCPPCKCPANLL 118  
 Qy 259 GGPVSFLEFPKPKDPLMTSRPEVTCVVVDVSHEDPEPKFNNYVDGVVEVHNAKTKPREQ 318  
 Db 119 GGPVSFIEFPKIKDVLMTSLPIVTCVVVDVSEDDPDQVQISFNFNVEVHTAQGTQTHRED 178  
 Qy 319 YNSTYRVVSVLTVLHODMLNCKEYKCKYSKALPAPIEKTISKAKGQPREPOVYTLPPSR 378  
 Db 179 YNSTLRVVSALPIQHODMWSGKEFKCKVNNKDLPAPIERTISKPKGSVRAFOVYVLPPE 238

Qy 379 EEMTKNQVSLTCLVKRGYFPYSDIAWVESNGQPENNYKTPPPLDSDGSGFLYSLKTVDKS 438  
 Db 239 EEMTKNQVSLTCLVKRGYFPYSDIAWVESNGQPENNYKTPPPLDSDGSGFLYSLKTVDKS 238  
 Qy 439 RMOQGNVFSCTSVNHEALHNYHTQKSLSLSPGK 470  
 Db 299 NWVERNSYSCVYVHEGLHNNHTTKFSRTPGK 330  
 RESULT 14  
 GCC\_RAT  
 ID GCC\_RAT STANDARD; PRT; 329 AA.  
 AC P20762;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig gamma-2c chain C region.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88166903; PubMed=3127222;  
 RA Brueggemann M., Delmastro-Galire P., Waldmann H., Calabi F.;  
 RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant  
 RT region CDNA: extensive homology to mouse gamma 3.";  
 RL Eur. J. Immunol. 18:317-319(1988).  
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 CC -----  
 DR EMBL; X07189; CAA30169.1; -;  
 DR PIR; S00847; S00847.  
 DR HSSP; P01857; 1FC1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003597; Ig-cl.  
 DR InterPro; IPR003600; Ig\_like.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00410; Ig\_like; 1.  
 DR SMART; SM00407; IGcl; 2.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Immunoglobulin domain; Immunoglobulin C region.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 97 CH1.  
 FT DOMAIN 98 113 HINGE.  
 FT DOMAIN 114 222 CH2.  
 FT DOMAIN 223 329 CH3.  
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).  
 FT DISULFID 27 82  
 FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).  
 FT DISULFID 143 203  
 FT DISULFID 249 307  
 SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;  
 Query Match 44.8%; Score 1127.5; DB 1; Length 329;  
 Best Local Similarity 62.8%; Pred. No. 4.5e-71;  
 Matches 209; Conservative 51; Mismatches 66; Indels 7; Gaps 3;  
 Qy 141 ASTKGPSVFLPAPSKSTSGGTAALGCLVKDYFPEPTVWNSGALTSGVHTFPAVLQSS 200  
 Db 1 ARTTAPSVYPLVPGCGSTSGSLVTLGCLVKGYFPEPTVTKWNSGALSSGVHTFPAVLQ-S 59  
 Qy 201 GLYLSVVTPVPSSSLGTQTYICNVNHNKPSNTKVDKRVKPKSCDKTHTCPP--CPAPEL 257  
 Db 60 GLYTLSSSVTVPSSTWSSQTVTCSVAHPATKSNLIKRIEPR---RPKPRPTDICSDDN 116

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QY 258 LGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREE 317
|||:|||||:||||:|||||:|||||:||||:|||||:||||:|||||:||||:|||||:||||:
Db 117 LGRPSVFEIPEPKDKILMITLTPKVTCCVVVDVSEEPDQVQSFVDNVRVFTAQTPHEE 176
|||:|||||:||||:|||||:|||||:||||:|||||:||||:|||||:||||:|||||:||||:
QY 318 QYNSTRVVSVLVLVHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 377
|||:|||||:||||:|||||:|||||:||||:|||||:||||:|||||:||||:|||||:||||:
Db 177 OLNGTRFVSTLHIOHODWMSGKEFKCKVNNKDLPSPIEKTISKPRGKARTPQVYIIPP 236
|||:|||||:||||:|||||:|||||:||||:|||||:||||:|||||:||||:|||||:||||:
QY 378 REDMTKNOVSLTCLVKGFPYSDIAVWESNGQPENNYKTTTPPVLDSDGSFELYSKLTVDK 437
|||:|||||:||||:|||||:|||||:||||:|||||:||||:|||||:||||:|||||:||||:
Db 237 REOMSKNKVSLTQWTSFYPASISVWERNGELEDQDKNTLPVLDSDSEYFLYSKUSVDT 296
|||:|||||:||||:|||||:|||||:||||:|||||:||||:|||||:||||:|||||:||||:
QY 438 SRMQQGNVFCSCYMHREALHNHYTKLSLSPGK 470
|||:|||||:||||:|||||:|||||:||||:|||||:||||:|||||:||||:|||||:||||:
Db 297 DSWMRGDIYTCVVVREALHNHHTQKNLSRSPGK 329
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RESULT 15
GCAB_MOUSE STANDARD; PRT; 335 AA.
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2A chain C region, B allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
RT IgG2a and IgG2b alleles of the mouse."
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN [2]
RP SEQUENCE.
RX MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwereys M., Strosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
RT chain FC regions of Ig1a and Ig1b allotypic forms."
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -1- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
CC FROM BALB/C MICE, AT 15% OF THE POSITIONS.
CC -----
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CC -----
DR EMBL; J00479; -; NOT_ANNOTATED_CDS.
DR PIR; A02153; G2MSAB.
DR HSP; P01857; 1FCL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; IGCL; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER
FT SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;
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Query Match 44.7%; Score 1126.5; DB 1; Length 335;  
Best Local Similarity 61.6%; Pred. No. 5.3e-71;

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Matches 207; Conservative 52; Mismatches 70; Indels 7; Gaps 2;
QY 141 ASTKGPSVFLPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 200
|||:|||||:||||:|||||:|||||:||||:|||||:||||:|||||:||||:|||||:||||:
Db 1 AKTAPSVYPLVPVCGGTGSSVTLCGLVKGYPEPTVLTWNSGSLSSGVHTFPALLQ-S 59
|||:|||||:||||:|||||:|||||:||||:|||||:||||:|||||:||||:|||||:||||:
QY 201 GLYSLSVWTVPSSSLGTYIYNVNHKPKNTKVDKRVKPK-----SCDKTHTCTPCPCA 254
|||:|||||:||||:|||||:|||||:||||:|||||:||||:|||||:||||:|||||:||||:
Db 60 GLVTLSSSVTVTSNTWPSQITITCNVAHPASSTKVYDKKIEPRVPIQNCPPHQVRVPCAA 119
|||:|||||:||||:|||||:|||||:||||:|||||:||||:|||||:||||:|||||:||||:
QY 255 PELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTP 314
|||:|||||:||||:|||||:|||||:||||:|||||:||||:|||||:||||:|||||:||||:
Db 120 PDLGGPSVFEIPEPKIKDVLMSLSPMVTCCVVVDVSEDDPDQVQISWVFNVEVHTAQQT 179
|||:|||||:||||:|||||:|||||:||||:|||||:||||:|||||:||||:|||||:||||:
QY 315 REQYNSTRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTL 374
|||:|||||:||||:|||||:|||||:||||:|||||:||||:|||||:||||:|||||:||||:
Db 180 HREDYNSTLRVVSALPIOHODWMSGKEFKCKVNNRALPSPIEKTISKPRGPVRAPQVYVL 239
|||:|||||:||||:|||||:|||||:||||:|||||:||||:|||||:||||:|||||:||||:
QY 375 PPSREEMTKNOVSLTCLVKGFPYSDIAVWESNGQPENNYKTTTPPVLDSDGSFELYSKLT 434
|||:|||||:||||:|||||:|||||:||||:|||||:||||:|||||:||||:|||||:||||:
Db 240 PPAEEMTKKEFSLTCTMITGFLPAETAVDWTSGRTQYKNTATVLDSDGSYPMYSKLR 299
|||:|||||:||||:|||||:|||||:||||:|||||:||||:|||||:||||:|||||:||||:
QY 435 VDKSRMQQGNVFCSCYMHREALHNHYTKLSLSPGK 470
|||:|||||:||||:|||||:|||||:||||:|||||:||||:|||||:||||:|||||:||||:
Db 300 VQKSTWERSLFAFACSVVHEVLHNHLTKTISRSLGK 335
|||:|||||:||||:|||||:|||||:||||:|||||:||||:|||||:||||:|||||:||||:

Search completed: August 14, 2002, 15:23:17
Job time: 690 sec
```

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 15:22:19 ; Search time 187.61 Seconds  
(without alignments)  
433.386 Million cell updates/sec

Title: US-09-499-662-157  
Perfect score: 2518  
Sequence: 1 MWSCILFLVATATGVHSQ.....MHEALHHYTKLSLSLSPGK 470

Scoring table:

BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.19.\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1623.5	64.5	473	11 Q9D8L4	Q9d8l4 mus musculus
2	1612.5	64.0	463	11 Q99LC4	Q99lc4 mus musculus
3	1572.5	62.5	473	11 Q99L25	Q99l25 mus musculus
4	1350	61.6	468	11 Q99L31	Q99l31 mus musculus
5	1446.5	57.4	437	11 Q99L34	Q99l34 mus musculus
6	1434.5	57.0	473	11 Q91205	Q91205 mus musculus
7	1263.5	50.2	337	6 Q95M34	Q95m34 equus caball
8	1257	49.9	701	4 Q96P08	Q96p08 homo sapien
9	967	38.4	278	11 Q92L1	Q92l1 mus musculus
10	944.5	37.5	614	4 Q96GA6	Q96ga6 homo sapien
11	875.5	34.8	481	11 Q91WT3	Q91wt3 mus musculus
12	866	34.4	500	4 Q9BRV0	Q9brv0 homo sapien
13	826.5	32.8	597	4 Q96BB9	Q96bb9 mus musculus
14	824.5	32.7	481	11 Q91WT1	Q91wt1 mus musculus
15	812	32.2	496	4 Q96DK0	Q96dk0 homo sapien
16	798	31.7	488	11 Q91WR1	Q91wr1 mus musculus

#### ALIGNMENTS

RESULT 1  
ID Q9D8L4 PRELIMINARY; PRT; 473 AA.

AC Q9D8L4;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE 181006009RIK PROTEIN.  
GN IGH-1 OR 1810060009RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=PANCREAS;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Famanaka I.,  
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto J.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RT Hayashizaki Y.;  
RL Nature 409:685-690(2001).  
DR EMBL; AK007918; BAB25349.1; -.  
DR HSSP; P01842; 7FAB.

17 764.5 30.4 597 4 Q9BU10  
18 760.5 30.2 597 4 Q9BOB8  
19 754.5 30.0 618 4 Q96AA6  
20 753 29.9 484 11 Q99LA6  
21 748 29.7 494 4 Q96K68  
22 738.5 29.3 487 11 Q99KA4  
23 735.5 29.2 479 11 Q91WP5  
24 731 29.0 613 4 Q96EY0  
25 714 28.4 486 11 Q91X07  
26 706.5 28.1 480 11 Q91XE1  
27 669 26.6 479 11 Q99M22  
28 667 26.5 482 11 Q91X92  
29 643 25.5 496 4 Q96KX8  
30 591.5 23.5 416 4 Q9NPP6  
31 586 23.3 426 11 Q9DCD9  
32 523.5 20.8 143 11 Q91V67  
33 523 20.8 150 4 Q9Y298  
34 520 20.7 157 4 Q95978  
35 508.5 20.2 143 11 Q924P9  
36 508.5 20.2 159 4 Q96OS0  
37 495 19.7 142 11 Q924Q2  
38 494.5 19.6 145 11 Q924R3  
39 482.5 19.2 124 4 Q9UL92  
40 480.5 19.1 384 4 Q9UP60  
41 479.5 19.0 143 11 Q924Q5  
42 477 18.9 144 11 Q924P5  
43 475 18.9 146 11 Q924R8  
44 473.5 18.8 145 11 Q924Q7  
45 473 18.8 119 4 Q9UL94

Q9bu10 homo sapien  
Q9bqb8 homo sapien  
Q96aa6 homo sapien  
Q99la6 mus sapien  
Q96k68 homo sapien  
Q99ka4 mus musculus  
Q91wp5 mus musculus  
Q96ey0 homo sapien  
Q91x07 mus musculus  
Q91xe1 mus musculus  
Q99m22 mus musculus  
Q91x92 mus musculus  
Q96kx8 homo sapien  
Q9npp6 homo sapien  
Q9dcd9 mus musculus  
Q91v67 mus musculus  
Q9y298 homo sapien  
Q95978 homo sapien  
Q924p9 mus musculus  
Q96os0 homo sapien  
Q924q2 mus musculus  
Q924r3 mus musculus  
Q9ul92 homo sapien  
Q9up60 homo sapien  
Q924q5 mus musculus  
Q924p5 mus musculus  
Q924r8 mus musculus  
Q924q7 mus musculus  
Q9ul94 homo sapien

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DR MGD; MGI:96443; Igh-1.
DR InterPro: IPR003597; Ig.
DR InterPro: IPR003599; Ig.cl.
DR InterPro: IPR003600; Ig.Like.
DR InterPro: IPR003006; Ig.MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00409; Igc1; 3.
DR SMART: SM00406; Igv; 1.
DR SMART: SM00410; Ig.Like; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 64.5%; Score 1623.5; DB 11; Length 473;
Best Local Similarity 62.8%; Pred. No. 1e-128;
Matches 299; Conservative 73; Mismatches 95; Indels 9; Gaps 4;

QY 1 MGWSCILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFYTMQWVVRQAP 60
DB 1 MENSWFLELLSVTAGVHCQVQLKQSGAEELVKPGASVKISCKASGYTFDYINWVKRP 60

QY 61 GQGLEWMEIDPSDSTNYNKKFGRVITITRDTSTSTAYMELSLRSEDYAVYICARNRD 120
DB 61 GQGLEWIGIKPGSGSTYYNEKFKGKATLTADKSSSTAYMQLSLSLTSSEDSAVYFCARS-G 119

QY 121 YSNWYFDWEGEGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYRPEPTVS 180
DB 120 YDWDW-FAYWGQGLTVTVSAAKTATPSVPLAPVCGGTGSSVTLGCLVKGYFPEPTLT 178

QY 181 WNSGALTSVGHVTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRV 240
DB 179 WNSGSLSSGVHTFPALLO-SGLYTLSSSVTVTSNTWPSQITTCNVNHNKPSNTKVDK 237

QY 241 K-----SCDKTHTCCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 294
DB 238 RVPTQNCPPLKECPCCAAPDLLGGPSVFIFPPKIKDVLMISSLPMVTTCVVVDVSEDDP 297

QY 295 EVKFNKYVDGEVHNNAKTPREEQYNSYRYVSVLTVLHODWLNKGEYCKVSNKALPAP 354
DB 298 DVOISFVNVEVHTAQTHREDYNSLTVVSAALPTQHODWMSGKEFKCKVNNRPLSP 357

QY 355 IEKTSKAKGQPREPVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 414
DB 358 IEKTSKPRGPVPAPQVYVLPPEAEEMTKKEFSLTCTMITGFLPAEIAVDWTSNGRTEQNY 417

QY 415 KTTVPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
DB 418 KNTATVLDSDGSFYMFYSKLRVQKSTWERSLFACSVVHEGLHNHLTKTISRSLGK 473

RESULT 2
Q99LC4 PRELIMINARY; PRT; 463 AA.
AC Q99LC4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -.
DR HSP; P01842; 7FAB.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig.cl.
DR InterPro: IPR003600; Ig.Like.
```

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DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00409; Igc1; 2.
DR SMART: SM00407; Igc1; 2.
DR SMART: SM00406; Igv; 1.
DR SMART: SM00410; Ig.Like; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Query Match 64.0%; Score 1612.5; DB 11; Length 463;
Best Local Similarity 62.7%; Pred. No. 8.2e-128;
Matches 296; Conservative 75; Mismatches 90; Indels 11; Gaps 5;

QY 1 MGWSCILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFYTMQWVVRQAP 60
DB 1 MENTWIFLFLISGTAGVHSQVQLQSGAELARPASVRLSCKASGYTFYTGCVSNVQRT 60

QY 61 GQGLEWMEIDPSDSTNYNKKFGRVITITRDTSTSTAYMELSLRSEDYAVYICARNRD 120
DB 61 GQGLEWVGEIYPGSGNTYYSEKFKGKATLTDDKSSSTAYMHLSSLTSEDSAYIFCARSSY 120

QY 121 YSNWYFDWEGEGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYRPEPTVS 180
DB 121 YSYD-LFAYWGQGLTVTVSAAKTTPPSVYPLAPGAAQTNSMVTLGCLVKGYFPEPTVT 179

QY 181 WNSGALTSVGHVTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRV 240
DB 180 WNSGSLSSGVHTFPAYLQSD-LYTLSSSVTVTPSSVTPSETVCNVNHNKPSNTKVDK 238

QY 241 KSCDKTHTCCP--CPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVF 298
DB 239 RDCG----CKPCICTVPEV---SSVFIFPPKPKDVLITLTPKVTCTVVVDISKDDPEVQ 291

QY 299 NWYVDGVEVHNNAKTPREEQYNSYRYVSVLTVLHODWLNKGEYCKVSNKALPAPIEKT 358
DB 292 SWFVDDDEVHVAQTPREEQNSYRYVSVLPIHODWLNKGEYCKVSNKALPAPIEKT 351

QY 359 ISKAKGQPREPVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 418
DB 352 ISKTKGRPKAPQVYTIPTPPKEQMAKDKVSLTCTMITDFPEDITVEMQWNGQPAENYKNTQ 411

QY 419 PVLSDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
DB 412 PIMTDGDSFYIYSKLVNOKSNWEAGNTFTCSVLHEGLHNHHTKSLSHSPGK 463

RESULT 3
Q99L25 PRELIMINARY; PRT; 473 AA.
AC Q99L25;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AAH03888.1; -.
DR HSP; P01842; 7FAB.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig.cl.
DR InterPro: IPR003600; Ig.Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00409; Igc1; 2.
```

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DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 62.5%; Score 1572.5; DB 11; Length 473;
Best Local Similarity 62.5%; Pred. No. 2e-124;
Matches 297; Conservative 64; Mismatches 107; Indels 7; Gaps 5;

Qy 1 MGWSCIILFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWRQAP 60
Db 1 MEWSWVLFELFVATATGVHSGVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWRQAP 60
Qy 61 GQLEWMEIGIDPSDYSYNNQKFKGRVITRTDTSTSTAYMELSSLRSEDTAYVYCARNR 120
Db 61 EGQLEWIGWIDEDGETKYPKFKGKATITADKSSSTAYMQLNSLTSEDVAVCFCSRGGS 120
Qy 121 --YSNN--WFDVWEGTGLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDVKYFPEPV 177
Db 121 IYGYGLYFDYWGOGTTITVSSAKTTAPSVYPLAPVCGDTTGGSVTLGCLVKGYFPEPV 180
Qy 178 TVWNSGALTSGVHTFPAVLQSSGLYSLSVYVPSSSLGTQTYICNVNHHKPSNTKVDKR 237
Db 181 TLTWNSGSLSGVHTFPAVLQSD--LYTLSSSVTVTSSTWPSQSIICNVNHAHPASSTKVDKK 239
Qy 238 VEPKSCDTHTCPP--CPAPELGGPSVFLPPPKDILMISRTPEVTCVVDVSHEDPE 295
Db 240 IEPKRG--PTIKPCPCPCAPNLLGGPSVFIIPPKIKDVLMLSLSPMVTVCVVDVSEDDPD 298
Qy 296 VKENYVDGVEVHNKTPREEQYNSTYRVSVLTFLVHODWLNGLKYEKCKVSNKALPAPI 355
Db 299 VOISWVNVVETLRATQTHREDYNSTLRVVSALPIQHDWMSGKEFKCKVNNKALPAPI 358
Qy 356 EKTISKAKGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 415
Db 359 ERTISKPKGSRAPQVYVLPPEEEMTKQVTLTCMTDFMPEDIVVEVNTNGKTELNYK 418
Qy 416 TTPVLDSDGSFFLYSKLTVDSKRNQGVNFCVSVHHEALHNHYTQKSLSLSPGK 470
Db 419 NTEPVLDSDGSFYMFYSKLRVEKNVYERNVSCSVVHEGLHNHHTTKFSRTPGK 473

RESULT 4
Q99L31 PRELIMINARY; PRT; 468 AA.
AC Q99L31;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AAH03878.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003600; IG_like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR
```

```
SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match 61.6%; Score 1550; DB 11; Length 468;
Best Local Similarity 62.3%; Pred. No. 1.6e-122;
Matches 294; Conservative 63; Mismatches 109; Indels 6; Gaps 4;

Qy 1 MGWSCIILFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWRQAP 60
Db 1 MKCSWVIFFLMAVIGVNSEYVQLQSGAEVLRPGASVKLSCTASGFNIKDSLHMHVQKRP 60
Qy 61 GQLEWMEIGIDPSDYSYNNQKFKGRVITRTDTSTSTAYMELSSLRSEDTAYVYCARNR 120
Db 61 EGQLEWIGWIDEDGETKYPKFKGKATITADTSSNTAYLQLSSLTSEDTAYVYCARNLL 120
Qy 121 YSNNNYEDVWEGTGLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDVKYFPEPV 180
Db 121 YGG--YIDVWOGTGLTIVSSAKTTAPSVYPLAPVCGDTTGGSVTLGCLVKGYFPEVTLT 178
Qy 181 WNSGALTSGVHTFPAVLQSSGLYSLSVYVPSSSLGTQTYICNVNHHKPSNTKVDKRVEP 240
Db 179 WNSGSLSGVHTFPAVLQSD--LYTLSSSVTVTSSTWPSQSIICNVNHAHPASSTKVDKKIEP 237
Qy 241 KSCDTHTCPP--CPAPELGGPSVFLPPPKDILMISRTPEVTCVVDVSHEDPEVKF 298
Db 238 RG--PTIKPCPCPCAPNLLGGPSVFIIPPKIKDVLMLSLSPMVTVCVVDVSEDDPDVQI 296
Qy 299 NKVVDGVEVHNKTPREEQYNSTYRVSVLTFLVHODWLNGLKYEKCKVSNKALPAPIEKT 358
Db 297 SWFVNVVETLRATQTHREDYNSTLRVVSALPIQHDWMSGKEFKCKVNNKALPAPIERT 356
Qy 359 ISKAKGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 418
Db 357 ISKPKGSRAPQVYVLPPEEEMTKQVTLTCMTDFMPEDIVVEVNTNGKTELNYKNT 416
Qy 419 PVLDSGDSFFLYSKLTVDSKRNQGVNFCVSVHHEALHNHYTQKSLSLSPGK 470
Db 417 PVLDSGDSGYMFYSKLRVEKNVYERNVSCSVVHEGLHNHHTTKFSRTPGK 468

RESULT 5
Q9RIA4 PRELIMINARY; PRT; 437 AA.
AC Q9RIA4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G.; Yu X.; Ekramoddoullah A.K.M.; Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003600; IG_like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;
```

Query Match 57.4%; Score 1446.5; DB 11; Length 437;  
Best Local Similarity 59.7%; Pred. No. 7.9e-114;  
Matches 270; Conservative 70; Mismatches 95; Indels 17; Gaps 7;

QY 21 VOLVQSGAEVKKPGASVKVSCKAGSYFTFSYWMQVWQAPQGQGLEWGEIDPSDYNNYN 80  
Db 1 VOLQESGGGLVKPGSLKLSCAASGFTFSYAMSWVRQTPEKRLWVASFS-SGGIYYT 59  
QY 81 QKFGKRVITRTDSTAYMELSLRSEDYAVYYCARNRDYNNWYFDVWGEGLTVYSS 140  
Db 60 DSVKGRFTIYKDKRNLTLQMSLSRSEDYAVYYCARG-DYS-----AYWPGGLTVYSA 113  
QY 141 ASTKGPSEVFLAPSSKSTSGTAAALGCLVXDYFPEPTVSNWNSGALTSVHTFFAVLQSS 200  
Db 114 AKTPPSVYFLAPGSAQAQTMVTLGCLVKGYPPEPTVTVNWSGSLSSGVTFFAVLQSD 173  
QY 201 GLYSLSSWVTPSSSLGTQTYICNVNHPKNTKVKRVEPKSCDKTHTCPP--CPAPPELL 258  
Db 174 -LITLSSSVTPSSWTPSEIVTCNVHPASTKVDKILVPRDCG---CKPCICTVPEV- 227  
QY 259 GGSVFLFPKPKKDTLMISRTPEVTCVVDVSHEDPEKFNWYVDGVEVHNNAKTKPREEQ 318  
Db 228 --SSVFIFPPKPKDVLITLTPKVTCTVVDVSKDDPEVQFSWFVDDVEVHTAQTPREEQ 285  
QY 319 YNSTYRVSVTLVTHODWLNKGEYKCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSR 378  
Db 286 FNSTFRSVSELPVHQDLNKGFEKCRVNSAAPPAPTEKTSIKTKGRKPAQVYTIPTPK 345  
QY 379 EEMTKNOVSLTCLVKGFYPSPDIKAVESNGQPNENYKTTPEVLDSGSLFLSKLTVDKS 438  
Db 346 EQMAKDKVSLTCLMTDFPEPDIIVEMQWNGQPAENYKNTQIPMDTDSGFYVSKLVNQS 405  
QY 439 RWQGNVFCVSNVMEALHNNHYTKQSLSPGK 470  
Db 406 NWEAGNTFTCSVLHGLEHNNHHTKNIHSPGK 437

RESULT 6  
Q91Z05 PRELIMINARY; PRT; 473 AA.  
AC Q91Z05;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE HYPOTHETICAL 51.9 KDA PROTEIN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC010327; AAH10327.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 57.0%; Score 1434.5; DB 11; Length 473;  
Best Local Similarity 57.5%; Pred. No. 9.1e-113;  
Matches 272; Conservative 73; Mismatches 113; Indels 15; Gaps 5;

QY 7 ILFLVATATGVHSQVLQVSGAEVKKPGASVKVSKASGYFTFSYWMQVWQAPQAGGLEW 66  
Db 7 LVFLVLILKGVQCEVLQVSGGLVKPGGSRKLSLCAASGFTFSDYGMHWVRQAPEKGLEW 66  
QY 67 MEIDPSDSYNNYKQFKGRVITRTDSTAYMELSLRSEDYAVYYCARNRDYNNY 126  
Db 67 VAYINSGSTIYADTVKGRFTISRDNNAKNTLFLQMTLSRSEDYAVYYCAREL-----WL 121  
QY 127 --FDVWGEGLTVYSSASVTPSEIVTCNVHPASTKVDKILVPRDCG---CKPCICTVPEV- 227  
Db 122 RRDVWQGTITVSSAKTTPPSVFLAPGCGDTTGGSSVTLGCLVKVGFPSVTVTNWSG 181

QY 185 ALTSCVHTFPVAVLQSSGLSYSSVTVTPSSSLGTQTYICNVNHPKNTKVKRVEPKSCD 244  
Db 182 SLSSSVHTFPALLQ-SGLYTWSSSVTVTPSSWTPSTVCTCSVAHPASSITVDKLEPSGPI 240  
QY 245 KT-HTCPP-----CPAPPELLGGPSVFLFPKPKKDTLMISRTPEVTCVVDVSHEDPEVK 297  
Db 241 STINPCPPCKECHKCPAPNLEGGPSVFIFFPNKIDVLMISLTPKVTCTVVDVSEDDPDVQ 300  
QY 298 FNWYVDGVEVHNNAKTKPREEOYNSYRVSVTLVTHODWLNKGEYKCKVSNKALPAPIEK 357  
Db 301 ISWFNVNVEVHTAQTHREDYNSTIRVSALPIHQDMSCKEFCCKVNNKDLPSPIER 360  
QY 358 TISKAKGQPREPQVYTLPPSREEMTKNOVSLTCLVKGFYPSPDIKAVESNGQPNENYKTT 417  
Db 361 TISKIKGLVRAQVYTLPPPAEQLSRKDVSLTCLVVGFPNGDISVEMTNSGHTENYKDT 420  
QY 418 PPVLDSGSLFLSKLTVDKSRWQGNVFCVSNVMEALHNNHYTKQSLSPGK 470  
Db 421 APVLDSGSLFYISKLDIKTSKEKIDTSFSCNVRHEGLKNYLYKKTISRSPGK 473

RESULT 7  
Q95M34 PRELIMINARY; PRT; 337 AA.  
AC Q95M34;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE IMMUNOGLOBULIN GAMMA 1 HEAVY CHAIN CONSTANT REGION  
DE (FRAGMENT).  
GN IGHC1.  
OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wagner B.;  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98383416; PubMed=9717671;  
RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,  
RA Leibold W., Radbruch A.;  
RT "Organization of the equine immunoglobulin heavy chain constant region  
genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes."  
RL Immunobiology 199;105-119(1998).  
DR EMBL; AJ300675; CAC44624.1; -  
FT NON\_TER 1  
SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;

Query Match 50.2%; Score 1263.5; DB 6; Length 337;  
Best Local Similarity 68.9%; Pred. No. 1.5e-98;  
Matches 233; Conservative 44; Mismatches 52; Indels 9; Gaps 3;

QY 141 ASTKGPSEVFLAPSSKSTSGTAAALGCLVXDYFPEPTVSNWNSGALTSVHTFFAVLQSS 200  
Db 1 ASTAPKVFALAPCGGTTSDTVALGCLVSGYFPEPKVSVNWSGSLTSGVHTFFSVLQSS 60  
QY 201 GLYSLSSWVTPSSSLGTQTYICNVNHPKNTKVKRVEP-----KSCDKTHTCPPCPA 254  
Db 61 GFYSLSWVTPASTWTSEYICNVVHAASNFVKDKKIEFIPDNHQKVDMS-KCPKCPA 119  
QY 255 PELLGSPSVFLFPKPKKDTLMISRTPEVTCVVDVSHEDPEKFNWYVDGVEVHNNAKTKP 314  
Db 120 PELLGSPSVFIFFPNPKDLMITRTPEVTCVVDVSDQENPDVFNWMDGVEVHTATRP 179  
QY 315 REQOYNSTYRVSVTLVTHODWLNKGEYKCKVSNKALPAPIETKISKAKGQPREPQVYTL 374  
Db 180 KEQFNSTYRVSVTLVTHODWLNKGEYKCKVNNQALPQPIERTITTKTKGRSQEPQVYL 239



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QY 375 PPSREMTKNOVSLTCLVKGFPSPDIWESNGQP--ENNYKTTTPPVLDSDGSEFLYSK 432
Db 240 AHPDELKSKSVSLVKDFYPPINTEWQNGPELETETSTQAQDSDGSEFLYSK 299

QY 433 LTVDKSRWQGNVFCSCVMHEALHNYHTQKLSLSPGK 470
Db 300 LSVDRNRWQGTTCGVMHEALHNYHTQKNVSKNPGK 337

RESULT 8
Q96P08 PRELIMINARY; PRT; 701 AA.
AC Q96P08;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.;
RT "targeting tissue factor on tumor vascular endothelial cells and tumor
RL cells for immunotherapy in mouse models of prostatic cancer.";
DR EMBL; AF272774; AAK58686.1; -.
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;

Query Match 49.9%; Score 1257; DB 4; Length 701;
Best Local Similarity 99.1%; Pred. No. 1.6e-97;
Matches 230; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 239 EPKCDKTHTPPCPAPPELLGGPSVFLPPKPKDILMSRTPETVTCVVVDVSHEDPEVKF 298
Db 470 EPKCDKTHTPCCPAPPELLAGPSVFLPPKPKDILMSRTPETVTCVVVDVSHEDPEVKF 529

QY 299 NWYDGVGVHNAKTPREQYNSTYRVSVLTVLHQDLMLNGKEYCKVSNKALPAPIEKT 358
Db 530 NWYDGVGVHNAKTPREQYNSTYRVSVLTVLHQDLMLNGKEYCKVSNKALPAPIEKT 589

QY 359 ISKAGQPREQVYTLPPSREEMTKNQVSLTCLVKGFPSPDIWESNGQPPENNYKTPP 418
Db 590 ISKAGQPREQVYTLPPSREELTKNQVSLTCLVKGFPSPDIWESNGQPPENNYKTPP 649

QY 419 PVLDSDGSEFLYSKLTVDKSRWQGNVFCSCVMHEALHNYHTQKLSLSPGK 470
Db 650 PVLDSDGSEFLYSKLTVDKSRWQGNVFCSCVMHEALHNYHTQKLSLSPGK 701

RESULT 9
Q92IK1 PRELIMINARY; PRT; 278 AA.
AC Q92IK1;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE UNKNOWN (PROTEIN FOR MGC:18977).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012207; AAH12207.1; -.
SQ SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;

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Query Match 38.4%; Score 967; DB 11; Length 278;
Best Local Similarity 65.7%; Pred. No. 1.3e-73;
Matches 182; Conservative 35; Mismatches 52; Indels 8; Gaps 3;

QY 1 MGWSCIILFLVATATGVSQVQLVQSGAEVKKPKGASVKVSKASGYFTFTSYMMQWVRQAP 60
Db 1 MGWNCIILFLVATATGVSQVQLVQSGAEVKKPKGASVKVSKASGYFTFTSYMMHWVQR 60

QY 61 GQGLEWMGEIDPSDSTYNNQKFKGRVTITRDTSTSTAYMELSLRSEDATVAVYCARNRD 120
Db 61 GQGLEWIGNINPNSSGGTNTYNEKPKKATLAVDKSSSTVYMQLSLTSSEDAVYCTRGY 120

QY 121 YSNWTFDVMGEGTLVTVSASTKGPSVFPLAPSSKSTSGCTAAALGCLVDYFPEPPTVS 180
Db 121 Y-DDVYFDMGAGTTVTVSAAKTPAPSVPLAPVCGGTGGTSTGLGVLGYPPEPVTLT 179

QY 181 WNSGALTSGVHTPFAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKNTKYDKRVEP 240
Db 180 WNSGSLSSGVHTPFAVLQ-SGLYTLSSSVTVTNTWFSQITCNVAHPASSTKYDKKIEP 238

QY 241 K-----SCDKTHTCPPCPAPPELLGGPSVFLFPPKPK 271
Db 239 RVPIITQNPCLKECPKCAAPDLGGPSVFIEPPRSR 275

RESULT 10
Q96GA6 PRELIMINARY; PRT; 614 AA.
AC Q96GA6;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE UNKNOWN (PROTEIN FOR MGC:15420).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009851; AAH09851.1; -.
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match 37.5%; Score 944.5; DB 4; Length 614;
Best Local Similarity 37.3%; Pred. No. 3.1e-71;
Matches 215; Conservative 83; Mismatches 164; Indels 115; Gaps 17;

QY 1 MGWSCIILFLVATATGVSQVQLVQSGAEVKKPKGASVKVSKASGYFTFTSYMMQWVRQAP 60
Db 1 MDWTWRLFLVAAATDAYSQMLVQSGAEVKKGTSSVKVSKASGYFTFTSYLHWRQAP 60

QY 61 GQGLEWMGEIDPSDSTYNNQKFKGRVTITRDTSTSTAYMELSLRSEDATVAVYCARNRD 120
Db 61 GQALEWMGMITPFGNGTNTAQKFDQRTVITRDRSMNTAYMELSLRSEDATVAVYCARG-- 118

QY 121 YSNW--YFDVMGEGTLVTVSASTKGPSVFPLAPSSKSTG-GTAALGCLVDYFPEPV 177
Db 119 YSSWDADFIDWGGTMTVTVSASAPTLFPLVSCNSPDSSTSSVAVGCLAQFLPDSI 178

QY 178 TVSW--NSGALTSGVHTFAVLQSSGLYSLSSVTVTPSSSL--GTQTY-ICNVNHPKSN- 231
Db 179 TFSWKYKNSDISSTRGFPSVLR-GGKYAATSOVLLPSKDVMTQGTDEHVVKVQHPNGK 237

QY 232 -----TKYDKRVEPKS-----CDKTHTCP----- 250
Db 238 EKNVPLPVAELPPKVSFVFPFPRDGFNGPKSKLIQATGFSRQIQVSWLREGKQVGS 297

QY 251 -----PCPAPPELLGGPS----- 262
Db 298 GVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMTFCRVDRHRLTFOQNASSMCVDP 357

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Qy	395	FYPSDIAVESNGQ--PENNYKTTTPVLVD-SDG--SFFLYSKLTVDKSRWQQGNVFSCS	4489
Dd	402	FSPKDVLVRWLOGSQELPREKYLTWASRQPSTQTTFATVTSILRVAAEDKKGDFTSCM	461
Qy	450	VMHEALHNHYTKQSLSLSPCK	470
Dd	462	VGHEALPLAFTQETIDRLAGK	482
RESULT 13			
Q96BB9	ID	Q96BB9 PRELIMINARY;	PRT; 597 AA.
AC	Q96BB9;		
DT	01-DEC-2001	(TrEMBLrel. 19, Created)	
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)	
DT	01-DEC-2001	(TrEMBLrel. 19, Last annotation update)	
DE	HYPOTHETICAL 65_0 KDA PROTEIN.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
NCBI_TaxID=9606;			
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=PRIMARY B-CELLS FROM TONSILLS;		
RA	Strausberg R.;		
RL	Submitted (Oct-2001) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; BC015760; AAH15760.1; -.		
KW	Hypothetical protein.		
SQ	SEQUENCE 597 AA; 56039 MW; 4FCA3AD8ECE263D9 CRC64;		

Query Match	32.8%;	Score	826.5;	DB	4;	Length	597;		
Best local Similarity	33.0%;	Pred.	No. 2.8e-61;						
Matches	192;	Conservative	93;	Mismatches	178;	Indels	119;	Gaps	18;
Qy	1	MGWSCIIILFVATATGVHSSQVQLVQSGAEVKKPKGASVKVSKCASGYTSTSYMMQWVROAP	60						
Db	5	LSW-----LFLVAILKVOCEVOLLSEGGVLVOPGGSURLSCAAGSFSSYAMNVRQAP	60						
Qy	61	GGQLEWGEIDPDSDSYNYNOKFKRGVYITRDTSTSTAYMELLSILRSEDSTAVYICARN-R	119						
Db	61	GKGLEWYSAISGSGSTVYADSVKGRFTISRDNSRDTLYLQMNLSRAEDTAVYICAKDPR	120						
Qy	120	DYSNNWTF--DWGEGTLTYTVSSASTKGPSVFPLAIPSSKSTSG-GTAAALGCLVKDYDPE	175						
Db	121	GYSAGNYTRDYWGQGTFLTVSSGSAAPTLFPLVSCENSPDSTSSVAVGCLAQADFLPD	180						
Qy	176	PVTYSW--NSGALTSVGHTTFAVLQSSGLYSLSSVTVVPSSSL--GTQTY-ICNVNHHKPS	230						
Db	181	SITFSWKYKNSDLSISRGFPSVL-R-GGKYAATSOVLLPSKDVMOGQTDHVVCKVQHFG	239						
Qy	231	N-----TKVDRKVEPS-----CDKTHTCP-----	250						
Db	240	NKEKNVPLVIAELPPKVSVPFPRDGFPGNPKSKLICQATGFSPTQIQVSWLREGKVQ	299						
Qy	251	-----PCPAPELLGGS-----	262						
Db	300	GSVTTDQVQAEAKESGTTVYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFTQNASMCV	359						
Qy	263	-----VFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP	314						
Db	360	PQDQTAIRVFAIPLPS-FASIFLTKSLTCLVTLDTLTYD-SVYTSWTQNGEAVKTHINI	417						
Qy	315	REQYNSTYRVVSVLTVLHQDWLNGKEYKCKVKNKALPAPIEKTSIKAKGQP-REPQVYT	373						
Db	418	SESHPNATFSAVGEASICEDDWNISGERTCVTHTDLPSPLKQATISRPKGVALLHRPQVYL	477						
Qy	374	LPPSREEMT-KNOVSLTCLVKGFYPSDIAVWESNGQP--ENNYKTTTPVLD--SDGSFF	428						
Db	478	LPPAREQLNRESATITCLVTFGFPADVFGQMQRGQPLSPKEPKYTSAPMPEPQAPGRY	537						
Qy	429	LYSKLTVDKDSWQOQNVFSCVMHEALHNHYTQKSLSLSPGK	470						

Db	538	AHSILTVSEEWNTGEYITCVVAHEALPNRVTERTVTDKSTCK	579
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RESULT	14		
Q91WT1			
ID	Q91WT1	PRELIMINARY;	PRT; 481 AA.
AC	Q91WT1;		
DT	01-DEC-2001	(TrEMBLrel. 19, Created)	
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)	
DT	01-DEC-2001	(TrEMBLrel. 19, Last annotation update)	
DE	HYPOTHEtical 52.1 KDA PROTEIN.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae		
ON	NCBI_TaxID=10090;		
OX	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=COLON;		
RA	Strausberg R.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ datab.		
DR	EMBL; BC013490; AAH13490.1; -.		
KW	Hypothetical protein.		
SQ	SEQUENCE	481 AA; 52105 MW; 97DF68D159463F65 CRC32	

  

Query Match	32.7%	Score	824.5;	DB	11;
Best Local Similarity	39.6%	pred. No.	3e-61;		
Matches	191;	Conservative	76;	Mismatches	184;

  

Qy	1	MWSCIILFLVATGATGHSQVOLVOSGAEVKKPGASVKVSKCASGY	
Db	1	MGRWIFLLSAGTAGVQCQVQLLQSGPELVKPGASVKAIKSCASGY	
Qy	61	GGLEWGEIDPSDSTYNNOKFKGRVTITRDTSTSTAYMELSLRL	
Db	61	GGGLVMIGVIYPGDGTKYNEKFKGKTLTADKSSSTAYMFLSSLT	
Qy	121	YSNNWYFDVWCEGLTVTVSSASTKPGSVFPLAPSKTSGGTAALGSG	
Db	118	GGWAFDYWGQGITLVSESEPAEPTIYPLT-FPQALLSDPVIIG	
Qy	180	SWNSGALTSGVHTFPVAVLQSSGLYSLSVTVTPSSSLGT-QTYICN	
Db	176	TWKGSGKDITTVNFPALASGRYTMSSQLTLPAVECPGESEVKCS	
Qy	239	EPKCDKTHTCPPCPAPELLGGPSVFLPPPKPDTLMISRTPVETC	
Db	235	NCPGICSPPTTPPPSCQ----PSLSQRPALSD-LLLGSDASITC	
Qy	298	FNWYDGVGEVHNATKPREQYNST---YRVVSVLTVLHQDWLNGK	
Db	288	FTW-----EPSTGDADVQKAVQNSCGYSSVSLVPGCAERNNSGA	
Qy	355	IEKTSIKAKGPREFQVTVLPPSPREMTKNO-VSLTCLVKGFPSPD	
Db	342	LTGTIAKTVVNTFPQVHLLPPSEELNELVSLTCLVRAFNPKE	
Qy	411	ENNYKTPPVLDSDG--SFFLYLKLTVDKSWQOQNVFSCSVMEHA	
Db	402	ESYLVFPEKPEFGEGATTLYLTVSLVSAEIIWKGQDQYSCHVGEHA	
Qy	469	GK 470	
Db	462	GK 463	

  

RESULT	15		
Q96DK0			
ID	Q96DK0	PRELIMINARY;	PRT; 496 AA.
AC	Q96DK0;		
DT	01-DEC-2001	(TrEMBLrel. 19, Created)	
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)	

RESULT	15
Q96DK0	
ID	Q96DK
AC	Q96DK
DT	01-DEC
DT	01-DEC

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE CDNA FLJ25298 FIS, CLONE STM07683, HIGHLY SIMILAR TO PROTEIN TRO  
DE ALPHA H, MYELOMA.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=GASTRIC MUCOSA;  
RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,  
RA Hotta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,  
RA Watanabe M., Fujinori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,  
RA Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,  
RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,  
RA Kawakami B., Nagai K., Tsogai T., Sugano S.;  
RT "NEDO human cDNA sequencing project."  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK058027; BAB71633.1; -  
SQ SEQUENCE 496 AA; 53532 MW; C72EE1E247C86FED CRC64;  
  
Query Match 32.2%; Score 812; DB 4; Length 496;  
Best Local Similarity 39.6%; Pred. No. 3.6e-60;  
Matches 197; Conservative 65; Mismatches 189; Indels 46; Gaps 16;  
  
QY 1 MGWSCILFLVATGATGVHSGVQVQSGAEVVKPGASVKVSKASGYFTFTSYMMQWVRQAP 60  
DQ 1 MDKTRFLFVAVTGVQSVHLVQSGAEKMPGSSVKVSKASANNFRSYAFATWVRQAP 60  
QY 61 GQLEWMEIDPSDSTNTNPKFKGRVTITRDTSTSTAYMELSLRSEDFAVYICARNRD 120  
DQ 61 GQLEWMEIDPSDSTNTNPKFKGRVTITRDTSTSTAYMELSLRSEDFAVYICARNRD 120  
QY 121 Y---SNNWYFDVWEGTLYTVSSASTKGPSVFPPLAPSSKSTSGTAAALGLVKDYFP-EP 176  
DQ 121 YGSGSYIYLQHWGGTLYTVSSASTSPKVPFLSLCS-TQPDGNVVIACLVQGFPPQEP 179  
QY 177 VTVSMNSGALTSGVHTFFPAVLQSSG-LYSLSSVTVTPSSS-LGTQTVICNVNHKPSNTKV 234  
DQ 180 LSVTWSESGGVARTNEPPSQDASGDLTYTSSQLTLPATOCLAGKSVTCHKHY-TNPSQ 238  
QY 235 DKRVEPKSCDKHTCCPAPPELLGGPSVFLFPPKPK-----DTLMISRT 279  
DQ 239 DVTV-----PCVPSTPTPTSPST-PPTPSPSCCHPRLSLHRPALEDLLIGSE 285  
QY 280 PEVTCVVVDVSHEDPEVKENWYDVGVEVHNAKTKPREEQYNSTYRVYVSLTFLHODWLG 339  
DQ 286 ANLTCTLTGL-RDASGVTTWTTPSSSK--SAVGGPPDRDLCCGYSVSSVLPGCAEPWNHG 342  
QY 340 KEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ-VSLTCLVKGFYPS 398  
DQ 343 KFTFTCAAYPESKPTLTATLSKS-GNTFRPEVHLLPPPSSEALNELVTLTCLARGFSPK 401  
QY 399 DTAVERESNGQ--PENNYKTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHE 453  
DQ 402 DVLVRWLGQSQELPREKYLTVASRQPSQGTTFVAVTSILRVAEDWKKGDFTSCVMYGE 461  
QY 454 ALHNHYTOKSLSLSPCK 470  
DQ 462 ALPLAFTQRTIDRLAGK 478

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